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**Identificação de RNAs longos não-codificadores em  
pacientes pediátricos naturalmente infectados pelo vírus  
*Chikungunya***

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Dissertação apresentada à Faculdade de Medicina Veterinária de Araçatuba da Universidade Estadual Paulista “Júlio de Mesquita Filho” – UNESP, como parte dos requisitos para obtenção do título de Mestre em Ciência Animal (Medicina Veterinária Preventiva e Produção Animal)

Orientadora: Profa. Dra. Flávia Lombardi Lopes

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**“ Em algum lugar, algo incrível está esperando para ser descoberto.”**

**(Carl Sagan)**

FELIX, J. S. **Identificação de RNAs longos não-codificadores em pacientes pediátricos naturalmente infectados pelo vírus *Chikungunya***. 2023. 154 f. Dissertação (Mestrado) – Faculdade de Medicina Veterinária, Universidade Estadual Paulista, Araçatuba, 2023.

## RESUMO

A febre chikungunya é uma doença tropical negligenciada, onde o vírus de mesmo nome é transmitido por mosquitos da espécie *Aedes* (*A. aegypti* e *A. albopictus*). Após a infecção, o primeiro sítio de replicação do vírus *Chikungunya* é a pele humana, principalmente nos fibroblastos da derme, e sua disseminação é através dos gânglios linfáticos e do sistema circulatório, atingindo compartimentos musculares e articulares. A fase aguda da doença dura aproximadamente 2 semanas, entretanto, alguns pacientes progridem para um estágio crônico, apresentando intensas artralguas que podem durar de meses a anos. Sabe-se que os interferons do tipo I são essenciais para a resposta imune antiviral, contudo, a persistência do vírus nas articulações foi associada à intensa expressão dessa citocina. As infecções virais são capazes de modificar o transcriptoma do hospedeiro. Além dos RNAs mensageiros (mRNAs), outra classe importante de transcritos são os RNAs longos não-codificadores (lncRNAs), que diferem dos mRNAs pois não são traduzidos em proteínas. Os lncRNAs podem regular a expressão gênica de maneira transcricional e pós-transcricional, podendo modular a resposta do hospedeiro frente a infecções. Visto que a infecção pelo vírus *Chikungunya* altera a expressão de genes do hospedeiro, o presente estudo visa elucidar se a expressão de lncRNAs está correlacionada com a alteração de expressão de possíveis mRNAs alvos, e o papel dessas interações durante a infecção por *Chikungunya* em sangue total de meninos adolescentes. Foram utilizados dados de RNA-Seq disponíveis publicamente (GeoDatasets, GSE99992), que dispõe de 34 amostras de sangue total de adolescentes do sexo masculino, com idade entre 11 e 15 anos, coletadas do mesmo paciente nas fases aguda e convalescente. Utilizando a plataforma *Galaxy*, alinhamos as amostras, contamos as *reads* e analisamos a expressão diferencial ( $FDR < 0.05$ ;  $\log_2(FC) \geq 1$ ). Identificamos os pares de lncRNA-mRNA coexpressos utilizando a correlação de Pearson ( $|r| \geq 0.95$ ;  $FDR < 0.01$ ), calculamos o potencial de ligação e identificamos a distância em pares de

base entre lncRNAs e mRNAs. Todos os mRNAs alvos de lncRNAs que atenderam aos critérios de coexpressão e potencial de ligação ou coexpressão e localização próxima (100kbps) foram utilizados para a análise de enriquecimento funcional, utilizando o *g:Profiler*. Dos transcritos diferencialmente expressos entre a fase aguda e a convalescença, 1975 foram classificados como mRNAs e 793 como lncRNAs, sendo que destes, 569 lncRNAs apresentaram expressão aumentada durante a fase aguda, enquanto 224 estavam menos expressos. O lncRNA BISPR está mais expresso na fase aguda e correlacionado com o mRNA OASL, em uma possível interação *trans*, e com o mRNA BST2 em uma possível interação *cis*. Ao regular o mRNA OASL, BISPR favorece o reconhecimento de RNA viral através dos receptores RIG-I, que induzem a expressão de IFN-I. BISPR também é capaz de regular a região promotora de seu gene vizinho BST2, promovendo sua transcrição. Sendo assim, nossos resultados sugerem que a infecção por *Chikungunya* altera a expressão de mRNAs e lncRNAs, e que esses mRNAs são potencialmente regulados a nível transcricional e pós-transcricional por lncRNAs, influenciando assim a resposta imune do indivíduo.

**Palavras-chave:** Arboviroses. Bioinformática. Epigenética.

FELIX, J. S. **Identification of long non-coding RNAs in pediatric patients naturally infected with the *Chikungunya* virus.** 2023. 154 f. Dissertação (Mestrado) – Faculdade de Medicina Veterinária, Universidade Estadual Paulista, Araçatuba, 2023.

## ABSTRACT

Chikungunya fever is a neglected tropical disease, in which the virus of the same name is transmitted by mosquitoes of the *Aedes* species (*A. aegypti* and *A. albopictus*). After infection, the first replication site of the *Chikungunya* virus is the human skin, mainly in dermal fibroblasts, and its dissemination is through the lymph nodes and the circulatory system, reaching muscle and joint compartments. The acute phase of the disease lasts approximately 2 weeks, however, some patients progress to a chronic stage, presenting intense arthralgias that can last from months to years. It is known that type I interferons are essential for the antiviral immune response, although, the persistence of the virus in the joints was associated with the intense expression of this cytokine. Viral infections are able to modify the host transcriptome. In addition to messenger RNAs (mRNAs), another important class of transcripts are the long non-coding RNAs (lncRNAs), which differ from mRNAs in their inability to be translated into proteins. lncRNAs can regulate gene expression in a transcriptional and post-transcriptional level, and can modulate the host's response to infections. Since *Chikungunya* virus infection alters host gene expression, the present study aims to elucidate whether the expression of lncRNAs is correlated with differentially expressed target mRNAs, and the role of these interactions during *Chikungunya* infection in whole blood from adolescent boys. Publicly available RNA-Seq data were used (GeoDatasets, GSE99992) containing 34 whole blood samples from male adolescents, aged between 11 and 15 years, collected from the same patient in the acute and convalescent phases. Using the Galaxy platform, we aligned the samples, counted the reads and analyzed the differential expression ( $FDR < 0.05$ ;  $\log_2(FC) \geq 1$ ). We identified co-expressed lncRNA-mRNA pairs using Pearson's correlation ( $|r| \geq 0.95$ ;  $FDR < 0.01$ ), calculated the binding potential, and identified the distance in base pairs between lncRNAs and mRNAs. All lncRNA target mRNAs that met the criteria for co-expression and binding potential or co-expression and close location (100kbp) were used for functional enrichment analysis using g:Profiler. Of the differentially expressed

transcripts between the acute and convalescent phases, 1975 were classified as mRNAs and 793 as lncRNAs and, of these, 569 lncRNAs showed increased expression during the acute phase, while 224 were less expressed. BISPR lncRNA is more expressed in the acute phase and is correlated with OASL mRNA, in a possible *trans* interaction, and with BST2 mRNA in a possible *cis* interaction. By regulating OASL mRNA, BISPR favors viral RNA recognition through RIG-I receptors, which induce IFN-I expression. BISPR is also capable of regulating the promoter region of its neighbor gene BST2, promoting its transcription. Therefore, our results suggest that *Chikungunya* infection alters the expression of mRNAs and lncRNAs, and these mRNAs are potentially regulated at the transcriptional and post-transcriptional level by lncRNAs, consequently influencing immune response.

**Keywords:** Arbovirosis. Bioinformatics. Epigenetics.

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## 1 INTRODUÇÃO GERAL

Os arbovírus são um grupo de diversos vírus transmitidos através de vetores artrópodes, como mosquitos, carrapatos e flebotomíneos. Uma importante família de arbovírus é a *Togaviridae* (gênero *Alphavirus*), que compreende vírus de RNA de sentido positivo, lineares, envelopados e de cadeia simples. Um representante importante deste gênero é o vírus *Chikungunya* (CHIKV), um alfavírus artritogênico (VU; JUNGKIND; LABEAUD, 2017).

O vírus causa a febre chikungunya (CHIKF), uma doença tropical negligenciada capaz de impactar a economia global, devido às dores incapacitantes que alguns infectados desenvolvem. O primeiro relato da doença foi descrito em uma região onde atualmente se localiza a Tanzânia, a partir de um surto que ocorreu entre 1952 a 1953. Os infectados apresentavam febre, erupções cutâneas e intensa artralgia, que diferenciava dos relatos anteriores de surtos de dengue. A população passou a chamar a doença de chikungunya, um termo do idioma maconde que significa “aquilo que se curva”, em referência à posição dos acometidos pela artralgia (MASON; HADDOW, 1957).

O primeiro surto de CHIKF nas Américas, confirmado através de métodos de detecção modernos, foi relatado em 2013 em Saint Martin, no Caribe (FISCHER; STAPLES, 2014). Devido à grande semelhança de sintomas, é possível que tenham ocorrido surtos anteriores de CHIKF nas Américas, e que estes tenham sido atribuídos ao vírus da dengue (HALSTEAD, 2015). Em Setembro de 2014 foi confirmado o primeiro caso autóctone no Brasil, no Oiapoque, estado do Amapá (BRASIL, 2017). De Janeiro a Novembro de 2022 foram notificados 169.574 casos prováveis de infecção por CHIKV no Brasil; um crescimento de 81,9% dos casos, quando comparado ao mesmo período do ano de 2021 (BRASIL, 2022).

A transmissão de CHIKV ocorre por meio de fêmeas de mosquitos do gênero *Aedes*, principalmente *Aedes aegypti* e *Aedes albopictus* (TSETSARKIN; CHEN; WEAVER, 2016). Após o repasto sanguíneo de um hospedeiro infectado, os vírus multiplicam no intestino médio do inseto para então infectarem os tecidos adjacentes causando uma infecção disseminada, resultando em uma alta carga viral principalmente nas glândulas salivares (DUBRULLE et al., 2009). Os vírus são então transmitidos para novos hospedeiros vertebrados durante a picada dos vetores infectados. A transmissão pode ocorrer através de dois diferentes ciclos; o ciclo

urbano, onde a infecção ocorre entre humanos através do mosquito, ou o ciclo silvestre, onde a infecção ocorre entre animais e humanos, através do mosquito. Os mosquitos se reproduzem em água limpa acumulada em objetos próximos às residências, e se alimentam do sangue humano em áreas sombreadas durante o dia e início da noite (SINGH; UNNI, 2011). O Brasil apresenta diversos fatores que o predispõe à ocorrência de grandes epidemias de CHIKF, considerando a ampla difusão dos vetores por todo o território brasileiro, favorecida pelo clima tropical.

As células hospedeiras endocitam o CHIKV através de receptores de membrana, formando o endossomo. O endossomo possui um pH ácido que causa a fusão entre a membrana do hospedeiro e o vírus, liberando o nucleocapsídeo no citoplasma hospedeiro (SILVA; DERMODY, 2017). Iniciam então os processos de tradução do genoma viral em proteínas que posteriormente formarão o nucleocapsídeo, onde o RNA viral será empacotado dando origem a novos vírions. Esses vírions maduros são liberados através da membrana plasmática da célula hospedeira, onde adquirem um envelope de bicamada lipídica e formam vírus maduros, capazes de infectar novas células (SOLIGNAT et al., 2009).

Posteriormente a infecção por CHIKV, o primeiro sítio de replicação viral é a pele humana, principalmente nos fibroblastos da derme. Outras células também são suscetíveis à infecção, como as células epiteliais e endoteliais, e os macrófagos derivados de monócitos (SOURISSEAU et al., 2007). O vírus é disseminado através dos gânglios linfáticos e do sistema circulatório, atingindo os compartimentos musculares e articulares ao infectar os fibroblastos musculares primários e esqueléticos (HUA; COMBE, 2017).

Após o período de incubação de 2 a 7 dias, a maior parte dos indivíduos infectados apresentam manifestações clínicas características da doença. Os sintomas clássicos da fase inicial incluem doença febril abrupta (com temperaturas superiores a 38,9°C), erupções cutâneas maculopapulares e dor nas articulações. Os danos nas articulações costumam afetar principalmente as extremidades, como as mãos, tornozelos e junções dos dedos (BORGHERINI et al., 2008; MANIMUNDA et al., 2010; SISSOKO et al., 2009). Alguns infectados também podem apresentar outros sintomas inespecíficos, como cefaleia, fadiga, náusea, diarreia, vômito, dor abdominal, calafrios, conjuntivite, neurite, faringite e mialgias (STAPLES; BREIMAN; POWERS, 2009). Esses sinais e sintomas costumam desaparecer em menos de 2 semanas; entretanto, alguns pacientes progridem para o estágio crônico da doença,

apresentando manifestações reumáticas que duram por mais de 3 meses (MANIMUNDA et al., 2010).

A febre chikungunya crônica pode durar de meses a anos, e o que leva alguns pacientes a desenvolvê-la não está completamente elucidado. A evolução para esse estágio pode estar associada a capacidade do CHIKV persistir em algumas regiões do corpo, através de mecanismos ainda pouco compreendidos. Estudos sugerem que um defeito na regulação da inflamação durante a fase aguda e a convalescença favorece o desenvolvimento da doença crônica (CHOW et al., 2011; DUPUIS-MAGUIRAGA et al., 2012; LABADIE et al., 2010).

Os principais fatores da imunidade inata contra infecções virais são os macrófagos, as células dendríticas e células *natural killer*, que culminam na ativação de linfócitos T e B mediando a imunidade adaptativa. As evidências demonstram que durante a fase crônica, os macrófagos atuam como reservatórios de CHIKV nas articulações, favorecendo a persistência do vírus (DUPUIS-MAGUIRAGA et al., 2012; LABADIE et al., 2010). A ativação de células não hematopoiéticas estimula a produção de interferon do tipo I (IFN  $\alpha$  e  $\beta$ ). Sabe-se que os interferons do tipo I (IFN-I) são essenciais para a resposta imune antiviral, entretanto, a persistência do vírus nas articulações foi associada à intensa expressão de IFN- $\alpha$ , um potente inibidor da replicação de CHIKV (HOARAU et al., 2010).

Logo após a infecção, o INF atua nas células infectadas por vírus de forma que o núcleo dessa célula passe a sintetizar proteínas antivirais, que inibem a síntese proteica do vírus (FORTE, 2007). Diversas citocinas e quimiocinas estão presentes em elevados níveis durante a infecção aguda, dentre elas: a interleucina 7 (IL-7), responsável pelo crescimento e maturação de linfócitos B e ativação de linfócitos T, e a interleucina 12 (IL-12), que tem como principal função aumentar a secreção e atividade de INF- $\gamma$  (um interferon do tipo II), aumentando a resposta citotóxica que é extremamente importante na defesa antiviral (WAUQUIER et al., 2011). O INF também induz uma alta expressão de prostaglandinas nas células infectadas pelo vírus, contribuindo para mecanismos de ativação e sensibilização dos nociceptores. Assim como ocorre nas osteoartrites, leva ao quadro de artralgia que é característico da febre chikungunya (FITZPATRICK; STRINGFELLOW, 1980; MALFAIT; SCHNITZER, 2013)

As infecções virais são capazes de modificar o transcriptoma do hospedeiro, como já relatado em outras arboviroses (GEDDES et al., 2021;

MICHLMAYR et al., 2018, 2020; POONPANICHAKUL et al., 2021). Essas modificações no transcriptoma hospedeiro podem favorecer os mecanismos de defesa afim de eliminar os vírus, assim como também podem regular mecanismos de evasão viral, contribuindo para a persistência do vírus no hospedeiro. Além dos RNAs mensageiros (mRNAs), outra importante classe são os RNAs longos não-codificadores (lncRNAs), que diferem do primeiro pelo fato de não serem traduzidos em proteínas.

Os lncRNAs são transcritos pela RNA polimerase II e consistem em sequências superiores a 200 nucleotídeos. São encontrados dentro de frações nucleares ou citosólicas, estando ou não poliadenilados e podem ser transcritos a partir de qualquer uma das fitas de DNA. Os lncRNAs podem ser classificados de acordo com a sua localização no genoma em: 1) *sense* ou *antisense*, quando sobrepõe um ou mais exons de outro transcrito, na mesma fita ou na oposta, respectivamente; 2) *bidirectional*, quando a transcrição do lncRNA e de um transcrito codante, localizado na fita oposta, iniciam em uma região próxima do genoma; 3) *intronic*, quando é transcrito a partir de uma região de íntron de um segundo transcrito; 4) *intergenic*, quando está localizado entre dois genes (PONTING; OLIVER; REIK, 2009).

A função dos lncRNAs se dá através da regulação da expressão gênica, atuando de maneira transcricional e pós-transcricional. Podem interagir com moléculas de DNA ou RNA através da complementariedade de sequências, assim como também são capazes de se dobrar em complexos tridimensionais e interagir com proteínas (SCHMITZ; GROTE; HERRMANN, 2016; WERNER; RUTHENBURG, 2015). Baseado no local de atuação, os lncRNAs podem exercer suas funções em *cis* ou em *trans*. Os lncRNAs de ação *cis* regulam a expressão de genes próximos ao seu locus transcricional através de diferentes mecanismos: recrutando ou modulando fatores reguladores no locus; o lncRNA transcrito é capaz de regular um gene próximo independente da sequência do RNA; o locus do lncRNA pode atuar como região promotora e regular o gene próximo mesmo sem ser transcrito. Por sua vez, os lncRNAs de ação *trans* são transcritos e exercem suas funções por toda a célula. Além de regular a expressão gênica em regiões distantes do seu sítio de transcrição, podem interagir com outras moléculas de RNA e também com proteínas (KOPP; MENDELL, 2018). Devido à escassez de bancos de dados de funções de lncRNAs

experimentalmente observadas, a análise de coexpressão entre lncRNAs e mRNAs é utilizada para inferir o papel de lncRNAs em contextos biológicos.

Considerando que a infecção pelo vírus *Chikungunya* altera a expressão de genes do hospedeiro, o presente estudo visa elucidar se a expressão de lncRNAs está correlacionada com possíveis mRNAs alvos, e o papel dessas interações durante a infecção por *Chikungunya* em sangue total de meninos adolescentes.

## **2 CAPÍTULO 1 - NETWORK ANALYSIS OF LNCRNA-MRNA CO-EXPRESSION DURING ACUTE *CHIKUNGUNYA* FEVER REVEALS INCREASED EXPRESSION OF LNCRNA BISPR IN ADOLESCENT BOYS**

### **ACUTE *CHIKUNGUNYA* FEVER INCREASES LNCRNA BISPR EXPRESSION IN ADOLESCENT BOYS**

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## 2.1 Resumo

O vírus *Chikungunya* (CHIKV) é um arbovírus que causa a doença tropical negligenciada febre chikungunya, comum em áreas tropicais do mundo. Há evidências de que os arbovírus alteram o transcriptoma do hospedeiro e modulam a resposta imune. Essas alterações no transcriptoma do hospedeiro podem estar relacionadas a mecanismos de controle transcricionais e pós-transcricionais mediados por longos RNAs não-codificadores (lncRNAs). Neste estudo, avaliamos a coexpressão de lncRNAs e seus supostos mRNAs alvo durante a infecção natural por CHIKV em meninos adolescentes. Utilizamos um banco de dados público de RNA-Seq e identificamos 1.975 mRNAs e 793 lncRNAs que foram expressos diferencialmente entre as fases aguda e convalescente da infecção. Entre os 569 lncRNAs regulados positivamente na fase aguda, identificamos o *BISPR* que é coexpresso positivamente com os mRNAs *OASL* e *BST2*. A potencial regulação do *OASL* pelo *BISPR* é pós-transcricional, pois *BISPR* tem potencial de ligação ao *OASL*, facilitando o reconhecimento viral por meio do receptor RIG-I. Além disso, *BISPR* potencialmente regula, a nível transcricional, seu gene vizinho *BST2*, que controla a liberação de CHIKV para células não infectadas. Nossos achados indicam que a infecção aguda por CHIKV induz alterações na expressão de mRNAs e lncRNAs em meninos adolescentes, contribuindo para uma resposta imune antiviral.

## 2.2 Abstract

*Chikungunya* virus (CHIKV) is an arbovirus that causes the neglected tropical disease chikungunya fever, common in tropical areas of the world. There is evidence that arboviruses alter host transcriptome and modulate immune response. These changes in host transcriptome may be related to transcriptional and post-transcriptional control mechanisms mediated by long non-coding RNAs (lncRNAs). Herein, we evaluate co-expression of lncRNAs and their putative target mRNAs during natural CHIKV infection in adolescent boys. We used a public RNA-Seq dataset and identified 1975 mRNAs and 793 lncRNAs that were differentially expressed between acute and convalescent stages of infection. Among the 569 lncRNAs upregulated in the acute phase, we identified *BISPR* which is positively co-expressed with the mRNAs *OASL* and *BST2*. The putative regulation of *OASL* by *BISPR* is post-transcriptional, as *BISPR* has binding potential to *OASL*, facilitating viral recognition through the RIG-I like receptor. Also, *BISPR* potentially regulates, at a transcriptional level, its neighboring gene *BST2*, which contributes to control the release of CHIKV to uninfected cells. Our findings indicate that acute CHIKV infection induces alterations in mRNA and lncRNA expression in adolescent boys, contributing to an antiviral immune response.

## 2.3 Author Summary

*Chikungunya* virus is transmitted by mosquitoes, such as *Aedes aegypti* and *Aedes albopictus*. Chikungunya fever is a neglected tropical disease, meaning that it affects millions of people annually, but receives little investment in research and development of therapies. RNAs are important molecules that translate genetic information from the DNA, their effects can be based on their translation into proteins or by regulating other RNAs, and their expression may be altered in response to infections. By studying the expression of host RNAs, we sought to clarify the interaction between two classes of RNAs in response to natural *Chikungunya* infection in adolescent boys. The first class are mRNAs, which guide the production of proteins, essential for any organism; the second class are long non-coding RNAs, which are not translated into proteins and act as regulatory molecules. Our results suggest that *Chikungunya* infection increases expression of coding and non-coding RNAs during the initial phase of the disease, and these are directly related to the innate immune response, promoting an antiviral state in the host immune cells in order to eliminate the virus. Our study broadens our understanding of host-pathogen interactions through non-coding RNAs, which may be potential therapeutic targets.

## 2.4 Introduction

The reemerging mosquito-borne alphavirus known as the *Chikungunya* virus (CHIKV) is responsible for epidemics affecting tropical areas of the world. CHIKV is mainly spread by infected mosquitoes belonging to the *Aedes* species (*A. aegypti* and *A. albopictus*) [1]. According to the European Centre for Disease Prevention and Control (ECDC) [2], 113,052 Chikungunya cases were reported in 15 countries up to June 2022, with all 14 deaths and the vast majority of cases (92,349) coming from Brazil.

Most CHIKV infections are symptomatic and common clinical manifestations are high fever, rash, headache and severe polyarthralgia that can last from months to years [3]. Arthralgia lasting longer than three months characterizes the chronic stage of Chikungunya. Acute infection might last up to 21 days and viremia is prevalent for 5-7 days, although intensity of symptoms usually decreases after a couple of weeks [4]. Currently, there are no vaccines or specific drugs against CHIKV approved for use in humans, and treatment is based on symptom relief.

Understanding the dynamics of host-pathogen interaction can help identify potential therapeutic targets; a key molecule for the antiviral immune response is type I interferon (IFN-I). Following host cells recognition of pathogen-associated molecular patterns (PAMPs), expression of IFN-I and other proinflammatory cytokines is induced. IFN signaling leads to transcription of IFN-stimulated genes (ISGs), which have a variety of antiviral effector properties [5].

Several reports evidence that viral infections significantly alter host transcriptome, including CHIKV [6–8]. These changes may be related to transcriptional and post-transcriptional control mechanisms mediated by long non-coding RNAs (lncRNAs) in several ways [9,10]. lncRNAs are tissue-specific transcripts with poor

coding potential, that can be classified as *cis* or *trans*, based on the chromosomal distance to their targets. *Cis*-acting lncRNAs are those that act at the same loci where they are transcribed [11]; in turn, *trans*-acting lncRNAs are transcribed, processed, and then leave their transcription site to execute their function in another region, either in the nucleus or in the cytoplasm of the cell [12]. Several lncRNAs were identified in response to infection by other arboviruses, including Dengue and Zika Virus, indicating that altered lncRNA expression may participate in host response and immunity [13,14].

In view of the role of lncRNAs in epigenetic regulation during other arboviral infections, we aimed to elucidate whether the expression of lncRNAs is correlated with their presumptive target mRNAs during natural Chikungunya infection in adolescents, and whether these interactions may play key roles in the pathogenesis of the disease and antiviral response.

## **2.5 Methods**

### **2.5.1 Dataset**

Publicly available RNA-Seq data were collected from the Gene Expression Omnibus (GEO) database, bioproject PRJNA390289 and accession number GSE99992. To generate this data, Michlmayr *et al.* [8] performed whole-blood RNA-Seq of acute and convalescent phase samples from 42 children who were spontaneously infected with CHIKV. Acute phase samples were taken on days 1-2 post-symptom onset, and convalescent phase samples of these same individuals were taken on days 15-17, after the resolution of symptoms and viremia. To decrease confounding factors, we excluded samples from girls, samples without acute viral load and convalescent IgG titer, and samples from children under 11 years of age. A total of 34 samples (17 from each phase), collected from adolescent boys (11-15 years old), were used for our analyses.

### **2.5.2 RNA-Seq analysis**

Paired-end files from both phases of illness were retrieved from the sequence read archive (SRA) database and converted to FASTQ format using Download and Extract Reads in the FASTA/Q (Galaxy Version 2.10.8+galaxy0) tool, available at the Galaxy web platform ([www.usegalaxy.org](http://www.usegalaxy.org)) [15]. Quality of reads was checked with FastQC (Galaxy Version 0.73+galaxy0) and then aligned to the human genome reference (assembly GENCODE GRCh38.p13) using HISAT2 (Galaxy Version 2.1.0+galaxy5) [16]. Read counts were performed using HTSeq-count (Galaxy Version 0.9.1) with comprehensive gene annotation GENCODE V34 [17]. Quality reports of all steps were analyzed with MultiQC (Galaxy Version 1.8+galaxy1) [18].

### **2.5.3 Differential gene expression analysis**

Using DESeq2 (Galaxy Version 2.11.40.6+galaxy1), we estimated variance-mean dependence in count data and used the Wald test to identify transcripts that were differentially expressed ( $FDR < 0.05$ ;  $\log_2(FC) \geq 1$ ) between acute and convalescent phases of the disease [19]. Next, we used the BioMart tool (release 103) to obtain the classification of our differentially expressed transcripts according to their biotype [20]. Annotation relied on Ensembl coding/non-coding classification and those transcripts of the “lncRNA” type were considered as lncRNAs, while those of the “protein\_coding” type were considered as mRNAs.

### **2.5.4 Co-expression analysis of lncRNAs and mRNAs**

Due to the scarcity of comprehensive databases that serve as a resource for experimentally verified lncRNA function, co-expression analysis is often employed to infer the role of lncRNAs in all biological and pathological contexts. To identify co-expressed lncRNA-mRNA pairs, Pearson correlation coefficients were calculated based on the expression value of every differentially expressed (DE) lncRNA and

mRNA pair. Threshold for Pearson correlation coefficient was set to  $|r| \geq 0.95$  and the corresponding FDR was set to  $<0.01$ . Using the FEELnc (Flexible Extraction of Long non-coding RNAs) tool, the putative interactions between lncRNA-mRNA were classified in *cis*- or *trans*-acting, based on the chromosomal distance between the transcripts, with the FEELnc classifier module, considering a sliding window of 10kbps and up to 100kbps in distance [21]. Further, potential of ligation between *trans* lncRNAs and putative target mRNAs with significant correlation was evaluated based on the estimates of free energy (normalized dG (ndG) was set to -0.10), using the LncTar tool [22].

### 2.5.5 Functional Enrichment Analysis

All mRNAs targeted by lncRNAs for which the criteria of co-expression ( $|r| \geq 0.95$  and  $FDR < 0.01$ ) and potential of ligation (for all *trans*-acting transcripts) or nearby genes (for all *cis*-acting transcripts) were met, were analyzed by Kyoto Encyclopedia of Genes and Genomes (KEGG), using the g:GOST tool in g:Profiler web server, applying the Benjamini-Hochberg FDR multiple testing correction method set at 0.05 [23].

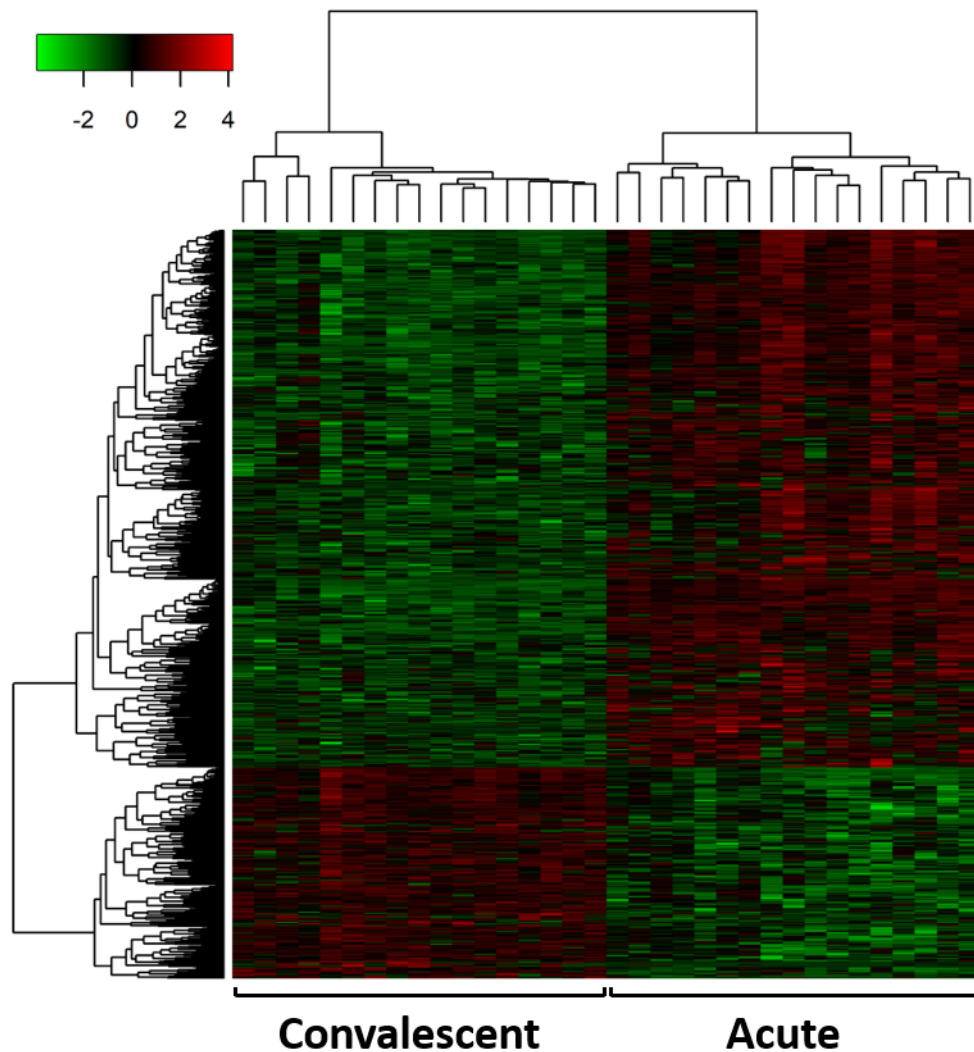
### 2.5.6 Construction of lncRNA-mRNA co-expression network

Gene co-expression network were built using the Cytoscape software (version 3.9.0) (<https://cytoscape.org/>) and the top five KEGG pathways, according to the highest percentage of our target mRNAs in the pathways, were evaluated. Cytoscape combines all the identified interactions among the genes and generates the final integrated regulatory network.

## 2.6 Results

Out of all 3461 differentially expressed transcripts ( $FDR < 0.05$ ;  $\log_2(FC) \geq 1$ ) in whole blood cells of adolescent boys positive for CHIKV, between acute and

convalescent stages, 1975 transcripts were classified as mRNAs and 793 as lncRNAs, according to the Ensembl definition as available in the BioMart tool (S1A and S1B Table). Regarding those 793 lncRNAs, 569 DE lncRNAs showed elevated expression while 224 were downregulated in the acute phase (Fig 1).



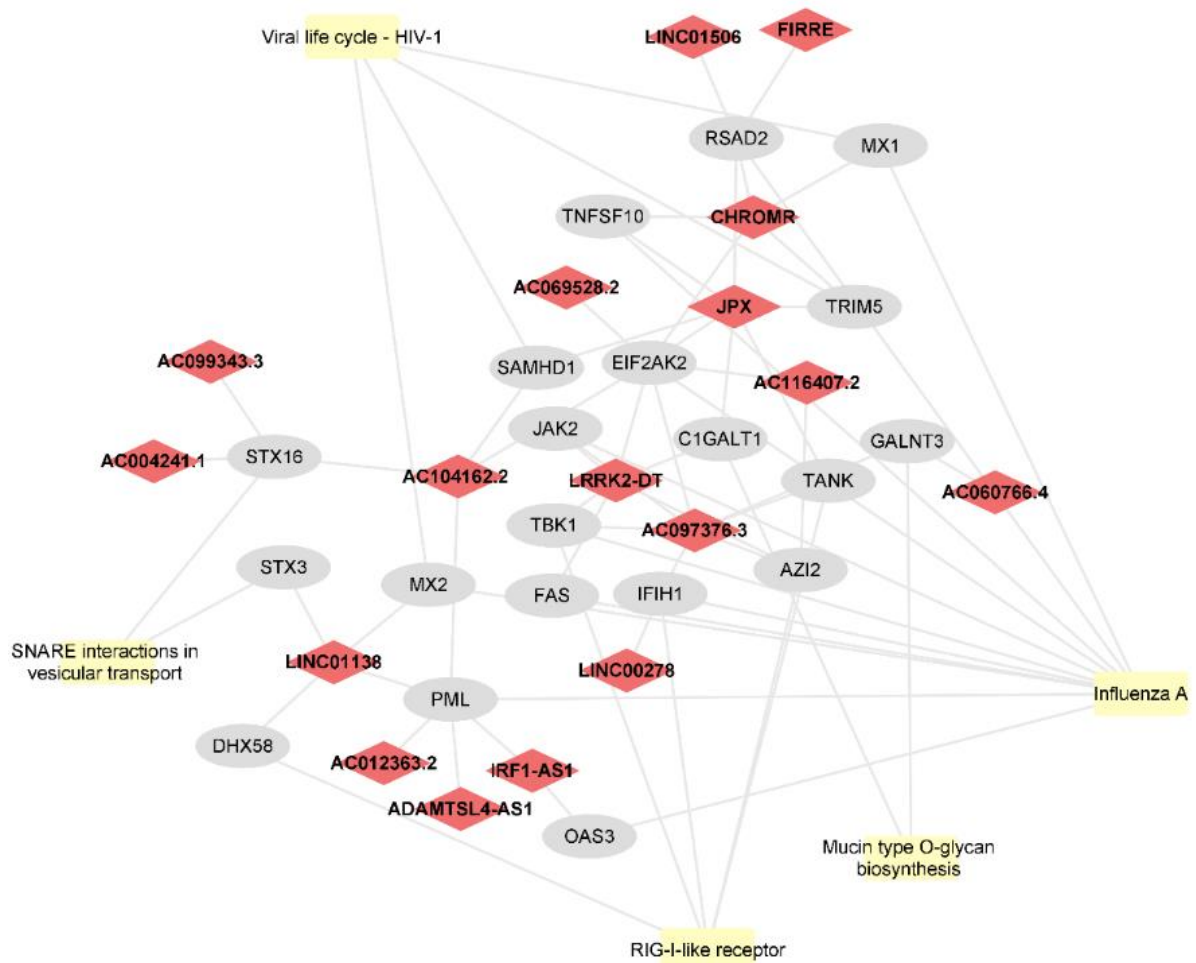
**Fig 1. Heatmap of differentially expressed lncRNAs between acute and convalescent phases of chikungunya infection.**

Expression of 793 lncRNAs, differentially expressed in whole blood cells of male children aged 11 to 15 years old, is hierarchically grouped (hierarchical clustering used the complete linkage method with Euclidean distance) and represented according to

the color scale in z-score (green indicates lower expression, whereas red indicates higher expression).

From a correlation matrix containing 774 potential lncRNA-mRNA interactions ( $|r| \geq 0.95$ ;  $FDR < 0.01$ ), we classified the distance between lncRNA and the putative mRNA by the FEELnc algorithm, which result in 9 lncRNAs-mRNAs interactions predicted to have *cis* activity (S2 Table). We performed free energy analysis in LncTar ( $\Delta G \leq -0.10$ ), which resulted in 357 interactions with a potential of ligation between lncRNA-mRNA (S3 Table), that here we considered to have a *trans* activity.

After pathway enrichment analysis, 52 KEGG pathways were significantly enriched by 78 DE mRNAs which were potentially regulated by 43 DE lncRNAs. These pathways are mainly related to immune response and viral infections. To better visualize the relationship between the co-expressed transcripts, Cytoscape was used to assemble in a network the top five KEGG pathways (Fig 2), ranked according to the highest ratio between our significant target mRNAs and the total of genes in the pathway (S4 Table).



**Fig 2. Network analysis of the top 5 pathways and related mRNAs and lncRNAs.**

All lncRNAs and mRNAs depicted were upregulated in acute phase of CHIKV infection.

Node shape legends: Ellipses correspond to mRNAs; Diamonds to lncRNAs; Round rectangles to KEGG pathways.

Given the relevance of the type I interferon response to viral infections, we used the INTERFEROME database v2.01 (INTERFEROME.org) to determine which of our lncRNAs and mRNAs are classified as ISGs. Among our 366 significant interactions between lncRNA-mRNA (9 *cis* interactions and 357 *trans* interactions), we identified 160 ISGs, 154 were classified as mRNAs and 6 as lncRNA (S5 Table). The criteria for

inclusion was any experiment where IFN (type I, II or III) was employed and genes were differentially expressed on human blood cells [24].

## 2.7 Discussion

Previous reports revealed that viral infections modify the host transcriptome, including both coding and non-coding transcripts [6–9]; moreover, lncRNAs induced by infection may influence viral pathogenesis and replication (reviewed by [25]). Despite current research being done on CHIKV infection and pathogenesis, the mechanisms mediating host-virus interactions are still elusive. Among several mechanisms involved in these interactions, altered expression of cellular lncRNA may follow CHIKV infection, and can influence the antiviral pathways induced by infection.

Therefore, using a publicly RNA-Seq data produced by Michlmayr *et al.* [8], we analyzed the co-expression profiles of lncRNA-mRNA in adolescent boys, naturally infected with CHIKV. Out of the 774 lncRNA-mRNA pairs, we identified 357 with potential for ligation and, therefore, target regulation in *trans*, and 9 lncRNAs-mRNAs interactions in *cis*. Pathway enrichment analysis indicates that the co-expressed putative targets of the differentially expressed lncRNAs are involved in immune response and viral infection pathways mediated by ISGs. Indeed, IFNs are important immune regulators for viral infections and appear to regulate the lncRNA *BISPR* (*BST2* IFN-Stimulated Positive Regulator) expression [26,27]. In the report that generated the dataset used for our analysis, Michlmayr *et al.* [8] found elevated serum levels of IFN- $\alpha$  and IFN- $\gamma$ , which may be inducing the overexpression of *BISPR* we reported here.

Our analysis reveals that *BISPR* was upregulated in the acute phase of CHIKV and is correlated in a *trans* action with *OASL* (2'-5'-Oligoadenylate Synthetase Like; an ISG transcript), also upregulated in acute phase. Viral infections lead to synthesis of IFN and interferon regulatory factor (IRF)-3, and these proteins induce transcription of

*OASL* [28]. By enhancing the sensitivity of RIG-I (Retinoic acid-inducible gene I) activation, *OASL* promotes an antiviral host response. The putative ligation between *BISPR* and *OASL* may support the stability of *OASL* in cytoplasm, increasing viral recognition and IFN synthesis.

*OASL* activates RIG-I by mimicking the K63-linked polyubiquitin (pUb) to promote transcription of immunoregulatory antiviral genes. In the absence of viral nucleic acid, RIG-I is in a stable auto-inhibited conformation. The C-terminal domain of RIG-I detects and binds to the viral RNA, in this case, causing a conformational shift in RIG-I, consequently exposing the RIG-I N-terminal caspase activation and recruitment domains (CARDs). CARDs then connect to K63-linked polyubiquitin (pUb) and convert RIG-I to an active state, enabling RIG-I to interact with a CARD domain also found in the mitochondrial antiviral-signaling protein (MAVS). MAVS are essential adaptor proteins for RIG like receptors (RLR) signal transduction and, through activation of TANK-binding kinase 1 (TBK1) and I $\kappa$ B kinase- $\epsilon$  (IKK $\epsilon$ ), activate IRF3 (Interferon Regulatory Factor 3) and IRF7 (Interferon Regulatory Factor 7), triggering transcription of *IFN-I*, *OASL* and other antiviral immunoregulatory genes. After the onset of viral infection and stimulation of *OASL* expression in infected and surrounding cells, *OASL* connects and activates RIG-I by simulating pUb, further increasing expression of IFN [29].

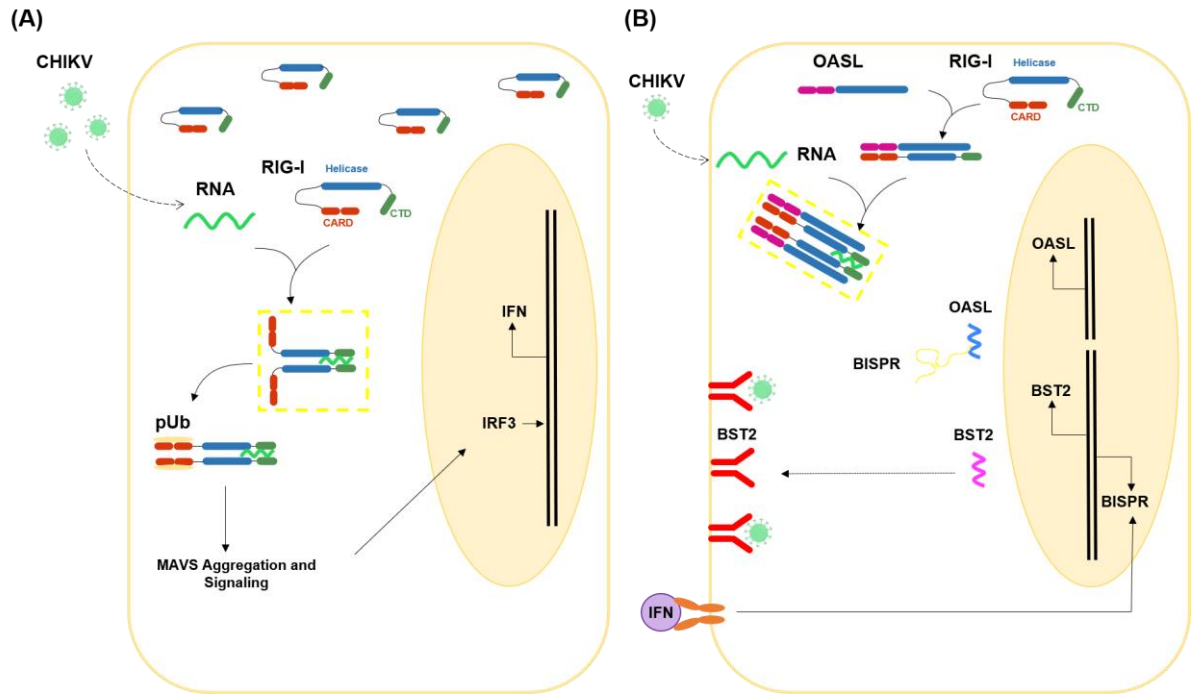
The relevance of *BISPR-OASL-RIG-I* interaction to this infection process is further highlighted by the fact that RIG-I like receptor signaling pathway (KEGG term: map04622) is enriched by five of our DE target mRNAs (*AZI2*, *TBK*, *TANK*, *IFIH1*, and *DHX58*). Since this pathway starts with recognition of viral RNA leading to the synthesis of IFN-I and other inflammatory cytokines, we emphasize the relevance of the interaction between *OASL* and RIG-I.

Furthermore, *BISPR* is also correlated (Pearson Correlation Coefficient 0.89; p-value 0.002) in a *cis* action with their upregulated neighboring gene *BST2* (Bone Marrow Stromal Antigen 2), with whom *BISPR* shares a bidirectional promoter. We observed that *BISPR* does not have binding potential with *BST2*, suggesting that regulation could take place at the pre-transcriptional level. In accordance, Kambara and colleagues [27] demonstrated that *BISPR* may increase the expression or stability of *BST2* by attracting transcription factors to the proximal promoter. These transcription factors may induce local chromatin remodeling or activate transcriptional complexes directly to the transcription start site.

The positive regulation of *BST2* by *BISPR* is important to control release of CHIKV into uninfected cells. *BST2*, a host membrane protein induced by interferon, blocks the exit of many enveloped viruses by directly tethering budded particles to the cell surface [30,31]. Although, the highly organized structures of alphaviruses and the exclusion of host membrane proteins from the site of budding, raise the possibility that tetherin inhibition may not affect the release of these pathogens [32,33]. Notwithstanding, Mahauad-Fernandez [34] demonstrated that *BST2* was co-localized with infectious CHIKV, thus suppressing CHIKV release from infected mouse embryonic fibroblasts and macrophages during acute infection. We suggest that *BISPR* is regulating *BST2* expression in whole-blood cells, in an attempt to block the release of new viruses to neighboring cells.

Our findings indicate that *Chikungunya* infection alters mRNA expression, which may be regulated at transcription or transcript stability, by differentially expressed lncRNAs (Fig 3). Regulation of mRNAs by lncRNAs can facilitate viral recognition through the RIG-I like receptor, which stimulates interferon production and an antiviral immune response. Additionally, *BST2* is regulated by the nearby gene lncRNA *BISPR*,

which helps to suppress viral release. Our research also raises the question of whether altered lncRNA-mRNA interactions mediate the establishment of chronic illness.



**Fig 3. Putative interactions between *BISPR* and two mRNAs: *BST2* and *OASL*.**

(A) By endocytosis, CHIKV enter host cells and release viral RNA in the cytoplasm. After viral recognition, RIG-I undergoes a conformational change exposing CARDs; where the pUb connects and activates RIG-I. Further, RIG-I interacts with the CARD domain also found in the MAVS, which in turn activates IRF3 and IRF7, promoting transcription of *IFN-1* and *OASL*. (B) After the onset of infection, IFN stimulates *BISPR* expression. *BISPR* is predicted to bind *OASL* mRNA by sequence complementarity and also to regulate the promoter of *BST2*. By regulating *OASL*, *BISPR* favors that *OASL* connects and activates RIG-I by simulating pUb, as highlighted by the yellow square, increasing *IFN* expression. Also, *BISPR* positively regulates *BST2* expression, thus interfering with the release of new viruses to neighboring cells.

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## **2.9 Supporting Information**

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

**S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.**

**S2 Table. LncRNA-mRNA *cis* interactions according to FEELnc.**

**S3 Table. LncRNA-mRNA *trans* interactions with potential of ligation according to LncTar.**

**S4 Table. Top 5 KEGG pathways ranked according to the highest ratio between our significant target mRNAs and the total of genes in the pathway.**

**S5 Table. Interferon Stimulated Genes according to Interferome Database and KEGG pathways related to them.**

## APÊNDICE A – Referências da Introdução Geral

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## APÊNDICE B – Material Suplementar Referente ao Capítulo 1

S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.

(Continua)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000165029.16	ABCA1	2.95	UP	3.25E-99
ENSG00000063046.17	EIF4B	-1.55	DOWN	1.28E-95
ENSG00000174748.22	RPL15	-1.37	DOWN	3.96E-73
ENSG00000132669.13	RIN2	3.23	UP	2.58E-68
ENSG00000078098.14	FAP	4.95	UP	4.23E-66
ENSG00000186468.13	RPS23	-1.69	DOWN	2.06E-65
ENSG00000121797.10	CCRL2	3.74	UP	4.22E-65
ENSG00000125355.15	TMEM255A	4.81	UP	1.47E-64
ENSG00000171860.5	C3AR1	3.04	UP	1.47E-64
ENSG00000169508.7	GPR183	-1.60	DOWN	5.53E-64
ENSG00000255221.3	CARD17	5.05	UP	3.47E-63
ENSG00000143344.15	RGL1	2.83	UP	3.61E-62
ENSG00000136689.18	IL1RN	4.18	UP	5.33E-62
ENSG00000175390.14	EIF3F	-1.00	DOWN	2.06E-61
ENSG00000067082.15	KLF6	1.66	UP	2.95E-59
ENSG00000112343.11	TRIM38	2.29	UP	6.66E-58
ENSG00000196141.14	SPATS2L	4.94	UP	3.63E-57
ENSG00000165185.14	KIAA1958	3.12	UP	1.00E-56
ENSG00000116251.11	RPL22	-1.57	DOWN	1.00E-56
ENSG00000122406.14	RPL5	-1.75	DOWN	1.07E-55
ENSG00000244617.2	ASPRV1	3.91	UP	1.55E-55
ENSG00000135334.9	AKIRIN2	1.91	UP	3.46E-55
ENSG00000143891.17	GALM	3.68	UP	7.47E-55
ENSG00000163823.4	CCR1	2.73	UP	2.80E-54
ENSG00000035681.9	NSMAF	1.63	UP	4.13E-54
ENSG00000213903.9	LTB4R	2.10	UP	5.85E-53
ENSG00000007944.15	MYLIP	1.47	UP	1.97E-52
ENSG00000108771.13	DHX58	3.67	UP	2.95E-52
ENSG00000143947.13	RPS27A	-1.52	DOWN	3.69E-52
ENSG00000145016.16	RUBCN	2.46	UP	7.82E-52
ENSG00000124256.15	ZBP1	3.21	UP	1.38E-51
ENSG00000184979.10	USP18	5.10	UP	1.84E-51
ENSG00000135211.6	TMEM60	1.76	UP	2.09E-50
ENSG00000155926.14	SLA	2.01	UP	1.30E-49
ENSG00000138642.15	HERC6	3.01	UP	1.76E-49
ENSG00000177294.7	FBXO39	4.25	UP	2.82E-49
ENSG00000111912.20	NCOA7	3.50	UP	3.37E-49
ENSG00000178562.18	CD28	-1.52	DOWN	9.26E-49
ENSG00000132357.14	CARD6	1.49	UP	6.98E-48

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000123689.6	G0S2	4.15	UP	2.31E-47
ENSG00000059378.13	PARP12	2.79	UP	2.39E-47
ENSG00000158481.13	CD1C	-2.86	DOWN	2.67E-47
ENSG00000258227.7	CLEC5A	3.02	UP	4.67E-47
ENSG00000109452.12	INPP4B	-1.68	DOWN	8.92E-47
ENSG00000144843.11	ADPRH	1.98	UP	9.97E-47
ENSG00000133101.10	CCNA1	4.20	UP	1.02E-46
ENSG00000117834.12	SLC5A9	3.20	UP	1.08E-46
ENSG00000196358.11	NTNG2	3.30	UP	1.51E-46
ENSG00000135047.15	CTSL	3.26	UP	3.29E-46
ENSG00000100129.18	EIF3L	-1.73	DOWN	5.15E-46
ENSG00000188786.10	MTF1	1.60	UP	6.05E-46
ENSG00000108984.15	MAP2K6	2.27	UP	1.02E-45
ENSG00000123130.17	ACOT9	2.20	UP	2.00E-45
ENSG00000173208.4	ABCD2	-1.70	DOWN	3.59E-45
ENSG00000141664.10	ZCCHC2	2.31	UP	1.41E-44
ENSG00000114942.14	EEF1B2	-1.73	DOWN	1.46E-44
ENSG00000116954.8	RRAGC	1.22	UP	1.63E-44
ENSG00000008988.9	RPS20	-1.22	DOWN	4.34E-44
ENSG00000110079.18	MS4A4A	3.27	UP	1.21E-43
ENSG00000165097.16	KDM1B	1.41	UP	4.33E-43
ENSG00000183486.13	MX2	2.67	UP	6.33E-43
ENSG00000130813.18	SHFL	2.15	UP	6.34E-43
ENSG00000108424.10	KPNB1	2.23	UP	7.97E-43
ENSG00000196116.8	TDRD7	2.61	UP	9.79E-43
ENSG00000117010.17	ZNF684	3.35	UP	5.56E-42
ENSG00000135114.12	OASL	3.80	UP	1.22E-41
ENSG00000197548.12	ATG7	1.11	UP	1.39E-41
ENSG00000178175.12	ZNF366	3.52	UP	1.39E-41
ENSG00000072121.16	ZFYVE26	2.06	UP	1.90E-41
ENSG00000188215.10	DCUN1D3	1.59	UP	2.29E-41
ENSG00000183621.15	ZNF438	2.34	UP	2.33E-41
ENSG00000213741.11	RPS29	-1.34	DOWN	2.40E-41
ENSG00000088827.12	SIGLEC1	5.31	UP	3.04E-41
ENSG00000110700.7	RPS13	-1.21	DOWN	3.67E-41
ENSG00000165929.13	TC2N	-1.63	DOWN	4.20E-41
ENSG00000105968.19	H2AZ2	-1.04	DOWN	4.99E-41
ENSG00000139132.14	FGD4	1.47	UP	5.15E-41
ENSG00000121281.13	ADCY7	1.33	UP	1.06E-40
ENSG00000185862.7	EVI2B	1.62	UP	1.16E-40
ENSG00000127334.11	DYRK2	-1.39	DOWN	2.70E-40

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000149311.18	ATM	-1.19	DOWN	4.84E-40
ENSG00000140379.8	BCL2A1	2.59	UP	5.24E-40
ENSG00000166889.14	PATL1	1.95	UP	5.51E-40
ENSG00000132825.7	PPP1R3D	1.34	UP	6.91E-40
ENSG00000159882.13	ZNF230	1.52	UP	7.32E-40
ENSG00000136816.16	TOR1B	2.77	UP	1.18E-39
ENSG00000119321.9	FKBP15	1.50	UP	1.47E-39
ENSG00000137462.8	TLR2	1.64	UP	1.48E-39
ENSG00000198785.7	GRIN3A	4.70	UP	1.60E-39
ENSG00000163666.10	HESX1	5.64	UP	1.82E-39
ENSG00000188282.12	RUFY4	5.16	UP	2.64E-39
ENSG00000145425.10	RPS3A	-1.73	DOWN	3.66E-39
ENSG00000132780.17	NASP	1.42	UP	5.51E-39
ENSG00000185880.13	TRIM69	2.31	UP	5.63E-39
ENSG00000181163.13	NPM1	-1.15	DOWN	6.68E-39
ENSG00000109046.15	WSB1	1.69	UP	8.30E-39
ENSG00000130066.16	SAT1	2.79	UP	8.30E-39
ENSG00000204397.8	CARD16	2.45	UP	8.30E-39
ENSG00000162614.18	NEXN	3.04	UP	1.18E-38
ENSG00000165949.12	IFI27	4.63	UP	4.41E-38
ENSG00000138760.10	SCARB2	1.94	UP	7.30E-38
ENSG00000120280.6	CXorf21	2.09	UP	1.02E-37
ENSG00000124357.13	NAGK	1.89	UP	1.15E-37
ENSG00000165030.4	NFIL3	2.29	UP	2.45E-37
ENSG00000147604.14	RPL7	-1.41	DOWN	3.22E-37
ENSG00000168026.18	TTC21A	3.00	UP	3.77E-37
ENSG00000173221.14	GLRX	1.96	UP	4.05E-37
ENSG00000067221.14	STOML1	3.34	UP	5.21E-37
ENSG00000184678.10	H2BC21	2.42	UP	5.21E-37
ENSG00000175471.19	MCTP1	1.56	UP	5.31E-37
ENSG00000164054.15	SHISA5	2.25	UP	5.65E-37
ENSG00000120690.16	ELF1	1.81	UP	7.36E-37
ENSG00000115956.10	PLEK	1.63	UP	8.73E-37
ENSG00000107736.21	CDH23	2.46	UP	1.43E-36
ENSG00000254470.3	AP5B1	2.20	UP	1.70E-36
ENSG00000152213.4	ARL11	1.46	UP	1.82E-36
ENSG00000111371.16	SLC38A1	-1.21	DOWN	1.90E-36
ENSG00000173821.19	RNF213	2.77	UP	1.90E-36
ENSG00000135899.17	SP110	1.94	UP	2.21E-36
ENSG00000117475.14	BLZF1	1.89	UP	2.22E-36

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000126262.4	FFAR2	2.84	UP	2.24E-36
ENSG00000285976.2	AL135905.2	2.54	UP	2.28E-36
ENSG00000079385.22	CEACAM1	2.96	UP	2.87E-36
ENSG00000152465.18	NMT2	-1.38	DOWN	3.02E-36
ENSG00000125148.7	MT2A	4.00	UP	3.63E-36
ENSG00000181778.5	TMEM252	3.47	UP	6.29E-36
ENSG00000136111.14	TBC1D4	-1.28	DOWN	6.45E-36
ENSG00000157693.15	TMEM268	2.20	UP	1.20E-35
ENSG00000117226.12	GBP3	2.62	UP	1.23E-35
ENSG00000117602.12	RCAN3	-1.77	DOWN	1.50E-35
ENSG00000185722.18	ANKFY1	1.84	UP	1.78E-35
ENSG00000143119.14	CD53	1.24	UP	2.00E-35
ENSG00000163746.11	PLSCR2	3.19	UP	2.73E-35
ENSG00000169439.12	SDC2	-4.29	DOWN	2.93E-35
ENSG00000183918.17	SH2D1A	-1.68	DOWN	2.99E-35
ENSG00000078589.13	P2RY10	-1.48	DOWN	3.83E-35
ENSG00000105967.16	TFEC	3.64	UP	3.83E-35
ENSG00000213722.9	DDAH2	2.21	UP	3.87E-35
ENSG00000112773.16	TENT5A	2.36	UP	5.05E-35
ENSG00000101150.17	TPD52L2	1.20	UP	5.96E-35
ENSG00000154217.15	PITPNC1	-1.29	DOWN	6.65E-35
ENSG00000142687.18	KIAA0319L	2.23	UP	9.40E-35
ENSG00000102317.18	RBM3	-1.89	DOWN	1.25E-34
ENSG00000160710.17	ADAR	1.99	UP	1.60E-34
ENSG00000121236.21	TRIM6	3.28	UP	3.32E-34
ENSG00000091409.15	ITGA6	-1.59	DOWN	4.10E-34
ENSG00000023171.18	GRAMD1B	3.05	UP	4.55E-34
ENSG00000172578.12	KLHL6	1.19	UP	4.55E-34
ENSG00000062598.18	ELMO2	1.79	UP	5.58E-34
ENSG00000020577.14	SAMD4A	3.68	UP	6.30E-34
ENSG00000169385.3	RNASE2	2.38	UP	7.71E-34
ENSG00000174444.15	RPL4	-1.68	DOWN	8.83E-34
ENSG00000111335.13	OAS2	3.40	UP	8.84E-34
ENSG00000155307.19	SAMSN1	1.83	UP	1.07E-33
ENSG00000156508.18	EEF1A1	-1.58	DOWN	1.52E-33
ENSG00000157827.20	FMNL2	2.38	UP	1.71E-33
ENSG00000104408.10	EIF3E	-1.09	DOWN	1.95E-33
ENSG00000172432.19	GTPBP2	2.17	UP	2.42E-33
ENSG00000012048.23	BRCA1	1.10	UP	2.43E-33
ENSG00000196954.14	CASP4	2.04	UP	2.64E-33

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000135363.12	LMO2	2.14	UP	3.51E-33
ENSG00000172936.15	MYD88	1.66	UP	3.59E-33
ENSG00000153823.18	PID1	-2.74	DOWN	3.63E-33
ENSG00000153283.13	CD96	-1.38	DOWN	3.98E-33
ENSG00000244482.10	LILRA6	2.41	UP	4.51E-33
ENSG00000137752.24	CASP1	1.90	UP	4.66E-33
ENSG00000100596.6	SPTLC2	2.21	UP	4.70E-33
ENSG00000168003.16	SLC3A2	2.31	UP	4.79E-33
ENSG00000163840.10	DTX3L	2.10	UP	5.61E-33
ENSG00000055332.18	EIF2AK2	2.93	UP	5.94E-33
ENSG00000115159.16	GPD2	2.31	UP	6.34E-33
ENSG00000164466.13	SFXN1	-1.14	DOWN	1.20E-32
ENSG00000163393.13	SLC22A15	1.75	UP	1.35E-32
ENSG00000089009.15	RPL6	-1.40	DOWN	1.90E-32
ENSG00000119917.14	IFIT3	4.05	UP	2.41E-32
ENSG00000154359.13	LONRF1	1.08	UP	2.56E-32
ENSG00000118922.17	KLF12	-1.32	DOWN	3.11E-32
ENSG00000121060.18	TRIM25	2.10	UP	3.86E-32
ENSG00000099290.17	WASHC2A	1.06	UP	4.13E-32
ENSG00000151835.16	SACS	-1.06	DOWN	4.60E-32
ENSG00000108700.5	CCL8	5.72	UP	5.37E-32
ENSG00000170989.10	S1PR1	-1.27	DOWN	5.65E-32
ENSG00000138246.17	DNAJC13	1.55	UP	6.70E-32
ENSG00000152778.9	IFIT5	2.91	UP	6.88E-32
ENSG00000189057.11	FAM111B	-2.12	DOWN	7.79E-32
ENSG00000116977.18	LGALS8	1.48	UP	8.54E-32
ENSG00000182774.13	RPS17	-1.33	DOWN	9.99E-32
ENSG00000266028.7	SRGAP2	2.45	UP	1.01E-31
ENSG00000104043.15	ATP8B4	1.63	UP	1.10E-31
ENSG00000203814.6	H2BC18	2.44	UP	1.16E-31
ENSG00000078081.8	LAMP3	4.81	UP	1.23E-31
ENSG00000102699.6	PARP4	1.10	UP	1.25E-31
ENSG00000158373.8	H2BC5	1.77	UP	1.36E-31
ENSG00000186409.18	CCDC30	1.25	UP	1.39E-31
ENSG00000067066.17	SP100	1.74	UP	1.55E-31
ENSG00000163606.11	CD200R1	-1.52	DOWN	1.58E-31
ENSG00000178075.20	GRAMD1C	-3.16	DOWN	1.62E-31
ENSG00000132256.19	TRIM5	2.40	UP	1.91E-31
ENSG00000101608.12	MYL12A	1.47	UP	3.59E-31
ENSG00000115267.8	IFIH1	3.26	UP	4.77E-31

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000163600.13	ICOS	-1.51	DOWN	5.02E-31
ENSG00000157601.14	MX1	3.72	UP	7.18E-31
ENSG00000086065.14	CHMP5	2.47	UP	9.63E-31
ENSG00000143367.16	TUFT1	2.39	UP	1.04E-30
ENSG00000134627.12	PIWIL4	1.40	UP	1.36E-30
ENSG00000185477.5	GPRIN3	-1.22	DOWN	1.36E-30
ENSG00000102897.10	LYRM1	1.67	UP	1.43E-30
ENSG00000205413.8	SAMD9	2.48	UP	1.65E-30
ENSG00000164674.15	SYTL3	1.85	UP	2.00E-30
ENSG00000152495.11	CAMK4	-1.67	DOWN	2.47E-30
ENSG00000133106.14	EPST11	2.72	UP	4.23E-30
ENSG00000091181.19	IL5RA	-3.04	DOWN	4.47E-30
ENSG00000075420.13	FNDC3B	1.54	UP	4.95E-30
ENSG00000148180.19	GSN	2.25	UP	5.04E-30
ENSG00000142875.19	PRKACB	-1.10	DOWN	5.56E-30
ENSG00000140464.20	PML	2.76	UP	6.32E-30
ENSG00000137200.13	CMTR1	2.34	UP	6.62E-30
ENSG00000136514.3	RTP4	3.37	UP	7.10E-30
ENSG00000003400.15	CASP10	1.34	UP	7.26E-30
ENSG00000163565.18	IFI16	2.43	UP	7.26E-30
ENSG00000119899.13	SLC17A5	1.10	UP	8.83E-30
ENSG00000089127.13	OAS1	3.35	UP	1.04E-29
ENSG00000111224.14	PARP11	2.07	UP	1.27E-29
ENSG00000197321.15	SVIL	1.17	UP	1.64E-29
ENSG00000115604.10	IL18R1	2.65	UP	1.73E-29
ENSG00000146859.6	TMEM140	2.37	UP	1.81E-29
ENSG00000156587.16	UBE2L6	2.63	UP	1.94E-29
ENSG00000143771.12	CNIH4	1.59	UP	2.05E-29
ENSG00000106785.15	TRIM14	1.77	UP	2.32E-29
ENSG00000152133.15	GPATCH11	-1.16	DOWN	2.43E-29
ENSG00000172183.15	ISG20	2.18	UP	2.76E-29
ENSG00000123728.10	RAP2C	1.22	UP	2.92E-29
ENSG00000108387.15	SEPTIN4	4.26	UP	4.47E-29
ENSG00000115155.18	OTOF	5.72	UP	4.72E-29
ENSG00000139618.15	BRCA2	2.14	UP	5.33E-29
ENSG00000137628.17	DDX60	2.68	UP	6.65E-29
ENSG00000204103.4	MAFB	2.16	UP	7.94E-29
ENSG00000138496.16	PARP9	2.53	UP	9.00E-29
ENSG00000158769.18	F11R	1.10	UP	9.04E-29
ENSG00000203880.12	PCMTD2	-1.11	DOWN	9.98E-29

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000126860.11	EVI2A	1.70	UP	1.01E-28
ENSG00000111331.13	OAS3	3.97	UP	1.05E-28
ENSG00000106617.15	PRKAG2	1.47	UP	1.25E-28
ENSG00000130449.6	ZSWIM6	1.01	UP	1.48E-28
ENSG00000167984.18	NLRC3	-1.14	DOWN	2.05E-28
ENSG00000173334.4	TRIB1	1.94	UP	2.16E-28
ENSG00000121486.12	TRMT1L	1.17	UP	2.19E-28
ENSG00000170345.10	FOS	1.87	UP	2.74E-28
ENSG00000183688.4	RFLNB	-2.00	DOWN	2.85E-28
ENSG00000185745.10	IFIT1	4.37	UP	2.88E-28
ENSG00000138119.17	MYOF	2.36	UP	3.73E-28
ENSG00000107864.15	CPEB3	1.85	UP	3.85E-28
ENSG00000174021.11	GNG5	1.64	UP	4.05E-28
ENSG00000138035.15	PNPT1	2.61	UP	4.95E-28
ENSG00000134709.12	HOOK1	-1.38	DOWN	5.23E-28
ENSG00000170525.21	PFKFB3	2.37	UP	5.35E-28
ENSG00000152558.15	TMEM123	2.21	UP	5.48E-28
ENSG00000164440.15	TXLNB	1.80	UP	5.48E-28
ENSG00000173110.8	HSPA6	2.02	UP	5.73E-28
ENSG00000148841.17	ITPRIP	1.74	UP	7.10E-28
ENSG00000154814.14	OXNAD1	-1.50	DOWN	7.21E-28
ENSG00000198242.14	RPL23A	-1.41	DOWN	1.24E-27
ENSG00000108691.9	CCL2	5.09	UP	1.25E-27
ENSG00000277443.3	MARCKS	2.02	UP	1.27E-27
ENSG00000188313.13	PLSCR1	3.14	UP	1.38E-27
ENSG00000143162.9	CREG1	1.48	UP	1.48E-27
ENSG00000146425.11	DYNLT1	2.22	UP	1.87E-27
ENSG00000204516.10	MICB	1.97	UP	2.21E-27
ENSG00000163512.14	AZI2	1.67	UP	2.30E-27
ENSG00000176597.12	B3GNT5	1.78	UP	2.35E-27
ENSG00000172673.10	THEMIS	-1.46	DOWN	2.77E-27
ENSG00000159885.14	ZNF222	1.20	UP	2.80E-27
ENSG00000145287.10	PLAC8	1.69	UP	2.91E-27
ENSG00000132530.17	XAF1	3.14	UP	2.91E-27
ENSG00000167232.14	ZNF91	-1.25	DOWN	4.66E-27
ENSG00000135148.12	TRAFD1	2.03	UP	5.14E-27
ENSG00000205352.11	PRR13	1.38	UP	5.49E-27
ENSG00000142541.17	RPL13A	-1.59	DOWN	5.51E-27
ENSG00000158406.4	H4C8	2.13	UP	6.68E-27
ENSG00000179562.3	GCC1	1.01	UP	7.70E-27

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000170581.14	STAT2	2.61	UP	8.21E-27
ENSG00000092036.18	HAUS4	2.12	UP	8.56E-27
ENSG00000103121.9	CMC2	1.73	UP	8.84E-27
ENSG00000204642.14	HLA-F	1.11	UP	8.84E-27
ENSG00000186407.7	CD300E	2.17	UP	9.23E-27
ENSG00000198833.7	UBE2J1	1.36	UP	1.02E-26
ENSG00000101842.13	VSIG1	-1.72	DOWN	1.14E-26
ENSG00000096968.14	JAK2	2.05	UP	1.26E-26
ENSG00000172575.12	RASGRP1	-1.33	DOWN	1.28E-26
ENSG00000185909.15	KLHDC8B	3.07	UP	1.37E-26
ENSG00000198755.11	RPL10A	-1.72	DOWN	1.71E-26
ENSG00000162714.12	ZNF496	2.04	UP	1.82E-26
ENSG00000155629.15	PIK3AP1	2.11	UP	1.91E-26
ENSG00000111728.10	ST8SIA1	-1.57	DOWN	2.36E-26
ENSG00000112053.14	SLC26A8	2.53	UP	2.70E-26
ENSG00000112419.14	PHACTR2	2.02	UP	2.81E-26
ENSG00000079263.19	SP140	2.12	UP	2.91E-26
ENSG00000124688.13	MAD2L1BP	1.49	UP	3.39E-26
ENSG00000097033.14	SH3GLB1	1.29	UP	3.73E-26
ENSG00000257743.8	MGAM2	2.75	UP	4.07E-26
ENSG00000169871.13	TRIM56	1.37	UP	4.37E-26
ENSG00000166920.12	C15orf48	3.40	UP	4.39E-26
ENSG00000112394.17	SLC16A10	-2.11	DOWN	4.49E-26
ENSG00000153029.14	MR1	1.30	UP	4.63E-26
ENSG00000197208.6	SLC22A4	2.29	UP	5.11E-26
ENSG00000171033.13	PKIA	-1.42	DOWN	6.40E-26
ENSG00000136147.18	PHF11	1.94	UP	6.80E-26
ENSG00000184613.10	NELL2	-2.37	DOWN	6.80E-26
ENSG00000204186.10	ZDBF2	-1.26	DOWN	6.96E-26
ENSG00000008130.15	NADK	1.97	UP	7.68E-26
ENSG00000128016.7	ZFP36	1.55	UP	8.04E-26
ENSG00000109854.13	HTATIP2	1.43	UP	8.55E-26
ENSG00000133104.14	SPART	1.24	UP	8.71E-26
ENSG00000145685.14	LHFPL2	2.33	UP	8.78E-26
ENSG00000185482.8	STAC3	2.42	UP	1.24E-25
ENSG00000241839.10	PLEKHO2	1.79	UP	1.49E-25
ENSG00000265681.7	RPL17	-1.13	DOWN	1.51E-25
ENSG00000137842.7	TMEM62	1.46	UP	1.51E-25
ENSG00000033867.16	SLC4A7	-1.20	DOWN	1.55E-25
ENSG00000064225.12	ST3GAL6	1.77	UP	1.63E-25

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000119686.10	FLVCR2	1.58	UP	1.70E-25
ENSG00000104320.14	NBN	1.91	UP	1.85E-25
ENSG00000166278.15	C2	3.49	UP	1.97E-25
ENSG00000158163.15	DZIP1L	3.98	UP	2.05E-25
ENSG00000118564.15	FBXL5	1.42	UP	2.08E-25
ENSG00000107201.10	DDX58	3.08	UP	2.73E-25
ENSG00000129355.7	CDKN2D	1.57	UP	3.52E-25
ENSG00000196547.15	MAN2A2	1.34	UP	3.72E-25
ENSG00000025039.15	RRAGD	1.26	UP	3.77E-25
ENSG00000196369.11	SRGAP2B	2.27	UP	3.77E-25
ENSG00000122643.22	NT5C3A	3.16	UP	4.24E-25
ENSG00000148019.14	CEP78	-1.37	DOWN	4.62E-25
ENSG00000107099.15	DOCK8	1.16	UP	4.67E-25
ENSG00000173611.18	SCAI	-1.49	DOWN	4.74E-25
ENSG00000113263.13	ITK	-1.10	DOWN	5.15E-25
ENSG00000111911.7	HINT3	1.77	UP	5.60E-25
ENSG00000204634.12	TBC1D8	2.06	UP	5.70E-25
ENSG00000172243.18	CLEC7A	1.34	UP	6.92E-25
ENSG00000182022.18	CHST15	1.32	UP	7.19E-25
ENSG00000185760.15	KCNQ5	-1.52	DOWN	7.32E-25
ENSG00000172159.16	FRMD3	2.92	UP	7.62E-25
ENSG00000157557.13	ETS2	1.60	UP	7.76E-25
ENSG00000147138.2	GPR174	-1.16	DOWN	9.93E-25
ENSG00000171943.12	SRGAP2C	2.03	UP	1.01E-24
ENSG00000100316.16	RPL3	-1.81	DOWN	1.14E-24
ENSG00000131446.16	MGAT1	1.47	UP	1.17E-24
ENSG00000155363.18	MOV10	2.29	UP	1.23E-24
ENSG00000059804.16	SLC2A3	1.80	UP	1.27E-24
ENSG00000181481.14	RNF135	1.51	UP	1.33E-24
ENSG00000103313.12	MEFV	2.06	UP	1.42E-24
ENSG00000249437.8	NAIP	2.27	UP	1.45E-24
ENSG00000150907.10	FOXO1	-1.26	DOWN	1.47E-24
ENSG00000116044.16	NFE2L2	1.01	UP	1.58E-24
ENSG00000178425.14	NT5DC1	-1.00	DOWN	1.61E-24
ENSG00000115339.14	GALNT3	1.90	UP	1.70E-24
ENSG00000186074.19	CD300LF	1.66	UP	1.76E-24
ENSG00000111860.14	CEP85L	-1.15	DOWN	1.82E-24
ENSG00000171291.8	ZNF439	-1.08	DOWN	2.02E-24
ENSG00000158470.5	B4GALT5	2.00	UP	2.03E-24
ENSG00000168394.11	TAP1	2.22	UP	2.17E-24

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000135318.12	NT5E	-2.03	DOWN	2.20E-24
ENSG00000068400.13	GRIPAP1	1.75	UP	2.20E-24
ENSG00000073331.18	ALPK1	1.48	UP	2.23E-24
ENSG00000272325.2	NUDT3	-1.50	DOWN	2.25E-24
ENSG00000138069.18	RAB1A	1.29	UP	2.60E-24
ENSG00000137038.8	DMAC1	-1.05	DOWN	2.65E-24
ENSG00000158869.11	FCER1G	2.16	UP	2.84E-24
ENSG00000138688.15	KIAA1109	1.62	UP	3.36E-24
ENSG00000079215.14	SLC1A3	2.37	UP	3.46E-24
ENSG00000105501.12	SIGLEC5	2.44	UP	3.46E-24
ENSG00000197121.15	PGAP1	2.29	UP	4.31E-24
ENSG00000068079.8	IFI35	2.92	UP	4.62E-24
ENSG00000123609.11	NMI	1.97	UP	4.80E-24
ENSG00000113368.12	LMNB1	2.41	UP	5.46E-24
ENSG00000076641.4	PAG1	1.15	UP	5.55E-24
ENSG00000144749.13	LRIG1	-1.23	DOWN	5.95E-24
ENSG00000033327.13	GAB2	1.73	UP	6.43E-24
ENSG00000124201.15	ZNFX1	1.87	UP	6.61E-24
ENSG00000198818.10	SFT2D1	1.16	UP	6.93E-24
ENSG00000141682.12	PMAIP1	1.76	UP	7.03E-24
ENSG00000229474.6	PATL2	1.26	UP	7.17E-24
ENSG00000196664.5	TLR7	1.67	UP	8.23E-24
ENSG00000138433.16	CIR1	1.51	UP	8.62E-24
ENSG00000133812.15	SBF2	1.20	UP	1.06E-23
ENSG00000072694.21	FCGR2B	2.46	UP	1.07E-23
ENSG00000107679.14	PLEKHA1	-1.20	DOWN	1.10E-23
ENSG00000149970.16	CNKS2	-1.64	DOWN	1.19E-23
ENSG00000149131.16	SERPING1	3.72	UP	1.51E-23
ENSG00000138646.9	HERC5	3.81	UP	1.53E-23
ENSG00000198918.8	RPL39	-1.20	DOWN	1.92E-23
ENSG00000121380.12	BCL2L14	3.63	UP	2.04E-23
ENSG00000132849.20	PATJ	-1.41	DOWN	2.13E-23
ENSG00000134326.11	CMPK2	3.72	UP	2.21E-23
ENSG00000151364.17	KCTD14	4.44	UP	2.25E-23
ENSG00000127152.18	BCL11B	-1.43	DOWN	2.33E-23
ENSG00000112182.15	BACH2	-1.57	DOWN	2.35E-23
ENSG00000104177.18	MYEF2	-1.08	DOWN	2.35E-23
ENSG00000145365.11	TIFA	1.98	UP	2.79E-23
ENSG00000177932.7	ZNF354C	-1.11	DOWN	2.79E-23
ENSG00000163568.15	AIM2	3.11	UP	3.08E-23

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000187608.10	ISG15	4.19	UP	3.09E-23
ENSG00000116991.10	SIPA1L2	2.04	UP	3.27E-23
ENSG00000132274.16	TRIM22	2.23	UP	3.27E-23
ENSG00000113273.17	ARSB	1.09	UP	3.38E-23
ENSG00000100802.15	C14orf93	1.20	UP	3.58E-23
ENSG00000073969.18	NSF	1.03	UP	3.71E-23
ENSG00000175518.8	UBQLNL	3.16	UP	3.73E-23
ENSG00000128512.23	DOCK4	2.56	UP	4.34E-23
ENSG00000068784.13	SRBD1	1.09	UP	4.55E-23
ENSG00000166908.18	PIP4K2C	1.22	UP	4.80E-23
ENSG00000070756.16	PABPC1	-1.10	DOWN	5.56E-23
ENSG00000136560.14	TANK	1.71	UP	5.56E-23
ENSG00000239920.2	AC104389.5	2.65	UP	5.94E-23
ENSG00000123096.11	SSPN	-1.84	DOWN	7.62E-23
ENSG00000170956.17	CEACAM3	1.93	UP	8.20E-23
ENSG00000198105.15	ZNF248	-1.09	DOWN	8.39E-23
ENSG00000271605.6	MILR1	1.94	UP	1.00E-22
ENSG00000075785.13	RAB7A	1.23	UP	1.01E-22
ENSG00000160654.11	CD3G	-1.36	DOWN	1.01E-22
ENSG00000101236.17	RNF24	1.63	UP	1.13E-22
ENSG00000068305.17	MEF2A	1.36	UP	1.21E-22
ENSG00000180871.8	CXCR2	1.56	UP	1.25E-22
ENSG00000135828.11	RNASEL	1.37	UP	1.27E-22
ENSG00000176928.7	GCNT4	-1.56	DOWN	1.39E-22
ENSG00000139178.11	C1RL	1.24	UP	1.45E-22
ENSG00000181690.8	PLAG1	-1.11	DOWN	1.50E-22
ENSG00000162946.23	DISC1	1.87	UP	1.56E-22
ENSG00000168062.10	BATF2	3.55	UP	1.88E-22
ENSG00000162772.17	ATF3	4.24	UP	1.89E-22
ENSG00000099860.9	GADD45B	2.09	UP	1.91E-22
ENSG00000110497.14	AMBRA1	1.52	UP	1.96E-22
ENSG00000185339.9	TCN2	3.94	UP	2.31E-22
ENSG00000156239.12	N6AMT1	-1.09	DOWN	2.34E-22
ENSG00000112763.17	BTN2A1	1.31	UP	2.39E-22
ENSG00000134070.5	IRAK2	1.63	UP	2.44E-22
ENSG00000085788.14	DDHD2	-1.07	DOWN	3.29E-22
ENSG00000137757.11	CASP5	3.50	UP	3.49E-22
ENSG00000171817.17	ZNF540	-1.42	DOWN	3.60E-22
ENSG00000198087.7	CD2AP	1.93	UP	3.60E-22
ENSG00000254087.8	LYN	1.47	UP	3.60E-22

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000241343.10	RPL36A	-1.14	DOWN	3.64E-22
ENSG00000066084.13	DIP2B	1.17	UP	3.82E-22
ENSG00000163964.16	PIGX	-1.26	DOWN	3.95E-22
ENSG00000132694.18	ARHGEF11	1.65	UP	4.19E-22
ENSG00000172007.7	RAB33B	1.78	UP	4.47E-22
ENSG00000087157.19	PGS1	1.92	UP	4.81E-22
ENSG00000110852.4	CLEC2B	1.92	UP	5.23E-22
ENSG00000134318.14	ROCK2	1.26	UP	5.34E-22
ENSG00000102245.8	CD40LG	-1.39	DOWN	5.66E-22
ENSG00000213462.5	ERV3-1	1.33	UP	5.88E-22
ENSG00000204592.9	HLA-E	1.27	UP	5.91E-22
ENSG00000117632.23	STMN1	-1.23	DOWN	6.01E-22
ENSG00000100342.21	APOL1	2.44	UP	6.20E-22
ENSG00000198040.10	ZNF84	-1.02	DOWN	6.37E-22
ENSG00000108679.13	LGALS3BP	3.58	UP	7.03E-22
ENSG00000147050.15	KDM6A	1.60	UP	7.07E-22
ENSG00000142961.14	MOB3C	1.93	UP	7.39E-22
ENSG00000158987.21	RAPGEF6	-1.11	DOWN	7.96E-22
ENSG00000171132.14	PRKCE	1.28	UP	8.76E-22
ENSG00000113319.13	RASGRF2	-1.04	DOWN	9.07E-22
ENSG00000140280.14	LYSMD2	1.83	UP	9.27E-22
ENSG00000107593.17	PKD2L1	3.90	UP	9.82E-22
ENSG00000181381.13	DDX60L	2.82	UP	1.04E-21
ENSG00000163694.15	RBM47	1.40	UP	1.07E-21
ENSG00000151743.11	AMN1	1.18	UP	1.13E-21
ENSG00000082512.15	TRAF5	-1.15	DOWN	1.16E-21
ENSG00000123610.5	TNFAIP6	3.42	UP	1.18E-21
ENSG00000165209.19	STRBP	-1.17	DOWN	1.19E-21
ENSG00000059728.11	MXD1	1.61	UP	1.50E-21
ENSG00000126709.15	IFI6	3.23	UP	1.61E-21
ENSG00000003402.20	CFLAR	1.16	UP	1.61E-21
ENSG00000130589.16	HELZ2	2.71	UP	1.71E-21
ENSG00000150782.12	IL18	1.38	UP	1.71E-21
ENSG00000137965.11	IFI44	3.40	UP	1.80E-21
ENSG00000102471.14	NDFIP2	-1.46	DOWN	1.93E-21
ENSG00000125826.21	RBCK1	1.89	UP	2.03E-21
ENSG00000135677.11	GNS	1.26	UP	2.09E-21
ENSG00000160888.7	IER2	1.62	UP	2.28E-21
ENSG00000120539.15	MASTL	1.87	UP	2.29E-21
ENSG00000143862.8	ARL8A	1.77	UP	2.33E-21

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000109743.11	BST1	1.39	UP	2.47E-21
ENSG00000103569.10	AQP9	1.87	UP	3.09E-21
ENSG00000187037.8	GPR141	1.88	UP	3.11E-21
ENSG00000172123.12	SLFN12	1.95	UP	3.11E-21
ENSG00000175538.10	KCNE3	1.15	UP	3.32E-21
ENSG00000182957.16	SPATA13	1.40	UP	3.38E-21
ENSG00000163191.6	S100A11	1.66	UP	3.82E-21
ENSG00000187607.16	ZNF286A	-1.15	DOWN	4.07E-21
ENSG00000197385.6	ZNF860	-1.91	DOWN	4.56E-21
ENSG00000091129.21	NRCAM	-2.28	DOWN	4.76E-21
ENSG00000131042.14	LILRB2	1.22	UP	4.83E-21
ENSG00000150457.9	LATS2	1.22	UP	4.83E-21
ENSG00000196177.13	ACADSB	-1.10	DOWN	5.38E-21
ENSG00000151413.17	NUBPL	-1.12	DOWN	6.74E-21
ENSG00000257093.7	DENND11	-1.10	DOWN	6.77E-21
ENSG00000136827.12	TOR1A	1.02	UP	6.79E-21
ENSG00000142089.16	IFITM3	3.51	UP	7.08E-21
ENSG00000171858.18	RPS21	-1.38	DOWN	7.26E-21
ENSG00000163754.18	GYG1	1.70	UP	7.28E-21
ENSG00000187231.14	SESTD1	1.43	UP	7.65E-21
ENSG00000174600.14	CMKLR1	1.91	UP	7.82E-21
ENSG00000168016.14	TRANK1	1.90	UP	8.33E-21
ENSG00000135205.15	CCDC146	1.67	UP	8.65E-21
ENSG00000096746.17	HNRNPH3	1.12	UP	9.16E-21
ENSG00000256223.6	ZNF10	-1.19	DOWN	9.79E-21
ENSG00000183474.15	GTF2H2C	1.16	UP	9.92E-21
ENSG00000173786.17	CNP	2.16	UP	1.13E-20
ENSG00000173281.5	PPP1R3B	1.53	UP	1.19E-20
ENSG00000160856.21	FCRL3	-1.29	DOWN	1.23E-20
ENSG00000128536.16	CDHR3	-1.50	DOWN	1.30E-20
ENSG00000132109.10	TRIM21	1.82	UP	1.30E-20
ENSG00000198829.6	SUCNR1	2.13	UP	1.42E-20
ENSG00000116514.16	RNF19B	1.27	UP	1.59E-20
ENSG00000119922.10	IFIT2	3.78	UP	1.59E-20
ENSG00000010539.11	ZNF200	1.66	UP	1.77E-20
ENSG00000135636.14	DYSF	2.50	UP	1.79E-20
ENSG00000102921.8	N4BP1	1.58	UP	1.80E-20
ENSG00000105205.7	CLC	-2.77	DOWN	1.81E-20
ENSG00000108950.12	FAM20A	3.28	UP	1.81E-20
ENSG00000128918.15	ALDH1A2	2.14	UP	1.83E-20

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000070269.14	TMEM260	1.01	UP	1.84E-20
ENSG00000157077.14	ZFYVE9	-1.47	DOWN	1.86E-20
ENSG00000168961.17	LGALS9	2.33	UP	1.91E-20
ENSG00000197635.10	DPP4	-1.41	DOWN	1.96E-20
ENSG00000258659.6	TRIM34	1.43	UP	2.10E-20
ENSG00000203666.12	EFCAB2	2.21	UP	2.27E-20
ENSG00000134146.12	DPH6	-1.30	DOWN	2.28E-20
ENSG00000142937.12	RPS8	-1.54	DOWN	2.35E-20
ENSG00000145687.16	SSBP2	-1.02	DOWN	2.43E-20
ENSG00000175197.12	DDIT3	1.97	UP	2.53E-20
ENSG00000105939.13	ZC3HAV1	1.76	UP	2.66E-20
ENSG00000135315.12	CEP162	1.03	UP	2.80E-20
ENSG00000186431.19	FCAR	2.17	UP	2.93E-20
ENSG00000138411.13	HECW2	1.34	UP	2.95E-20
ENSG00000187325.5	TAF9B	-1.01	DOWN	3.16E-20
ENSG00000113732.9	ATP6V0E1	1.02	UP	3.46E-20
ENSG00000108298.11	RPL19	-1.27	DOWN	3.65E-20
ENSG00000171115.4	GIMAP8	1.48	UP	3.89E-20
ENSG00000188404.10	SELL	1.62	UP	3.96E-20
ENSG00000109762.16	SNX25	-1.09	DOWN	4.14E-20
ENSG00000054523.17	KIF1B	1.52	UP	4.26E-20
ENSG00000138600.10	SPPL2A	1.09	UP	4.64E-20
ENSG00000154027.19	AK5	-2.00	DOWN	4.71E-20
ENSG00000167461.12	RAB8A	1.46	UP	4.95E-20
ENSG00000150048.10	CLEC1A	2.18	UP	5.08E-20
ENSG00000137767.14	SQOR	1.68	UP	5.40E-20
ENSG00000116793.16	PHTF1	1.27	UP	5.47E-20
ENSG00000047579.20	DTNBP1	1.11	UP	5.90E-20
ENSG00000106415.13	GLCC1	-1.16	DOWN	6.28E-20
ENSG00000235750.10	KIAA0040	1.44	UP	7.42E-20
ENSG00000123983.14	ACSL3	1.53	UP	7.86E-20
ENSG00000251369.8	ZNF550	-1.05	DOWN	7.95E-20
ENSG00000143889.16	HNRNPLL	2.09	UP	7.96E-20
ENSG00000118503.15	TNFAIP3	1.24	UP	9.16E-20
ENSG00000108861.9	DUSP3	1.38	UP	9.50E-20
ENSG00000135503.13	ACVR1B	1.42	UP	9.97E-20
ENSG00000168658.19	VWA3B	3.10	UP	1.03E-19
ENSG00000070190.13	DAPP1	1.63	UP	1.04E-19
ENSG00000130303.13	BST2	2.21	UP	1.14E-19
ENSG00000163492.15	CCDC141	-1.54	DOWN	1.16E-19

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000184860.10	SDR42E1	-1.20	DOWN	1.53E-19
ENSG00000172403.11	SYNPO2	2.20	UP	1.57E-19
ENSG00000234127.9	TRIM26	1.62	UP	1.77E-19
ENSG00000154589.7	LY96	2.00	UP	1.95E-19
ENSG00000185507.21	IRF7	4.02	UP	1.99E-19
ENSG00000173212.4	MAB21L3	2.20	UP	2.02E-19
ENSG00000167601.12	AXL	3.26	UP	2.26E-19
ENSG00000106804.8	C5	1.88	UP	2.43E-19
ENSG00000163519.14	TRAT1	-1.16	DOWN	2.46E-19
ENSG00000106829.19	TLE4	1.23	UP	2.47E-19
ENSG00000154122.14	ANKH	-1.29	DOWN	2.59E-19
ENSG00000120217.14	CD274	3.53	UP	2.74E-19
ENSG00000121858.11	TNFSF10	3.02	UP	2.82E-19
ENSG00000137575.12	SDCBP	1.27	UP	2.89E-19
ENSG00000136048.14	DRAM1	1.13	UP	2.92E-19
ENSG00000082397.17	EPB41L3	1.63	UP	2.97E-19
ENSG00000134243.12	SORT1	1.51	UP	2.97E-19
ENSG00000170837.3	GPR27	1.58	UP	3.13E-19
ENSG00000160932.11	LY6E	3.59	UP	3.23E-19
ENSG00000013374.16	NUB1	1.82	UP	3.38E-19
ENSG00000125900.13	SIRPD	1.87	UP	3.45E-19
ENSG00000164713.10	BRI3	1.79	UP	3.46E-19
ENSG00000174032.17	SLC25A30	1.04	UP	3.60E-19
ENSG00000023318.8	ERP44	1.01	UP	3.66E-19
ENSG00000099204.20	ABLIM1	-1.37	DOWN	3.66E-19
ENSG00000173559.14	NABP1	1.42	UP	3.68E-19
ENSG00000140396.13	NCOA2	1.21	UP	3.75E-19
ENSG00000196684.12	HSH2D	1.79	UP	3.83E-19
ENSG00000052795.13	FNIP2	1.07	UP	3.91E-19
ENSG00000169228.14	RAB24	1.99	UP	4.39E-19
ENSG00000154736.6	ADAMTS5	-3.43	DOWN	4.53E-19
ENSG00000168610.14	STAT3	1.44	UP	5.14E-19
ENSG00000101605.13	MYOM1	1.44	UP	5.38E-19
ENSG00000173369.16	C1QB	4.17	UP	5.57E-19
ENSG00000134809.9	TIMM10	2.54	UP	5.71E-19
ENSG00000064763.11	FAR2	1.41	UP	5.78E-19
ENSG00000138434.17	ITPRID2	1.51	UP	6.07E-19
ENSG00000183831.7	ANKRD45	4.05	UP	6.98E-19
ENSG00000128604.20	IRF5	1.80	UP	7.30E-19
ENSG00000116701.15	NCF2	1.09	UP	8.72E-19

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000105402.8	NAPA	2.17	UP	8.76E-19
ENSG00000184014.8	DENND5A	1.18	UP	8.78E-19
ENSG00000082074.18	FYB1	1.48	UP	8.86E-19
ENSG00000116106.12	EPHA4	-1.43	DOWN	9.01E-19
ENSG00000137414.6	FAM8A1	1.70	UP	9.89E-19
ENSG00000113088.6	GZMK	-1.71	DOWN	1.00E-18
ENSG00000215252.11	GOLGA8B	-1.53	DOWN	1.03E-18
ENSG00000131469.15	RPL27	-1.36	DOWN	1.18E-18
ENSG00000166900.17	STX3	1.43	UP	1.33E-18
ENSG00000104972.15	LILRB1	1.57	UP	1.41E-18
ENSG00000135535.17	CD164	1.38	UP	1.42E-18
ENSG00000131979.19	GCH1	2.51	UP	1.47E-18
ENSG00000183691.6	NOG	-2.52	DOWN	1.47E-18
ENSG00000167851.15	CD300A	1.72	UP	1.55E-18
ENSG00000189067.12	LITAF	1.34	UP	1.57E-18
ENSG00000184060.11	ADAP2	1.88	UP	1.57E-18
ENSG00000156110.14	ADK	-1.20	DOWN	1.65E-18
ENSG00000186818.12	LILRB4	1.79	UP	1.66E-18
ENSG00000231767.4	AL136454.1	-1.63	DOWN	1.69E-18
ENSG00000197054.12	ZNF763	1.15	UP	1.74E-18
ENSG00000180596.7	H2BC4	1.72	UP	1.81E-18
ENSG00000173114.13	LRRN3	-2.23	DOWN	1.92E-18
ENSG00000101596.16	SMCHD1	1.45	UP	2.01E-18
ENSG00000187554.14	TLR5	2.01	UP	2.09E-18
ENSG00000163464.8	CXCR1	1.95	UP	2.42E-18
ENSG00000087589.16	CASS4	-1.58	DOWN	2.43E-18
ENSG00000182158.15	CREB3L2	1.13	UP	2.54E-18
ENSG00000170776.22	AKAP13	1.15	UP	2.85E-18
ENSG00000135900.4	MRPL44	1.28	UP	2.91E-18
ENSG00000171863.15	RPS7	-1.16	DOWN	3.33E-18
ENSG00000124374.9	PAIP2B	-1.27	DOWN	3.43E-18
ENSG00000155313.15	USP25	1.42	UP	3.46E-18
ENSG00000197646.8	PDCD1LG2	3.17	UP	3.51E-18
ENSG00000185442.13	FAM174B	2.22	UP	3.77E-18
ENSG00000116663.11	FBXO6	2.97	UP	3.94E-18
ENSG00000136634.7	IL10	2.00	UP	4.11E-18
ENSG00000163251.4	FZD5	1.59	UP	4.15E-18
ENSG00000196778.3	OR52K1	1.84	UP	4.24E-18
ENSG00000114423.23	CBLB	-1.11	DOWN	4.25E-18
ENSG00000171700.14	RGS19	1.11	UP	4.25E-18

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000171476.22	HOPX	-1.59	DOWN	4.41E-18
ENSG00000156273.16	BACH1	1.13	UP	4.54E-18
ENSG00000198932.13	GPRASP1	-1.26	DOWN	4.66E-18
ENSG00000170909.13	OSCAR	1.92	UP	4.85E-18
ENSG00000197296.6	FITM2	-1.72	DOWN	5.05E-18
ENSG00000137449.16	CPEB2	1.50	UP	5.88E-18
ENSG00000106605.11	BLVRA	1.52	UP	6.54E-18
ENSG00000162654.9	GBP4	2.51	UP	7.26E-18
ENSG00000120832.10	MTERF2	-1.22	DOWN	7.89E-18
ENSG00000189007.16	ADAT2	-1.33	DOWN	8.46E-18
ENSG00000064999.15	ANKS1A	1.06	UP	8.48E-18
ENSG00000166340.17	TPP1	1.40	UP	8.49E-18
ENSG00000134532.19	SOX5	-1.89	DOWN	8.86E-18
ENSG00000106100.11	NOD1	1.49	UP	8.91E-18
ENSG00000150938.10	CRIM1	-1.32	DOWN	9.10E-18
ENSG00000132475.10	H3-3B	1.48	UP	9.16E-18
ENSG00000169180.11	XPO6	1.29	UP	1.01E-17
ENSG00000136026.14	CKAP4	1.22	UP	1.02E-17
ENSG00000168461.13	RAB31	1.13	UP	1.17E-17
ENSG00000124203.6	ZNF831	-1.25	DOWN	1.19E-17
ENSG00000113369.9	ARRDC3	1.32	UP	1.19E-17
ENSG00000164114.19	MAP9	-1.26	DOWN	1.25E-17
ENSG00000197063.11	MAFG	1.51	UP	1.45E-17
ENSG00000150977.10	RILPL2	1.27	UP	1.64E-17
ENSG00000035115.22	SH3YL1	-1.06	DOWN	1.72E-17
ENSG00000265972.6	TXNIP	1.13	UP	1.76E-17
ENSG00000182389.19	CACNB4	-2.11	DOWN	1.77E-17
ENSG00000173120.15	KDM2A	1.02	UP	1.80E-17
ENSG00000101846.8	STS	1.25	UP	1.85E-17
ENSG00000164430.16	CGAS	1.52	UP	1.95E-17
ENSG00000138670.17	RASGEF1B	1.55	UP	2.11E-17
ENSG00000136161.12	RCBTB2	1.16	UP	2.15E-17
ENSG00000112062.10	MAPK14	1.48	UP	2.16E-17
ENSG00000112367.11	FIG4	1.13	UP	2.23E-17
ENSG00000163625.15	WDFY3	1.41	UP	2.36E-17
ENSG00000178965.14	ERICH3	2.74	UP	2.41E-17
ENSG00000151490.15	PTPRO	1.19	UP	2.45E-17
ENSG00000133961.20	NUMB	1.04	UP	2.50E-17
ENSG00000183134.5	PTGDR2	-3.64	DOWN	2.57E-17
ENSG00000069667.16	RORA	-1.05	DOWN	2.72E-17

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000145247.12	OCIAD2	-1.11	DOWN	2.82E-17
ENSG00000100473.18	COCH	-1.77	DOWN	2.97E-17
ENSG00000168404.13	MLKL	1.64	UP	3.09E-17
ENSG00000215114.10	UBXN2B	1.15	UP	3.12E-17
ENSG00000105492.16	SIGLEC6	-1.82	DOWN	3.29E-17
ENSG00000154803.13	FLCN	1.48	UP	3.34E-17
ENSG00000148572.16	NRBF2	1.30	UP	3.44E-17
ENSG00000182782.8	HCAR2	2.06	UP	3.66E-17
ENSG00000172216.6	CEBPB	1.37	UP	3.83E-17
ENSG00000198216.12	CACNA1E	2.29	UP	4.06E-17
ENSG00000213928.9	IRF9	1.29	UP	4.06E-17
ENSG00000133818.14	RRAS2	-1.08	DOWN	4.19E-17
ENSG00000114698.15	PLSCR4	2.62	UP	5.28E-17
ENSG00000138336.9	TET1	-1.14	DOWN	5.31E-17
ENSG00000118420.17	UBE3D	-1.16	DOWN	5.47E-17
ENSG00000140743.8	CDR2	-1.04	DOWN	6.00E-17
ENSG00000138795.10	LEF1	-1.51	DOWN	6.28E-17
ENSG00000173258.13	ZNF483	-1.47	DOWN	6.31E-17
ENSG00000151470.13	C4orf33	1.23	UP	6.33E-17
ENSG00000111321.11	LTBR	1.32	UP	6.56E-17
ENSG00000196123.13	KIAA0895L	3.36	UP	7.09E-17
ENSG00000120784.16	ZFP30	-1.06	DOWN	7.22E-17
ENSG00000075151.20	EIF4G3	1.35	UP	7.36E-17
ENSG00000107796.13	ACTA2	2.34	UP	7.43E-17
ENSG00000102743.15	SLC25A15	-1.30	DOWN	8.44E-17
ENSG00000030419.16	IKZF2	-1.28	DOWN	8.57E-17
ENSG00000167208.15	SNX20	1.12	UP	8.92E-17
ENSG00000082898.17	XPO1	1.04	UP	1.01E-16
ENSG00000082293.13	COL19A1	-1.78	DOWN	1.07E-16
ENSG00000179630.11	LACC1	1.21	UP	1.14E-16
ENSG00000164241.13	C5orf63	-1.12	DOWN	1.23E-16
ENSG00000084234.17	APLP2	1.06	UP	1.26E-16
ENSG00000151726.14	ACSL1	1.84	UP	1.26E-16
ENSG00000241399.7	CD302	-1.16	DOWN	1.40E-16
ENSG00000204116.11	CHIC1	-1.04	DOWN	1.42E-16
ENSG00000159399.10	HK2	1.20	UP	1.53E-16
ENSG00000203747.11	FCGR3A	1.70	UP	1.56E-16
ENSG00000168028.14	RPSA	-1.36	DOWN	1.61E-16
ENSG00000169248.13	CXCL11	3.59	UP	1.62E-16
ENSG00000186260.17	MRTFB	-1.23	DOWN	1.67E-16

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000128335.14	APOL2	1.94	UP	1.71E-16
ENSG00000071082.11	RPL31	-1.08	DOWN	1.71E-16
ENSG00000181847.12	TIGIT	-1.19	DOWN	1.72E-16
ENSG00000182899.17	RPL35A	-1.14	DOWN	1.76E-16
ENSG00000187741.15	FANCA	1.97	UP	1.77E-16
ENSG00000204267.16	TAP2	1.56	UP	1.97E-16
ENSG00000116771.6	AGMAT	-1.59	DOWN	2.05E-16
ENSG00000186854.11	TRABD2A	-1.74	DOWN	2.10E-16
ENSG00000124102.5	PI3	-4.05	DOWN	2.21E-16
ENSG00000134827.8	TCN1	2.12	UP	2.21E-16
ENSG00000213809.9	KLRK1	-1.42	DOWN	2.25E-16
ENSG00000173193.15	PARP14	2.11	UP	2.38E-16
ENSG00000198673.10	TAF2	1.61	UP	2.38E-16
ENSG00000189060.5	H1-0	1.71	UP	2.47E-16
ENSG00000182240.16	BACE2	-1.99	DOWN	2.47E-16
ENSG00000102524.11	TNFSF13B	2.61	UP	2.48E-16
ENSG00000177409.12	SAMD9L	2.70	UP	2.48E-16
ENSG00000125691.14	RPL23	-1.41	DOWN	2.50E-16
ENSG00000133574.10	GIMAP4	1.33	UP	2.52E-16
ENSG00000073737.16	DHRS9	1.87	UP	2.57E-16
ENSG00000129682.16	FGF13	2.49	UP	2.63E-16
ENSG00000198160.14	MIER1	1.20	UP	2.63E-16
ENSG00000166527.8	CLEC4D	1.92	UP	2.64E-16
ENSG00000099139.14	PCSK5	-1.07	DOWN	2.72E-16
ENSG00000091106.19	NLRC4	1.35	UP	2.76E-16
ENSG00000168310.11	IRF2	1.26	UP	3.25E-16
ENSG00000137275.14	RIPK1	1.06	UP	3.27E-16
ENSG00000114745.13	GORASP1	1.41	UP	3.35E-16
ENSG00000076554.15	TPD52	-1.21	DOWN	3.41E-16
ENSG00000175928.6	LRRN1	2.22	UP	3.43E-16
ENSG00000144645.14	OSBPL10	-1.55	DOWN	3.66E-16
ENSG00000197705.10	KLHL14	-1.48	DOWN	3.95E-16
ENSG00000198034.11	RPS4X	-1.44	DOWN	4.08E-16
ENSG00000164109.14	MAD2L1	-1.22	DOWN	4.16E-16
ENSG00000101695.9	RNF125	-1.03	DOWN	4.50E-16
ENSG00000148926.10	ADM	2.54	UP	4.61E-16
ENSG00000125779.22	PANK2	1.13	UP	4.66E-16
ENSG00000167995.17	BEST1	1.17	UP	4.77E-16
ENSG00000148737.17	TCF7L2	1.37	UP	4.96E-16
ENSG00000102218.6	RP2	1.25	UP	4.98E-16

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000125753.14	VASP	1.29	UP	5.26E-16
ENSG00000074621.14	SLC24A1	2.86	UP	5.91E-16
ENSG00000133313.15	CNDP2	1.36	UP	5.92E-16
ENSG00000152380.10	FAM151B	1.28	UP	6.37E-16
ENSG00000109084.14	TMEM97	-1.26	DOWN	6.39E-16
ENSG00000164825.4	DEFB1	4.80	UP	6.44E-16
ENSG00000163932.15	PRKCD	2.19	UP	6.45E-16
ENSG00000161133.16	USP41	3.23	UP	7.12E-16
ENSG00000244734.4	HBB	3.68	UP	7.66E-16
ENSG00000166002.7	SMCO4	1.52	UP	8.28E-16
ENSG00000115318.12	LOXL3	1.67	UP	8.63E-16
ENSG00000129465.16	RIPK3	1.58	UP	8.83E-16
ENSG00000282988.2	AL031777.2	1.97	UP	9.00E-16
ENSG00000026950.17	BTN3A1	1.18	UP	9.46E-16
ENSG00000188895.12	MSL1	1.07	UP	9.55E-16
ENSG00000184898.7	RBM43	1.65	UP	9.98E-16
ENSG00000144354.14	CDCA7	-1.02	DOWN	1.01E-15
ENSG00000198780.12	FAM169A	-1.26	DOWN	1.04E-15
ENSG00000166405.15	RIC3	-1.26	DOWN	1.06E-15
ENSG00000196172.9	ZNF681	-1.08	DOWN	1.13E-15
ENSG00000144118.14	RALB	1.56	UP	1.19E-15
ENSG00000113742.14	CPEB4	1.12	UP	1.23E-15
ENSG00000221955.10	SLC12A8	2.67	UP	1.34E-15
ENSG00000285231.1	OOSP3	2.48	UP	1.37E-15
ENSG00000140044.13	JDP2	1.04	UP	1.41E-15
ENSG00000106392.11	C1GALT1	1.57	UP	1.43E-15
ENSG00000164398.15	ACSL6	-1.22	DOWN	1.44E-15
ENSG00000134954.14	ETS1	-1.09	DOWN	1.59E-15
ENSG00000171049.9	FPR2	1.65	UP	1.81E-15
ENSG00000124226.11	RNF114	1.12	UP	1.95E-15
ENSG00000152242.11	C18orf25	1.25	UP	1.97E-15
ENSG00000131873.7	CHSY1	1.43	UP	1.99E-15
ENSG00000164096.13	C4orf3	1.39	UP	2.02E-15
ENSG00000285444.1	AL162377.3	1.88	UP	2.07E-15
ENSG00000174125.8	TLR1	1.13	UP	2.08E-15
ENSG00000183690.13	EFHC2	-1.43	DOWN	2.17E-15
ENSG00000143384.13	MCL1	1.11	UP	2.19E-15
ENSG00000169245.6	CXCL10	3.94	UP	2.26E-15
ENSG00000141040.15	ZNF287	-1.16	DOWN	2.54E-15
ENSG00000128594.8	LRRC4	1.15	UP	2.55E-15

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000122025.15	FLT3	1.44	UP	2.56E-15
ENSG00000144655.15	CSRNP1	2.53	UP	2.70E-15
ENSG00000102554.14	KLF5	2.18	UP	2.77E-15
ENSG00000174500.13	GCSAM	-1.35	DOWN	2.79E-15
ENSG00000165682.14	CLEC1B	1.45	UP	2.99E-15
ENSG00000082996.19	RNF13	1.29	UP	3.05E-15
ENSG00000104375.17	STK3	1.59	UP	3.09E-15
ENSG00000169896.18	ITGAM	1.20	UP	3.14E-15
ENSG00000188107.15	EYS	1.64	UP	3.20E-15
ENSG00000083937.9	CHMP2B	1.05	UP	3.29E-15
ENSG00000137154.13	RPS6	-1.48	DOWN	3.31E-15
ENSG00000157654.19	PALM2AKAP2	1.71	UP	3.36E-15
ENSG00000134321.12	RSAD2	4.00	UP	3.52E-15
ENSG00000187475.6	H1-6	2.46	UP	3.69E-15
ENSG00000168675.18	LDLRAD4	-1.03	DOWN	3.80E-15
ENSG00000096060.14	FKBP5	1.57	UP	3.85E-15
ENSG00000177628.16	GBA	1.84	UP	4.13E-15
ENSG00000204388.7	HSPA1B	2.04	UP	4.43E-15
ENSG00000137959.16	IFI44L	3.61	UP	4.48E-15
ENSG00000253276.4	CCDC71L	1.39	UP	4.48E-15
ENSG00000095383.20	TBC1D2	1.61	UP	4.67E-15
ENSG00000078596.11	ITM2A	-1.41	DOWN	4.84E-15
ENSG00000077420.16	APBB1IP	1.20	UP	4.90E-15
ENSG00000143110.11	C1orf162	1.07	UP	5.03E-15
ENSG00000011422.12	PLAUR	1.76	UP	5.08E-15
ENSG00000062716.13	VMP1	1.05	UP	5.23E-15
ENSG00000105339.10	DENND3	1.19	UP	5.36E-15
ENSG00000107566.14	ERLIN1	1.24	UP	5.81E-15
ENSG00000132510.10	KDM6B	1.32	UP	5.85E-15
ENSG00000114770.17	ABCC5	-1.16	DOWN	6.17E-15
ENSG00000179021.10	C3orf38	1.18	UP	6.35E-15
ENSG00000114127.10	XRN1	1.87	UP	6.58E-15
ENSG00000120899.18	PTK2B	1.48	UP	6.79E-15
ENSG00000139083.11	ETV6	1.22	UP	6.87E-15
ENSG00000198556.14	ZNF789	-1.01	DOWN	6.96E-15
ENSG00000173198.6	CYSLTR1	1.02	UP	7.73E-15
ENSG00000140391.15	TSPAN3	-1.00	DOWN	8.11E-15
ENSG00000133943.20	DGLUCY	1.45	UP	8.21E-15
ENSG00000115415.20	STAT1	1.74	UP	8.47E-15
ENSG00000166523.8	CLEC4E	1.52	UP	8.52E-15

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000111796.4	KLRB1	-1.69	DOWN	8.55E-15
ENSG00000180479.14	ZNF571	-1.07	DOWN	8.57E-15
ENSG00000102794.10	ACOD1	3.51	UP	8.70E-15
ENSG00000101347.10	SAMHD1	1.38	UP	8.84E-15
ENSG00000164649.20	CDCA7L	-1.21	DOWN	9.41E-15
ENSG00000008086.13	CDKL5	1.00	UP	9.53E-15
ENSG00000184557.4	SOCS3	2.30	UP	9.68E-15
ENSG00000119655.11	NPC2	1.34	UP	1.02E-14
ENSG00000103064.15	SLC7A6	-1.09	DOWN	1.15E-14
ENSG00000073803.14	MAP3K13	1.20	UP	1.22E-14
ENSG00000110077.14	MS4A6A	1.07	UP	1.22E-14
ENSG00000089041.17	P2RX7	1.16	UP	1.24E-14
ENSG00000164124.11	TMEM144	1.18	UP	1.29E-14
ENSG00000198604.11	BAZ1A	1.51	UP	1.39E-14
ENSG00000129467.13	ADCY4	2.48	UP	1.47E-14
ENSG00000102034.17	ELF4	1.60	UP	1.49E-14
ENSG00000243667.7	WDR92	-1.02	DOWN	1.59E-14
ENSG00000204147.10	ASAH2B	-1.30	DOWN	1.70E-14
ENSG00000183735.10	TBK1	1.08	UP	1.77E-14
ENSG00000163412.13	EIF4E3	1.31	UP	1.85E-14
ENSG00000100644.17	HIF1A	1.15	UP	1.86E-14
ENSG00000165060.14	FXN	-1.07	DOWN	1.91E-14
ENSG00000076685.18	NT5C2	1.35	UP	2.23E-14
ENSG00000136014.12	USP44	-1.52	DOWN	2.30E-14
ENSG00000147697.9	GSDMC	2.45	UP	2.41E-14
ENSG00000100266.19	PACSIN2	1.11	UP	2.54E-14
ENSG00000163563.8	MNDA	1.18	UP	2.55E-14
ENSG00000109475.16	RPL34	-1.19	DOWN	2.63E-14
ENSG00000079277.21	MKKN1	1.27	UP	2.81E-14
ENSG00000117322.18	CR2	-1.55	DOWN	2.95E-14
ENSG00000102081.15	FMR1	1.19	UP	3.04E-14
ENSG00000059758.8	CDK17	1.28	UP	3.10E-14
ENSG00000181634.8	TNFSF15	2.00	UP	3.15E-14
ENSG00000204577.11	LILRB3	1.80	UP	3.23E-14
ENSG00000138439.12	FAM117B	-1.12	DOWN	3.54E-14
ENSG00000136231.14	IGF2BP3	1.41	UP	3.56E-14
ENSG00000139572.4	GPR84	2.11	UP	3.59E-14
ENSG00000159445.13	THEM4	-1.28	DOWN	3.67E-14
ENSG00000125844.16	RRBP1	1.57	UP	3.70E-14
ENSG00000120306.11	CYSTM1	2.48	UP	3.80E-14

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000110057.8	UNC93B1	2.41	UP	3.87E-14
ENSG00000115687.14	PASK	-1.53	DOWN	3.99E-14
ENSG00000148154.10	UGCG	1.22	UP	4.16E-14
ENSG00000125538.12	IL1B	1.70	UP	4.65E-14
ENSG00000058056.9	USP13	-1.13	DOWN	4.67E-14
ENSG00000182541.18	LIMK2	1.77	UP	5.05E-14
ENSG00000136040.9	PLXNC1	1.01	UP	5.22E-14
ENSG00000065911.12	MTHFD2	1.27	UP	5.40E-14
ENSG00000116157.6	GPX7	-1.33	DOWN	5.80E-14
ENSG00000102445.18	RUBCNL	-1.05	DOWN	6.45E-14
ENSG00000163682.16	RPL9	-1.41	DOWN	6.56E-14
ENSG00000145819.18	ARHGAP26	1.16	UP	6.59E-14
ENSG00000137502.10	RAB30	-1.21	DOWN	6.66E-14
ENSG00000122432.18	SPATA1	1.53	UP	6.89E-14
ENSG00000153064.12	BANK1	-1.18	DOWN	6.94E-14
ENSG00000156500.15	FAM122C	1.52	UP	7.11E-14
ENSG00000116016.14	EPAS1	1.92	UP	7.12E-14
ENSG00000185885.16	IFITM1	2.59	UP	7.35E-14
ENSG00000173200.13	PARP15	-1.03	DOWN	7.38E-14
ENSG00000151623.15	NR3C2	-1.20	DOWN	7.46E-14
ENSG00000172493.21	AFF1	1.57	UP	7.58E-14
ENSG00000005302.19	MSL3	1.08	UP	7.68E-14
ENSG00000152926.15	ZNF117	1.43	UP	7.79E-14
ENSG00000185338.6	SOCS1	3.06	UP	7.82E-14
ENSG00000180509.12	KCNE1	2.01	UP	8.05E-14
ENSG00000188559.15	RALGAPA2	1.20	UP	8.20E-14
ENSG00000198133.8	TMEM229B	1.76	UP	8.40E-14
ENSG00000131203.13	IDO1	3.72	UP	8.96E-14
ENSG00000127995.17	CASD1	-1.02	DOWN	9.23E-14
ENSG00000113916.18	BCL6	1.53	UP	9.30E-14
ENSG00000177600.9	RPLP2	-1.13	DOWN	9.56E-14
ENSG00000019169.10	MARCO	2.32	UP	9.57E-14
ENSG00000072110.13	ACTN1	1.08	UP	1.09E-13
ENSG00000240065.8	PSMB9	1.32	UP	1.10E-13
ENSG00000152818.18	UTRN	1.05	UP	1.12E-13
ENSG00000136960.12	ENPP2	1.61	UP	1.16E-13
ENSG00000139173.10	TMEM117	-1.31	DOWN	1.63E-13
ENSG00000173372.17	C1QA	3.43	UP	1.64E-13
ENSG00000206503.13	HLA-A	1.31	UP	1.68E-13
ENSG00000139505.11	MTMR6	1.00	UP	1.71E-13

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000108474.17	PIGL	-1.05	DOWN	1.73E-13
ENSG00000095794.19	CREM	1.34	UP	1.79E-13
ENSG00000127952.17	STYXL1	1.38	UP	1.87E-13
ENSG00000155657.27	TTN	-1.27	DOWN	1.92E-13
ENSG00000157551.19	KCNJ15	1.68	UP	1.94E-13
ENSG00000188897.9	AC099489.1	2.16	UP	2.05E-13
ENSG00000196683.10	TOMM7	-1.04	DOWN	2.10E-13
ENSG00000101577.9	LPIN2	1.23	UP	2.11E-13
ENSG00000234745.11	HLA-B	1.23	UP	2.26E-13
ENSG00000205927.5	OLIG2	-4.16	DOWN	2.27E-13
ENSG00000159228.13	CBR1	1.49	UP	2.41E-13
ENSG00000168661.14	ZNF30	-1.12	DOWN	2.56E-13
ENSG00000021355.13	SERPINB1	1.28	UP	2.57E-13
ENSG00000164327.13	RICTOR	1.18	UP	2.58E-13
ENSG00000176055.10	MBLAC2	-1.06	DOWN	2.76E-13
ENSG00000134108.13	ARL8B	1.03	UP	3.05E-13
ENSG00000126858.18	RHOT1	1.05	UP	3.30E-13
ENSG00000139832.5	RAB20	1.75	UP	3.36E-13
ENSG00000117228.10	GBP1	2.60	UP	3.51E-13
ENSG00000196381.11	ZNF781	-1.28	DOWN	3.51E-13
ENSG00000161905.13	ALOX15	-3.90	DOWN	3.56E-13
ENSG00000038945.15	MSR1	2.67	UP	3.83E-13
ENSG00000118515.11	SGK1	-1.31	DOWN	4.05E-13
ENSG00000118513.19	MYB	-1.03	DOWN	4.37E-13
ENSG00000114450.10	GNB4	1.43	UP	4.47E-13
ENSG00000213347.10	MXD3	1.77	UP	4.67E-13
ENSG00000121064.13	SCPEP1	1.02	UP	4.73E-13
ENSG00000175414.7	ARL10	-1.30	DOWN	4.88E-13
ENSG00000184924.5	PTRHD1	-1.12	DOWN	5.05E-13
ENSG00000085449.15	WDFY1	1.61	UP	5.31E-13
ENSG00000100084.14	HIRA	1.26	UP	5.59E-13
ENSG00000167565.13	SERTAD3	1.31	UP	5.83E-13
ENSG00000120051.15	CFAP58	1.68	UP	6.07E-13
ENSG00000183347.15	GBP6	2.75	UP	6.30E-13
ENSG00000161929.15	SCIMP	1.18	UP	6.33E-13
ENSG00000170456.16	DENND5B	-1.08	DOWN	6.43E-13
ENSG00000150961.15	SEC24D	1.26	UP	6.69E-13
ENSG00000170846.17	AC093323.1	-1.02	DOWN	6.71E-13
ENSG00000164587.13	RPS14	-1.38	DOWN	6.81E-13
ENSG00000111863.12	ADTRP	-1.66	DOWN	6.93E-13

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000099985.4	OSM	2.30	UP	7.08E-13
ENSG00000116711.10	PLA2G4A	1.12	UP	7.33E-13
ENSG00000111879.20	FAM184A	-1.47	DOWN	7.54E-13
ENSG00000104626.15	ERI1	1.30	UP	7.63E-13
ENSG00000108932.12	SLC16A6	1.13	UP	7.74E-13
ENSG00000025708.14	TYMP	1.86	UP	8.04E-13
ENSG00000105835.12	NAMPT	1.51	UP	8.36E-13
ENSG00000152229.18	PSTPIP2	1.82	UP	8.50E-13
ENSG00000181016.9	LSMEM1	1.23	UP	8.74E-13
ENSG00000197081.14	IGF2R	1.25	UP	8.75E-13
ENSG00000176595.4	KBTBD11	-1.09	DOWN	9.27E-13
ENSG00000134419.15	RPS15A	-1.13	DOWN	9.79E-13
ENSG00000115896.16	PLCL1	-1.06	DOWN	1.09E-12
ENSG00000185262.9	UBALD2	1.44	UP	1.11E-12
ENSG00000144935.15	TRPC1	-1.32	DOWN	1.17E-12
ENSG00000123095.6	BHLHE41	-1.76	DOWN	1.20E-12
ENSG00000187116.14	LILRA5	2.34	UP	1.34E-12
ENSG00000172116.23	CD8B	-1.63	DOWN	1.37E-12
ENSG00000154305.18	MIA3	1.21	UP	1.50E-12
ENSG00000135604.10	STX11	1.73	UP	1.52E-12
ENSG00000197903.8	H2BC12	1.14	UP	1.57E-12
ENSG00000123700.5	KCNJ2	1.54	UP	1.64E-12
ENSG00000129824.16	RPS4Y1	-1.15	DOWN	1.75E-12
ENSG00000179331.3	RAB39A	1.60	UP	1.77E-12
ENSG00000181789.14	COPG1	1.19	UP	1.97E-12
ENSG00000083223.18	TUT7	1.02	UP	2.03E-12
ENSG00000115129.14	TP53I3	1.74	UP	2.05E-12
ENSG00000197013.10	ZNF429	1.17	UP	2.18E-12
ENSG00000168646.13	AXIN2	-1.48	DOWN	2.31E-12
ENSG00000086730.17	LAT2	1.15	UP	2.41E-12
ENSG00000074410.14	CA12	2.25	UP	2.41E-12
ENSG00000169432.18	SCN9A	1.38	UP	2.49E-12
ENSG00000147180.16	ZNF711	-1.21	DOWN	2.50E-12
ENSG00000226479.4	TMEM185B	1.46	UP	2.52E-12
ENSG00000196873.15	CBWD3	1.16	UP	2.56E-12
ENSG00000149273.15	RPS3	-1.23	DOWN	2.61E-12
ENSG00000124222.22	STX16	1.19	UP	2.65E-12
ENSG00000163235.16	TGFA	1.34	UP	2.68E-12
ENSG00000035720.8	STAP1	1.62	UP	2.73E-12
ENSG00000152990.14	ADGRA3	-1.29	DOWN	2.90E-12

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000135821.19	GLUL	1.06	UP	2.91E-12
ENSG00000169435.14	RASSF6	-1.64	DOWN	3.00E-12
ENSG00000231925.12	TAPBP	1.11	UP	3.06E-12
ENSG00000111846.18	GCNT2	1.21	UP	3.12E-12
ENSG00000170464.10	DNAJC18	-1.13	DOWN	3.14E-12
ENSG00000119514.7	GALNT12	-1.15	DOWN	3.16E-12
ENSG00000111261.14	MANSC1	1.30	UP	3.18E-12
ENSG00000157456.8	CCNB2	-1.38	DOWN	3.19E-12
ENSG00000175073.8	VCPIP1	1.20	UP	3.21E-12
ENSG00000198846.6	TOX	-1.06	DOWN	3.31E-12
ENSG00000167065.13	DUSP18	1.23	UP	3.43E-12
ENSG00000101084.18	RAB5IF	1.13	UP	3.55E-12
ENSG00000122122.10	SASH3	1.39	UP	3.59E-12
ENSG00000167536.14	DHRS13	1.58	UP	3.60E-12
ENSG00000216490.4	IFI30	1.98	UP	3.63E-12
ENSG00000135426.16	TESPA1	-1.02	DOWN	3.64E-12
ENSG00000196663.16	TECPR2	1.42	UP	3.93E-12
ENSG00000105366.15	SIGLEC8	-3.65	DOWN	4.08E-12
ENSG00000080986.13	NDC80	1.30	UP	4.33E-12
ENSG00000134897.14	BIVM	-1.12	DOWN	4.54E-12
ENSG00000100462.16	PRMT5	1.29	UP	5.27E-12
ENSG00000170509.12	HSD17B13	1.40	UP	5.32E-12
ENSG00000138385.16	SSB	1.27	UP	5.41E-12
ENSG00000221963.6	APOL6	1.99	UP	5.43E-12
ENSG00000144848.11	ATG3	1.27	UP	5.61E-12
ENSG00000185947.15	ZNF267	1.14	UP	5.62E-12
ENSG00000042980.13	ADAM28	-1.15	DOWN	5.79E-12
ENSG00000100226.16	GTPBP1	1.77	UP	5.89E-12
ENSG00000100368.14	CSF2RB	1.47	UP	5.99E-12
ENSG00000198019.13	FCGR1B	2.14	UP	6.28E-12
ENSG00000106560.11	GIMAP2	1.22	UP	6.29E-12
ENSG00000035499.13	DEPDC1B	-1.00	DOWN	6.39E-12
ENSG00000197324.9	LRP10	1.30	UP	6.62E-12
ENSG00000167210.17	LOXHD1	1.98	UP	6.68E-12
ENSG00000089220.5	PEBP1	-1.08	DOWN	6.79E-12
ENSG00000165006.14	UBAP1	1.00	UP	6.86E-12
ENSG00000112137.17	PHACTR1	1.40	UP	6.88E-12
ENSG00000158079.16	PTPDC1	-1.03	DOWN	7.44E-12
ENSG00000103319.12	EEF2K	-1.31	DOWN	8.00E-12
ENSG00000104312.8	RIPK2	1.36	UP	8.27E-12

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000156738.18	MS4A1	-1.26	DOWN	8.48E-12
ENSG00000174749.6	FAM241A	1.43	UP	8.52E-12
ENSG00000136682.15	CBWD2	1.31	UP	8.86E-12
ENSG00000181963.5	OR52K2	2.16	UP	9.39E-12
ENSG00000136866.13	ZFP37	-1.23	DOWN	9.41E-12
ENSG00000158882.15	TOMM40L	1.28	UP	9.43E-12
ENSG00000143753.13	DEGS1	1.11	UP	9.85E-12
ENSG00000197818.11	SLC9A8	1.06	UP	1.10E-11
ENSG00000135960.10	EDAR	-1.77	DOWN	1.11E-11
ENSG00000146243.14	IRAK1BP1	-1.17	DOWN	1.16E-11
ENSG00000105355.9	PLIN3	1.38	UP	1.19E-11
ENSG00000085563.15	ABCB1	-1.02	DOWN	1.19E-11
ENSG00000163534.15	FCRL1	-1.41	DOWN	1.21E-11
ENSG00000137720.8	C11orf1	-1.16	DOWN	1.21E-11
ENSG00000183049.12	CAMK1D	-1.41	DOWN	1.23E-11
ENSG00000164342.13	TLR3	1.35	UP	1.24E-11
ENSG00000092295.12	TGM1	3.54	UP	1.37E-11
ENSG00000100220.12	RTCB	1.06	UP	1.56E-11
ENSG00000164111.15	ANXA5	1.10	UP	1.62E-11
ENSG00000148175.13	STOM	1.06	UP	1.69E-11
ENSG00000154188.10	ANGPT1	-1.63	DOWN	1.77E-11
ENSG00000163739.5	CXCL1	1.13	UP	1.81E-11
ENSG00000138772.13	ANXA3	2.42	UP	1.82E-11
ENSG00000174469.23	CNTNAP2	-1.88	DOWN	1.84E-11
ENSG00000188997.8	KCTD21	1.13	UP	1.85E-11
ENSG00000166128.13	RAB8B	1.00	UP	1.85E-11
ENSG00000243649.9	CFB	3.31	UP	1.90E-11
ENSG00000175550.8	DRAP1	1.43	UP	1.91E-11
ENSG00000182621.18	PLCB1	-1.28	DOWN	1.95E-11
ENSG00000178927.18	CYBC1	1.29	UP	1.97E-11
ENSG00000187944.3	C2orf66	2.28	UP	2.00E-11
ENSG00000082438.17	COBLL1	-1.17	DOWN	2.00E-11
ENSG00000175265.17	GOLGA8A	-1.44	DOWN	2.00E-11
ENSG00000185875.13	THNSL1	-1.08	DOWN	2.21E-11
ENSG00000114739.14	ACVR2B	-1.13	DOWN	2.44E-11
ENSG00000151320.11	AKAP6	-1.64	DOWN	2.46E-11
ENSG00000134765.10	DSC1	-1.71	DOWN	2.73E-11
ENSG00000092200.12	RPGRIP1	-1.30	DOWN	2.82E-11
ENSG00000112576.13	CCND3	1.08	UP	2.93E-11
ENSG00000118181.11	RPS25	-1.20	DOWN	2.93E-11

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000102796.11	DHRS12	1.54	UP	2.94E-11
ENSG00000121316.11	PLBD1	1.03	UP	2.96E-11
ENSG00000064601.19	CTSA	1.36	UP	2.96E-11
ENSG00000265817.4	FSBP	-1.61	DOWN	2.98E-11
ENSG00000119661.15	DNAL1	-1.03	DOWN	3.16E-11
ENSG00000183019.7	MCEMP1	2.74	UP	3.21E-11
ENSG00000090339.9	ICAM1	1.57	UP	3.26E-11
ENSG00000148450.13	MSRB2	1.22	UP	3.46E-11
ENSG00000068366.20	ACSL4	1.18	UP	3.50E-11
ENSG00000205730.6	ITPRIPL2	1.13	UP	3.58E-11
ENSG00000176273.15	SLC35G1	-1.03	DOWN	3.61E-11
ENSG00000254415.3	SIGLEC14	2.32	UP	3.61E-11
ENSG00000197249.14	SERPINA1	1.59	UP	3.81E-11
ENSG00000136999.5	CCN3	-1.93	DOWN	3.97E-11
ENSG00000204525.16	HLA-C	1.60	UP	4.00E-11
ENSG00000171649.12	ZIK1	-1.07	DOWN	4.16E-11
ENSG00000177954.14	RPS27	-1.33	DOWN	4.17E-11
ENSG00000005187.12	ACSM3	-1.08	DOWN	4.26E-11
ENSG00000185896.11	LAMP1	1.01	UP	4.50E-11
ENSG00000204856.12	FAM216A	-1.06	DOWN	4.56E-11
ENSG00000141293.16	SKAP1	-1.01	DOWN	4.60E-11
ENSG00000175643.10	RMI2	1.64	UP	4.77E-11
ENSG00000243646.10	IL10RB	1.05	UP	4.78E-11
ENSG00000135077.9	HAVCR2	1.01	UP	4.79E-11
ENSG00000173442.13	EHBP1L1	1.22	UP	4.89E-11
ENSG00000169660.16	HEXD	1.25	UP	5.01E-11
ENSG00000121691.7	CAT	-1.04	DOWN	5.21E-11
ENSG00000231500.7	RPS18	-1.54	DOWN	5.56E-11
ENSG00000118162.14	KPTN	2.01	UP	5.56E-11
ENSG00000165555.9	NOXRED1	1.13	UP	5.59E-11
ENSG00000157168.20	NRG1	-2.60	DOWN	5.79E-11
ENSG00000163053.11	SLC16A14	-1.98	DOWN	6.01E-11
ENSG00000109654.15	TRIM2	-1.25	DOWN	6.55E-11
ENSG00000239998.6	LILRA2	1.30	UP	6.55E-11
ENSG00000265118.5	AC134669.1	1.47	UP	6.69E-11
ENSG00000183696.14	UPP1	1.24	UP	6.89E-11
ENSG00000134489.7	HRH4	-1.56	DOWN	7.34E-11
ENSG00000186517.14	ARHGAP30	1.06	UP	7.64E-11
ENSG00000137054.16	POLR1E	-1.03	DOWN	7.71E-11
ENSG00000170962.13	PDGFD	-1.26	DOWN	7.72E-11

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000198900.6	TOP1	1.02	UP	7.81E-11
ENSG00000137364.5	TPMT	1.01	UP	8.19E-11
ENSG00000163644.15	PPM1K	1.14	UP	8.28E-11
ENSG00000089157.16	RPLP0	-1.57	DOWN	8.64E-11
ENSG00000112486.16	CCR6	-1.19	DOWN	8.95E-11
ENSG00000204439.4	C6orf47	1.05	UP	9.56E-11
ENSG00000153208.17	MERTK	1.86	UP	9.61E-11
ENSG00000157350.13	ST3GAL2	1.17	UP	9.81E-11
ENSG00000197978.9	GOLGA6L9	-1.23	DOWN	1.03E-10
ENSG00000119535.18	CSF3R	1.26	UP	1.04E-10
ENSG00000086061.16	DNAJA1	1.25	UP	1.04E-10
ENSG00000135506.16	OS9	1.08	UP	1.05E-10
ENSG00000221869.5	CEBPD	1.29	UP	1.11E-10
ENSG00000062194.16	GPBP1	1.01	UP	1.14E-10
ENSG00000167286.9	CD3D	-1.41	DOWN	1.24E-10
ENSG00000110944.9	IL23A	-2.15	DOWN	1.24E-10
ENSG00000171812.13	COL8A2	1.73	UP	1.27E-10
ENSG00000122862.5	SRGN	1.15	UP	1.28E-10
ENSG00000106772.18	PRUNE2	2.18	UP	1.29E-10
ENSG00000151746.15	BICD1	-1.05	DOWN	1.36E-10
ENSG00000198848.13	CES1	2.25	UP	1.46E-10
ENSG00000074660.16	SCARF1	1.76	UP	1.46E-10
ENSG00000147168.13	IL2RG	1.12	UP	1.50E-10
ENSG00000173715.17	C11orf80	-1.01	DOWN	1.59E-10
ENSG00000143546.10	S100A8	1.63	UP	1.62E-10
ENSG00000166803.13	PCLAF	-1.26	DOWN	1.73E-10
ENSG00000136869.16	TLR4	1.10	UP	1.74E-10
ENSG00000198814.12	GK	1.49	UP	1.80E-10
ENSG00000174944.9	P2RY14	2.31	UP	1.83E-10
ENSG00000204520.14	MICA	1.30	UP	1.88E-10
ENSG00000067182.8	TNFRSF1A	1.38	UP	1.91E-10
ENSG00000145555.15	MYO10	1.96	UP	1.95E-10
ENSG00000140853.15	NLRC5	1.30	UP	1.98E-10
ENSG00000180573.9	H2AC6	1.12	UP	1.99E-10
ENSG00000141574.8	SECTM1	1.84	UP	2.04E-10
ENSG00000026103.22	FAS	1.56	UP	2.08E-10
ENSG00000100784.12	RPS6KA5	-1.09	DOWN	2.08E-10
ENSG00000214226.9	C17orf67	1.48	UP	2.20E-10
ENSG00000002549.12	LAP3	2.34	UP	2.20E-10
ENSG00000188738.15	FSIP2	-1.91	DOWN	2.26E-10

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000138190.17	EXOC6	1.05	UP	2.30E-10
ENSG00000048462.11	TNFRSF17	-1.44	DOWN	2.37E-10
ENSG00000133030.21	MPRIP	-1.05	DOWN	2.53E-10
ENSG00000140795.13	MYLK3	1.73	UP	2.56E-10
ENSG00000182197.12	EXT1	1.08	UP	2.68E-10
ENSG00000146232.17	NFKBIE	1.41	UP	2.74E-10
ENSG00000186231.17	KLHL32	-1.26	DOWN	2.79E-10
ENSG00000138621.12	PPCDC	1.62	UP	2.95E-10
ENSG00000177663.14	IL17RA	1.05	UP	3.06E-10
ENSG00000105711.12	SCN1B	2.18	UP	3.25E-10
ENSG00000132952.12	USPL1	1.02	UP	3.26E-10
ENSG00000196550.10	FAM72A	1.89	UP	3.49E-10
ENSG00000164136.17	IL15	1.06	UP	3.56E-10
ENSG00000135404.11	CD63	1.14	UP	3.61E-10
ENSG00000120129.6	DUSP1	1.40	UP	3.63E-10
ENSG00000181616.9	OR52H1	2.63	UP	3.73E-10
ENSG00000213988.11	ZNF90	-1.22	DOWN	3.74E-10
ENSG00000161011.20	SQSTM1	1.01	UP	3.93E-10
ENSG00000178685.14	PARP10	2.55	UP	4.04E-10
ENSG00000162894.12	FCMR	-1.18	DOWN	4.27E-10
ENSG00000041357.16	PSMA4	1.17	UP	4.38E-10
ENSG00000134686.18	PHC2	1.44	UP	4.45E-10
ENSG00000171051.8	FPR1	1.50	UP	4.58E-10
ENSG00000173166.18	RAPH1	-1.12	DOWN	4.63E-10
ENSG00000156414.19	TDRD9	1.12	UP	4.78E-10
ENSG00000165997.5	ARL5B	1.15	UP	4.81E-10
ENSG00000072401.15	UBE2D1	1.22	UP	4.95E-10
ENSG00000128383.13	APOBEC3A	2.41	UP	5.01E-10
ENSG00000172164.15	SNTB1	1.04	UP	5.50E-10
ENSG00000115602.17	IL1RL1	-1.83	DOWN	5.70E-10
ENSG00000097096.9	SYDE2	-1.24	DOWN	5.80E-10
ENSG00000172915.18	NBEA	-1.08	DOWN	6.14E-10
ENSG00000204386.11	NEU1	1.33	UP	6.18E-10
ENSG00000286522.2	H3C2	-1.78	DOWN	6.41E-10
ENSG00000118960.13	HS1BP3	1.08	UP	6.44E-10
ENSG00000163220.11	S100A9	1.41	UP	6.80E-10
ENSG00000132932.17	ATP8A2	-1.33	DOWN	7.37E-10
ENSG00000000938.13	FGR	1.34	UP	7.40E-10
ENSG00000166707.11	ZCCHC18	-1.52	DOWN	7.43E-10
ENSG00000214113.10	LYRM4	-1.03	DOWN	7.52E-10

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000068323.17	TFE3	1.45	UP	7.60E-10
ENSG00000131634.14	TMEM204	-1.65	DOWN	7.62E-10
ENSG00000177674.16	AGTRAP	1.21	UP	7.72E-10
ENSG00000162630.6	B3GALT2	-1.70	DOWN	7.75E-10
ENSG00000124126.14	PREX1	1.11	UP	8.31E-10
ENSG00000138738.10	PRDM5	1.96	UP	8.92E-10
ENSG00000172878.14	METAP1D	-1.14	DOWN	1.02E-09
ENSG00000167207.13	NOD2	1.37	UP	1.07E-09
ENSG00000124762.14	CDKN1A	1.83	UP	1.11E-09
ENSG00000204852.16	TCTN1	-1.05	DOWN	1.14E-09
ENSG00000179088.14	C12orf42	-1.19	DOWN	1.23E-09
ENSG00000168918.14	INPP5D	1.03	UP	1.27E-09
ENSG00000146192.15	FGD2	1.09	UP	1.28E-09
ENSG00000145390.11	USP53	-1.12	DOWN	1.28E-09
ENSG00000075426.12	FOSL2	1.08	UP	1.29E-09
ENSG00000162616.9	DNAJB4	1.05	UP	1.36E-09
ENSG00000143382.15	ADAMTSL4	2.30	UP	1.38E-09
ENSG00000181982.18	CCDC149	1.17	UP	1.40E-09
ENSG00000170365.10	SMAD1	1.19	UP	1.41E-09
ENSG00000123612.16	ACVR1C	-1.28	DOWN	1.41E-09
ENSG00000188610.12	FAM72B	1.71	UP	1.41E-09
ENSG00000119669.5	IRF2BPL	1.26	UP	1.43E-09
ENSG00000130396.20	AFDN	-1.29	DOWN	1.51E-09
ENSG00000179750.16	APOBEC3B	2.74	UP	1.52E-09
ENSG00000172817.4	CYP7B1	-1.50	DOWN	1.59E-09
ENSG00000152804.11	HHEX	1.04	UP	1.68E-09
ENSG00000008394.13	MGST1	1.13	UP	1.70E-09
ENSG00000180096.12	SEPTIN1	-1.42	DOWN	1.70E-09
ENSG00000143226.14	FCGR2A	1.14	UP	1.72E-09
ENSG00000162645.13	GBP2	1.24	UP	1.74E-09
ENSG00000197275.14	RAD54B	-1.12	DOWN	1.74E-09
ENSG00000105948.13	TTC26	2.31	UP	1.80E-09
ENSG00000172728.16	FUT10	-1.04	DOWN	1.81E-09
ENSG00000144218.19	AFF3	-1.28	DOWN	1.87E-09
ENSG00000071967.12	CYBRD1	-1.40	DOWN	1.87E-09
ENSG00000163162.9	RNF149	1.08	UP	1.89E-09
ENSG00000105974.12	CAV1	-1.60	DOWN	2.27E-09
ENSG00000115828.17	QPCT	1.06	UP	2.34E-09
ENSG00000186806.5	VSIG10L	2.82	UP	2.37E-09
ENSG00000103496.15	STX4	1.36	UP	2.64E-09

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000156113.23	KCNMA1	2.38	UP	2.65E-09
ENSG00000121690.11	DEPDC7	-1.25	DOWN	2.65E-09
ENSG00000104290.11	FZD3	-1.09	DOWN	2.66E-09
ENSG00000270106.6	TSNAX-DISC1	1.80	UP	2.68E-09
ENSG00000155970.12	MICU3	-1.42	DOWN	2.73E-09
ENSG00000284194.3	SCO2	2.47	UP	2.75E-09
ENSG00000160570.14	DEDD2	1.31	UP	2.76E-09
ENSG00000165028.12	NIPSNAP3B	-1.51	DOWN	2.87E-09
ENSG00000117298.16	ECE1	1.60	UP	2.92E-09
ENSG00000135525.18	MAP7	-1.21	DOWN	2.96E-09
ENSG00000072952.18	MRV11	1.34	UP	2.99E-09
ENSG00000272398.6	CD24	-1.21	DOWN	3.14E-09
ENSG00000086300.16	SNX10	1.12	UP	3.15E-09
ENSG00000185201.16	IFITM2	1.96	UP	3.23E-09
ENSG00000284873.1	OOSP1	2.84	UP	3.24E-09
ENSG00000143452.16	HORMAD1	1.88	UP	3.41E-09
ENSG00000177575.12	CD163	1.24	UP	3.42E-09
ENSG00000148110.16	MFSD14B	1.22	UP	3.56E-09
ENSG00000143199.18	ADCY10	1.18	UP	3.68E-09
ENSG00000152894.14	PTPRK	-1.14	DOWN	3.68E-09
ENSG00000106034.18	CPED1	1.03	UP	3.78E-09
ENSG00000152689.18	RASGRP3	1.35	UP	3.84E-09
ENSG00000162836.12	ACP6	1.00	UP	4.01E-09
ENSG00000153563.15	CD8A	-1.15	DOWN	4.17E-09
ENSG00000163596.16	ICA1L	-1.09	DOWN	4.26E-09
ENSG00000152766.6	ANKRD22	2.83	UP	4.32E-09
ENSG00000107014.9	RLN2	-1.55	DOWN	4.33E-09
ENSG00000123360.12	PDE1B	1.20	UP	4.41E-09
ENSG00000089351.14	GRAMD1A	1.49	UP	4.45E-09
ENSG00000157856.12	DRC1	2.30	UP	4.45E-09
ENSG00000124785.9	NRN1	2.85	UP	4.59E-09
ENSG00000198736.11	MSRB1	1.40	UP	5.20E-09
ENSG00000157404.16	KIT	-1.32	DOWN	5.71E-09
ENSG00000168256.18	NKIRAS2	1.04	UP	5.84E-09
ENSG00000066336.12	SPI1	1.45	UP	6.05E-09
ENSG00000182463.16	TSHZ2	-1.28	DOWN	6.10E-09
ENSG00000255819.7	KLRC4-KLRK1	-1.46	DOWN	6.30E-09
ENSG00000158488.16	CD1E	-2.28	DOWN	6.51E-09
ENSG00000152207.7	CYSLTR2	-1.02	DOWN	6.52E-09
ENSG00000166068.13	SPRED1	-1.20	DOWN	6.54E-09

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000135903.20	PAX3	2.68	UP	6.63E-09
ENSG00000122877.16	EGR2	2.33	UP	6.85E-09
ENSG00000105287.12	PRKD2	1.66	UP	6.87E-09
ENSG00000005471.18	ABCB4	-1.14	DOWN	7.04E-09
ENSG00000186047.10	DLEU7	1.19	UP	7.40E-09
ENSG00000176788.9	BASP1	1.25	UP	7.44E-09
ENSG00000088298.13	EDEM2	1.16	UP	7.50E-09
ENSG00000132704.16	FCRL2	-1.08	DOWN	7.53E-09
ENSG00000132170.22	PPARG	1.77	UP	7.56E-09
ENSG00000171223.6	JUNB	1.08	UP	7.56E-09
ENSG00000137869.15	CYP19A1	1.84	UP	7.59E-09
ENSG00000066468.23	FGFR2	-1.90	DOWN	7.67E-09
ENSG00000204427.12	ABHD16A	1.01	UP	8.39E-09
ENSG00000186496.12	ZNF396	1.01	UP	8.72E-09
ENSG00000175536.7	LIPT2	-1.22	DOWN	8.80E-09
ENSG00000115607.9	IL18RAP	1.71	UP	9.34E-09
ENSG00000111837.11	MAK	1.36	UP	9.67E-09
ENSG00000186105.8	LRRC70	1.15	UP	1.01E-08
ENSG00000082641.16	NFE2L1	1.06	UP	1.03E-08
ENSG00000143554.14	SLC27A3	2.00	UP	1.05E-08
ENSG00000102024.18	PLS3	-1.35	DOWN	1.05E-08
ENSG00000157514.16	TSC22D3	1.02	UP	1.06E-08
ENSG00000118785.14	SPP1	-1.98	DOWN	1.07E-08
ENSG00000182489.9	XKRX	-1.62	DOWN	1.11E-08
ENSG00000166743.9	ACSM1	2.02	UP	1.18E-08
ENSG00000140332.17	TLE3	1.09	UP	1.19E-08
ENSG00000160179.18	ABCG1	1.33	UP	1.22E-08
ENSG00000183150.8	GPR19	-1.34	DOWN	1.27E-08
ENSG00000128040.11	SPINK2	-1.98	DOWN	1.41E-08
ENSG00000273173.5	SNURF	-1.04	DOWN	1.41E-08
ENSG00000117643.14	MAN1C1	-1.04	DOWN	1.42E-08
ENSG00000100605.17	ITPK1	1.20	UP	1.42E-08
ENSG00000089159.16	PXN	1.10	UP	1.46E-08
ENSG00000091972.18	CD200	-1.14	DOWN	1.49E-08
ENSG00000164509.15	IL31RA	2.08	UP	1.56E-08
ENSG00000038210.14	PI4K2B	1.71	UP	1.59E-08
ENSG00000172005.11	MAL	-1.54	DOWN	1.59E-08
ENSG00000172426.16	RSPH9	2.46	UP	1.71E-08
ENSG00000274349.4	ZNF658	-1.12	DOWN	1.78E-08
ENSG00000161970.15	RPL26	-1.04	DOWN	1.93E-08

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000163508.13	EOMES	-1.02	DOWN	1.95E-08
ENSG00000106714.17	CNTNAP3	-1.92	DOWN	2.01E-08
ENSG00000185272.14	RBM11	1.36	UP	2.09E-08
ENSG00000230797.3	YY2	-1.33	DOWN	2.20E-08
ENSG00000119915.5	ELOVL3	2.54	UP	2.27E-08
ENSG00000087074.8	PPP1R15A	1.49	UP	2.30E-08
ENSG00000204767.4	INSYN2B	1.89	UP	2.33E-08
ENSG00000167106.12	FAM102A	-1.45	DOWN	2.40E-08
ENSG00000197061.5	H4C3	-1.30	DOWN	2.40E-08
ENSG00000030582.18	GRN	2.22	UP	2.40E-08
ENSG00000146166.17	LGSN	2.57	UP	2.44E-08
ENSG00000257335.8	MGAM	1.03	UP	2.46E-08
ENSG00000054967.13	RELT	1.07	UP	2.48E-08
ENSG00000184226.15	PCDH9	-1.15	DOWN	2.61E-08
ENSG00000010030.14	ETV7	2.58	UP	2.66E-08
ENSG00000183542.5	KLRC4	-1.42	DOWN	2.68E-08
ENSG00000164715.6	LMTK2	1.02	UP	2.69E-08
ENSG00000188820.13	CALHM6	1.79	UP	2.80E-08
ENSG00000215784.6	FAM72D	1.72	UP	2.81E-08
ENSG00000110042.8	DTX4	-1.32	DOWN	2.88E-08
ENSG00000111732.11	AICDA	-2.10	DOWN	2.98E-08
ENSG00000197956.10	S100A6	1.04	UP	3.06E-08
ENSG00000155465.19	SLC7A7	1.01	UP	3.17E-08
ENSG00000113303.12	BTNL8	1.39	UP	3.26E-08
ENSG00000140105.18	WARS1	1.76	UP	3.35E-08
ENSG00000175556.17	LONRF3	1.02	UP	3.55E-08
ENSG00000175003.15	SLC22A1	1.42	UP	3.63E-08
ENSG00000132205.11	EMILIN2	1.09	UP	3.66E-08
ENSG00000173535.15	TNFRSF10C	1.10	UP	3.69E-08
ENSG00000163081.3	CCDC140	3.01	UP	3.70E-08
ENSG00000115271.11	GCA	1.22	UP	3.98E-08
ENSG00000197746.14	PSAP	1.25	UP	4.00E-08
ENSG00000170439.7	METTL7B	3.55	UP	4.09E-08
ENSG00000132589.16	FLOT2	1.72	UP	4.12E-08
ENSG00000270276.2	H4C15	1.14	UP	4.15E-08
ENSG00000171130.18	ATP6V0E2	-1.18	DOWN	4.21E-08
ENSG00000184922.14	FMNL1	1.22	UP	4.26E-08
ENSG00000101457.13	DNTTIP1	1.12	UP	4.32E-08
ENSG00000239887.6	C1orf226	3.18	UP	4.53E-08
ENSG00000197329.12	PELI1	1.04	UP	4.55E-08

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000101160.14	CTSZ	1.16	UP	4.63E-08
ENSG00000128641.19	MYO1B	-1.28	DOWN	4.64E-08
ENSG00000157445.15	CACNA2D3	-1.43	DOWN	4.65E-08
ENSG00000134470.21	IL15RA	1.21	UP	4.71E-08
ENSG00000103005.12	USB1	1.16	UP	4.75E-08
ENSG00000159588.15	CCDC17	1.43	UP	4.89E-08
ENSG00000165914.15	TTC7B	1.29	UP	5.01E-08
ENSG00000108774.15	RAB5C	1.01	UP	5.18E-08
ENSG00000133985.3	TTC9	-1.17	DOWN	5.27E-08
ENSG00000168275.16	COA6	1.11	UP	5.33E-08
ENSG00000141526.16	SLC16A3	1.71	UP	5.38E-08
ENSG00000213719.8	CLIC1	1.07	UP	5.61E-08
ENSG00000173801.17	JUP	2.12	UP	5.81E-08
ENSG00000135378.4	PRRG4	1.40	UP	6.30E-08
ENSG00000139970.17	RTN1	-1.21	DOWN	7.22E-08
ENSG00000165181.16	SHOC1	1.61	UP	7.92E-08
ENSG00000166016.6	ABTB2	2.56	UP	8.10E-08
ENSG00000278318.5	ZNF229	-1.31	DOWN	8.59E-08
ENSG00000029993.15	HMGB3	-1.09	DOWN	8.90E-08
ENSG00000147996.16	CBWD5	1.11	UP	8.95E-08
ENSG00000150625.16	GPM6A	-1.29	DOWN	8.97E-08
ENSG00000197756.10	RPL37A	-1.07	DOWN	9.08E-08
ENSG00000198929.13	NOS1AP	2.33	UP	1.02E-07
ENSG00000136541.14	ERMN	-1.04	DOWN	1.05E-07
ENSG00000060491.16	OGFR	1.35	UP	1.05E-07
ENSG00000137962.13	ARHGAP29	1.10	UP	1.06E-07
ENSG00000170458.14	CD14	1.26	UP	1.06E-07
ENSG00000163751.4	CPA3	-1.56	DOWN	1.07E-07
ENSG00000146094.14	DOK3	1.16	UP	1.18E-07
ENSG00000111181.12	SLC6A12	1.55	UP	1.24E-07
ENSG00000205846.4	CLEC6A	1.45	UP	1.28E-07
ENSG00000122952.17	ZWINT	-1.04	DOWN	1.31E-07
ENSG00000146021.15	KLHL3	-1.19	DOWN	1.34E-07
ENSG00000138166.6	DUSP5	1.20	UP	1.36E-07
ENSG00000118900.15	UBN1	1.00	UP	1.39E-07
ENSG00000197763.18	TXNRD3	-1.25	DOWN	1.44E-07
ENSG00000215126.10	CBWD6	1.00	UP	1.47E-07
ENSG00000134802.17	SLC43A3	1.04	UP	1.51E-07
ENSG00000072518.20	MARK2	1.00	UP	1.53E-07
ENSG00000139890.10	REM2	1.35	UP	1.55E-07

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000174684.7	B4GAT1	-1.53	DOWN	1.56E-07
ENSG00000169047.5	IRS1	1.05	UP	1.59E-07
ENSG00000155287.11	SLC25A28	1.33	UP	1.66E-07
ENSG00000151948.12	GLT1D1	1.07	UP	1.71E-07
ENSG00000142039.4	CCDC97	1.28	UP	1.75E-07
ENSG00000154451.14	GBP5	1.96	UP	1.76E-07
ENSG00000120278.16	PLEKHG1	-1.02	DOWN	1.76E-07
ENSG00000185215.10	TNFAIP2	1.07	UP	1.80E-07
ENSG00000120156.21	TEK	-1.75	DOWN	1.83E-07
ENSG00000130558.19	OLFM1	-2.72	DOWN	1.98E-07
ENSG00000125347.14	IRF1	1.13	UP	2.01E-07
ENSG00000022267.19	FHL1	-1.14	DOWN	2.10E-07
ENSG00000144713.13	RPL32	-1.12	DOWN	2.11E-07
ENSG00000006534.16	ALDH3B1	1.53	UP	2.16E-07
ENSG00000265590.10	C21orf59-TCP10L	-1.14	DOWN	2.27E-07
ENSG00000141551.14	CSNK1D	1.04	UP	2.32E-07
ENSG00000123405.14	NFE2	1.15	UP	2.36E-07
ENSG00000142634.13	EFHD2	1.14	UP	2.41E-07
ENSG00000067113.17	PLPP1	-1.06	DOWN	2.50E-07
ENSG00000121933.19	TMIGD3	1.76	UP	2.51E-07
ENSG00000214212.9	C19orf38	1.32	UP	2.55E-07
ENSG00000160321.15	ZNF208	-1.18	DOWN	2.55E-07
ENSG00000167658.16	EEF2	-1.14	DOWN	2.55E-07
ENSG00000117984.14	CTSD	1.90	UP	2.63E-07
ENSG00000171848.15	RRM2	-1.10	DOWN	2.63E-07
ENSG00000124657.1	OR2B6	1.24	UP	2.63E-07
ENSG00000184988.8	TMEM106A	1.05	UP	2.66E-07
ENSG00000164930.12	FZD6	-1.19	DOWN	2.77E-07
ENSG00000103642.12	LACTB	1.04	UP	2.79E-07
ENSG00000117318.9	ID3	-1.58	DOWN	2.84E-07
ENSG00000054598.9	FOXC1	2.21	UP	2.88E-07
ENSG00000139187.10	KLRG1	-1.09	DOWN	3.05E-07
ENSG00000182885.17	ADGRG3	1.94	UP	3.17E-07
ENSG00000250644.3	AC068580.4	2.44	UP	3.18E-07
ENSG00000204264.12	PSMB8	1.11	UP	3.22E-07
ENSG00000111886.11	GABRR2	1.26	UP	3.24E-07
ENSG00000180061.10	TMEM150B	2.56	UP	3.28E-07
ENSG00000174611.12	KY	1.48	UP	3.28E-07
ENSG00000277224.2	H2BC7	1.18	UP	3.39E-07
ENSG00000117650.13	NEK2	-1.16	DOWN	3.43E-07

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000179542.16	SLITRK4	1.01	UP	3.49E-07
ENSG00000114405.10	C3orf14	1.02	UP	3.65E-07
ENSG00000139567.13	ACVRL1	2.49	UP	3.70E-07
ENSG00000112232.9	KHDRBS2	-1.01	DOWN	4.12E-07
ENSG00000113494.17	PRLR	1.12	UP	4.20E-07
ENSG00000102057.10	KCND1	2.32	UP	4.34E-07
ENSG00000161921.16	CXCL16	1.28	UP	4.77E-07
ENSG00000183734.4	ASCL2	1.23	UP	4.77E-07
ENSG00000135116.9	HRK	-1.59	DOWN	5.03E-07
ENSG00000104432.14	IL7	-1.01	DOWN	5.08E-07
ENSG00000126561.16	STAT5A	1.06	UP	5.16E-07
ENSG00000227268.4	KLLN	1.11	UP	5.25E-07
ENSG00000154099.18	DNAAF1	2.85	UP	5.29E-07
ENSG00000087077.14	TRIP6	1.92	UP	5.30E-07
ENSG00000076067.13	RBMS2	1.16	UP	5.48E-07
ENSG00000160883.11	HK3	1.84	UP	6.07E-07
ENSG00000149577.16	SIDT2	1.46	UP	6.22E-07
ENSG00000165131.7	LLCFC1	2.49	UP	6.57E-07
ENSG00000180316.12	PNPLA1	1.39	UP	6.67E-07
ENSG00000167526.13	RPL13	-1.37	DOWN	6.72E-07
ENSG00000158301.18	GPRASP2	-1.15	DOWN	6.72E-07
ENSG00000061938.19	TNK2	1.54	UP	7.18E-07
ENSG00000253250.3	C8orf88	1.29	UP	7.30E-07
ENSG00000115590.14	IL1R2	1.11	UP	7.40E-07
ENSG00000147403.16	RPL10	-1.39	DOWN	7.50E-07
ENSG00000135540.11	NHSL1	1.23	UP	7.56E-07
ENSG00000100292.17	HMOX1	1.29	UP	7.63E-07
ENSG00000281106.4	TMEM272	1.08	UP	7.76E-07
ENSG00000134545.13	KLRC1	-1.25	DOWN	7.84E-07
ENSG00000146858.8	ZC3HAV1L	1.19	UP	7.98E-07
ENSG00000256812.2	CAPNS2	1.12	UP	8.01E-07
ENSG00000100365.16	NCF4	1.20	UP	8.05E-07
ENSG00000177989.13	ODF3B	2.46	UP	8.15E-07
ENSG00000184221.13	OLIG1	-1.75	DOWN	8.46E-07
ENSG00000137474.22	MYO7A	2.07	UP	8.88E-07
ENSG00000186310.10	NAP1L3	-1.19	DOWN	9.25E-07
ENSG00000196747.4	H2AC13	1.25	UP	9.69E-07
ENSG00000135052.16	GOLM1	1.20	UP	9.70E-07
ENSG00000206535.8	LNP1	-1.51	DOWN	9.90E-07
ENSG00000042832.12	TG	1.14	UP	9.96E-07

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000163116.10	STPG2	1.20	UP	1.02E-06
ENSG00000003096.14	KLHL13	-1.17	DOWN	1.03E-06
ENSG00000137312.15	FLOT1	1.35	UP	1.05E-06
ENSG00000162244.12	RPL29	-1.03	DOWN	1.06E-06
ENSG00000204531.19	POU5F1	2.49	UP	1.10E-06
ENSG00000101342.10	TLDC2	1.99	UP	1.14E-06
ENSG00000141434.12	MEP1B	1.65	UP	1.14E-06
ENSG00000166582.10	CENPV	-1.36	DOWN	1.18E-06
ENSG00000162591.16	MEGF6	-1.05	DOWN	1.20E-06
ENSG00000100055.21	CYTH4	1.10	UP	1.34E-06
ENSG00000128203.7	ASPHD2	1.10	UP	1.34E-06
ENSG00000204936.10	CD177	2.86	UP	1.34E-06
ENSG00000182866.17	LCK	-1.12	DOWN	1.40E-06
ENSG00000130052.13	STARD8	1.20	UP	1.47E-06
ENSG00000128394.17	APOBEC3F	1.11	UP	1.47E-06
ENSG00000132471.12	WBP2	1.03	UP	1.49E-06
ENSG00000105639.19	JAK3	1.38	UP	1.59E-06
ENSG00000171236.10	LRG1	1.73	UP	1.61E-06
ENSG00000141504.12	SAT2	1.37	UP	1.63E-06
ENSG00000158773.14	USF1	1.09	UP	1.65E-06
ENSG00000028137.19	TNFRSF1B	1.24	UP	1.65E-06
ENSG00000160796.18	NBEAL2	1.05	UP	1.66E-06
ENSG00000198915.11	RASGEF1A	1.00	UP	1.79E-06
ENSG00000072134.15	EPN2	-1.40	DOWN	1.81E-06
ENSG00000085063.17	CD59	1.19	UP	1.81E-06
ENSG00000030110.13	BAK1	1.45	UP	1.84E-06
ENSG00000181222.17	POLR2A	1.26	UP	1.90E-06
ENSG00000146122.17	DAAM2	1.61	UP	1.90E-06
ENSG00000108688.11	CCL7	2.52	UP	2.05E-06
ENSG00000204252.14	HLA-DOA	-1.17	DOWN	2.05E-06
ENSG00000080493.17	SLC4A4	-1.08	DOWN	2.11E-06
ENSG00000188822.8	CNR2	-1.12	DOWN	2.16E-06
ENSG00000273045.6	C2orf15	-1.54	DOWN	2.21E-06
ENSG00000180628.15	PCGF5	1.04	UP	2.23E-06
ENSG00000157152.17	SYN2	1.98	UP	2.25E-06
ENSG00000189325.7	BNIP5	2.24	UP	2.31E-06
ENSG00000163521.16	GLB1L	1.20	UP	2.32E-06
ENSG00000248385.8	TARM1	2.84	UP	2.34E-06
ENSG00000095370.20	SH2D3C	1.39	UP	2.36E-06
ENSG00000164105.4	SAP30	1.06	UP	2.39E-06

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000196935.9	SRGAP1	1.33	UP	2.53E-06
ENSG00000139537.11	CCDC65	-1.09	DOWN	2.59E-06
ENSG00000080824.19	HSP90AA1	1.08	UP	2.61E-06
ENSG00000214688.6	C10orf105	1.76	UP	2.62E-06
ENSG00000136942.15	RPL35	-1.19	DOWN	2.76E-06
ENSG00000142657.21	PGD	1.04	UP	3.00E-06
ENSG00000081059.20	TCF7	-1.17	DOWN	3.04E-06
ENSG00000276289.4	KCNE1B	2.52	UP	3.17E-06
ENSG00000215788.10	TNFRSF25	-1.31	DOWN	3.19E-06
ENSG00000214193.11	SH3D21	1.66	UP	3.19E-06
ENSG00000163421.9	PROK2	1.43	UP	3.23E-06
ENSG00000168779.19	SHOX2	2.31	UP	3.29E-06
ENSG00000100284.21	TOM1	1.69	UP	3.37E-06
ENSG00000257017.9	HP	1.91	UP	3.40E-06
ENSG00000167910.4	CYP7A1	2.13	UP	3.54E-06
ENSG00000134531.10	EMP1	1.36	UP	3.62E-06
ENSG00000143502.15	SUSD4	-1.46	DOWN	3.63E-06
ENSG00000196159.12	FAT4	-1.15	DOWN	3.65E-06
ENSG00000133216.16	EPHB2	1.92	UP	3.70E-06
ENSG00000180914.10	OXTR	-1.71	DOWN	3.72E-06
ENSG00000187987.9	ZSCAN23	-1.46	DOWN	3.78E-06
ENSG00000182983.15	ZNF662	-1.32	DOWN	3.80E-06
ENSG00000162747.12	FCGR3B	1.87	UP	3.84E-06
ENSG00000117115.13	PADI2	1.32	UP	3.92E-06
ENSG00000149054.16	ZNF215	-1.25	DOWN	3.92E-06
ENSG00000107018.8	RLN1	-1.18	DOWN	3.93E-06
ENSG00000169224.13	GCSAML	-1.20	DOWN	4.01E-06
ENSG00000119862.13	LGALS1	1.14	UP	4.06E-06
ENSG00000080845.17	DLGAP4	1.52	UP	4.26E-06
ENSG00000187824.9	TMEM220	-1.09	DOWN	4.42E-06
ENSG00000196189.13	SEMA4A	1.26	UP	4.44E-06
ENSG00000130985.17	UBA1	1.13	UP	4.53E-06
ENSG00000141161.11	UNC45B	-1.49	DOWN	4.54E-06
ENSG00000198417.7	MT1F	1.41	UP	4.84E-06
ENSG00000011600.12	TYROBP	1.29	UP	5.31E-06
ENSG00000124575.7	H1-3	-1.18	DOWN	5.43E-06
ENSG00000120915.14	EPHX2	-1.02	DOWN	5.82E-06
ENSG00000108179.14	PPIF	1.04	UP	5.88E-06
ENSG00000063177.13	RPL18	-1.16	DOWN	5.95E-06
ENSG00000176495.3	OR5AN1	-1.92	DOWN	5.99E-06

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000179222.18	MAGED1	-1.17	DOWN	6.09E-06
ENSG00000131759.18	RARA	1.41	UP	6.38E-06
ENSG00000139679.15	LPAR6	1.01	UP	6.38E-06
ENSG00000124019.10	FAM124B	-1.03	DOWN	6.40E-06
ENSG00000110987.9	BCL7A	-1.29	DOWN	6.68E-06
ENSG00000137936.18	BCAR3	-1.42	DOWN	6.70E-06
ENSG00000133134.11	BEX2	-1.05	DOWN	6.87E-06
ENSG00000100100.13	PIK3IP1	-1.14	DOWN	6.98E-06
ENSG00000169136.11	ATF5	1.52	UP	6.99E-06
ENSG00000170175.11	CHRN1	1.02	UP	7.14E-06
ENSG00000159958.6	TNFRSF13C	-1.31	DOWN	7.16E-06
ENSG00000152672.8	CLEC4F	2.27	UP	7.31E-06
ENSG00000104805.16	NUCB1	1.22	UP	7.49E-06
ENSG00000110080.18	ST3GAL4	1.56	UP	7.54E-06
ENSG00000235568.7	NFAM1	1.04	UP	7.74E-06
ENSG00000085514.16	PILRA	1.18	UP	8.20E-06
ENSG00000232810.4	TNF	1.48	UP	8.33E-06
ENSG00000116863.11	ADPRHL2	1.31	UP	8.54E-06
ENSG00000126353.3	CCR7	-1.20	DOWN	8.64E-06
ENSG00000188611.15	ASAH2	-1.08	DOWN	9.11E-06
ENSG00000161692.18	DBF4B	1.54	UP	9.20E-06
ENSG00000102007.11	PLP2	1.01	UP	9.29E-06
ENSG00000184730.11	APOBR	1.63	UP	9.41E-06
ENSG00000071539.14	TRIP13	-1.18	DOWN	9.45E-06
ENSG00000180758.12	GPR157	-1.36	DOWN	9.97E-06
ENSG00000124233.12	SEMG1	-1.90	DOWN	1.01E-05
ENSG00000105373.19	NOP53	-1.19	DOWN	1.01E-05
ENSG00000127074.14	RGS13	-1.34	DOWN	1.02E-05
ENSG00000168004.9	PLAAT5	-1.67	DOWN	1.02E-05
ENSG00000255398.3	HCAR3	1.25	UP	1.03E-05
ENSG00000181754.7	AMIGO1	-1.36	DOWN	1.04E-05
ENSG00000196653.12	ZNF502	-1.02	DOWN	1.07E-05
ENSG00000134574.12	DDB2	1.03	UP	1.09E-05
ENSG00000077152.11	UBE2T	-1.04	DOWN	1.10E-05
ENSG00000171714.12	ANO5	1.06	UP	1.14E-05
ENSG00000127084.19	FGD3	1.08	UP	1.14E-05
ENSG00000042493.16	CAPG	1.39	UP	1.14E-05
ENSG00000159840.16	ZYX	1.19	UP	1.14E-05
ENSG00000253958.2	CLDN23	1.35	UP	1.15E-05
ENSG00000158517.15	NCF1	1.38	UP	1.18E-05

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000244115.1	DNAJC25-GNG10	1.02	UP	1.19E-05
ENSG00000169116.11	PARM1	-1.22	DOWN	1.22E-05
ENSG00000134571.11	MYBPC3	2.04	UP	1.23E-05
ENSG00000145428.15	RNF175	-1.08	DOWN	1.27E-05
ENSG00000100336.17	APOL4	1.90	UP	1.27E-05
ENSG00000163221.9	S100A12	1.31	UP	1.28E-05
ENSG00000135127.11	BICDL1	-1.07	DOWN	1.29E-05
ENSG00000188676.13	IDO2	1.63	UP	1.30E-05
ENSG00000141194.6	OR4D1	-1.25	DOWN	1.33E-05
ENSG00000159915.12	ZNF233	-1.15	DOWN	1.38E-05
ENSG00000021762.20	OSBPL5	1.70	UP	1.39E-05
ENSG00000179639.10	FCER1A	-1.23	DOWN	1.40E-05
ENSG00000110492.15	MDK	2.44	UP	1.42E-05
ENSG00000270882.2	H4C14	1.20	UP	1.43E-05
ENSG00000153132.13	CLGN	-1.35	DOWN	1.49E-05
ENSG00000177105.10	RHOG	1.27	UP	1.50E-05
ENSG00000166188.2	ZNF319	1.16	UP	1.52E-05
ENSG00000147439.13	BIN3	1.08	UP	1.59E-05
ENSG00000056558.11	TRAF1	-1.08	DOWN	1.60E-05
ENSG00000133424.20	LARGE1	-1.37	DOWN	1.61E-05
ENSG00000130592.16	LSP1	1.17	UP	1.67E-05
ENSG00000083845.9	RPS5	-1.34	DOWN	1.68E-05
ENSG00000164106.8	SCRG1	1.73	UP	1.73E-05
ENSG00000105767.3	CADM4	1.90	UP	1.74E-05
ENSG00000169313.10	P2RY12	1.00	UP	1.79E-05
ENSG00000197748.13	CFAP43	2.04	UP	1.83E-05
ENSG00000141968.8	VAV1	1.10	UP	1.84E-05
ENSG00000162374.18	ELAVL4	1.45	UP	1.86E-05
ENSG00000197019.5	SERTAD1	1.14	UP	1.87E-05
ENSG00000183960.9	KCNH8	-1.01	DOWN	1.93E-05
ENSG00000198715.13	GLMP	1.17	UP	1.94E-05
ENSG00000188536.13	HBA2	2.53	UP	1.99E-05
ENSG00000162373.13	BEND5	-1.21	DOWN	2.07E-05
ENSG00000183307.4	TMEM121B	1.27	UP	2.16E-05
ENSG00000150337.13	FCGR1A	1.80	UP	2.18E-05
ENSG00000198355.5	PIM3	1.08	UP	2.29E-05
ENSG00000070087.14	PFN2	-1.12	DOWN	2.31E-05
ENSG00000182179.13	UBA7	1.41	UP	2.38E-05
ENSG00000162543.6	UBXN10	-1.15	DOWN	2.40E-05
ENSG00000111058.8	ACSS3	1.04	UP	2.50E-05

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000007350.17	TKTL1	-1.11	DOWN	2.53E-05
ENSG000000075399.14	VPS9D1	1.43	UP	2.54E-05
ENSG00000173825.7	TIGD3	-1.49	DOWN	2.56E-05
ENSG00000130402.12	ACTN4	1.16	UP	2.58E-05
ENSG00000129167.9	TPH1	-1.16	DOWN	2.60E-05
ENSG00000150630.4	VEGFC	1.28	UP	2.70E-05
ENSG00000079156.17	OSBPL6	1.39	UP	2.73E-05
ENSG00000144730.18	IL17RD	1.68	UP	2.80E-05
ENSG00000150687.12	PRSS23	-1.02	DOWN	2.81E-05
ENSG00000171302.17	CANT1	1.01	UP	2.83E-05
ENSG00000129667.12	RHBDF2	1.47	UP	2.84E-05
ENSG00000168899.5	VAMP5	1.86	UP	2.92E-05
ENSG00000271447.6	MMP28	-2.06	DOWN	2.93E-05
ENSG00000102053.12	ZC3H12B	-1.18	DOWN	2.96E-05
ENSG00000198933.9	TBKBP1	1.84	UP	3.05E-05
ENSG00000188375.5	H3-5	1.54	UP	3.09E-05
ENSG00000163874.11	ZC3H12A	1.16	UP	3.10E-05
ENSG00000118402.6	ELOVL4	-1.04	DOWN	3.27E-05
ENSG00000103723.15	AP3B2	1.69	UP	3.34E-05
ENSG00000172046.19	USP19	1.08	UP	3.36E-05
ENSG00000204020.5	LIPN	1.16	UP	3.50E-05
ENSG00000135437.10	RDH5	1.37	UP	3.65E-05
ENSG00000198792.13	TMEM184B	1.02	UP	3.65E-05
ENSG00000077984.6	CST7	1.29	UP	3.72E-05
ENSG00000164056.11	SPRY1	-1.04	DOWN	3.87E-05
ENSG00000130940.15	CASZ1	1.07	UP	3.95E-05
ENSG00000198046.12	ZNF667	-1.17	DOWN	4.06E-05
ENSG00000269720.2	CCDC194	2.36	UP	4.22E-05
ENSG00000108106.14	UBE2S	1.36	UP	4.27E-05
ENSG00000166148.4	AVPR1A	1.05	UP	4.43E-05
ENSG00000114315.4	HES1	-1.36	DOWN	4.44E-05
ENSG00000131080.15	EDA2R	1.78	UP	4.67E-05
ENSG00000158528.12	PPP1R9A	-1.10	DOWN	4.67E-05
ENSG00000101986.12	ABCD1	2.14	UP	4.69E-05
ENSG00000138669.9	PRKG2	-1.10	DOWN	4.71E-05
ENSG00000284773.1	AC114490.3	-1.24	DOWN	4.78E-05
ENSG00000146070.17	PLA2G7	-1.15	DOWN	4.83E-05
ENSG00000128011.4	LRFN1	1.37	UP	4.87E-05
ENSG00000129757.13	CDKN1C	1.61	UP	5.06E-05
ENSG00000164692.18	COL1A2	1.79	UP	5.17E-05

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000162512.16	SDC3	2.42	UP	5.22E-05
ENSG00000284931.1	AC104389.6	2.49	UP	5.32E-05
ENSG00000141837.21	CACNA1A	1.46	UP	5.44E-05
ENSG00000186635.14	ARAP1	1.07	UP	5.51E-05
ENSG00000198756.12	COLGALT2	-1.18	DOWN	5.54E-05
ENSG00000004809.14	SLC22A16	1.01	UP	5.56E-05
ENSG00000205809.9	KLRC2	-1.48	DOWN	5.57E-05
ENSG00000104112.9	SCG3	1.76	UP	5.86E-05
ENSG00000118292.9	C1orf54	1.09	UP	5.91E-05
ENSG00000181009.5	OR52N5	2.58	UP	6.05E-05
ENSG00000156398.13	SFXN2	-1.07	DOWN	6.20E-05
ENSG00000197457.10	STMN3	-1.40	DOWN	6.25E-05
ENSG00000064932.16	SBNO2	1.75	UP	6.59E-05
ENSG00000021300.14	PLEKHB1	-1.44	DOWN	6.72E-05
ENSG00000204389.10	HSPA1A	1.31	UP	6.81E-05
ENSG00000169031.20	COL4A3	-1.09	DOWN	6.88E-05
ENSG00000214711.10	CAPN14	-1.25	DOWN	6.92E-05
ENSG00000142512.15	SIGLEC10	-1.03	DOWN	6.95E-05
ENSG00000197992.7	CLEC9A	-1.01	DOWN	6.99E-05
ENSG00000280969.2	RPS4Y2	-1.61	DOWN	7.09E-05
ENSG00000125505.17	MBOAT7	1.10	UP	7.22E-05
ENSG00000284393.1	AC092111.3	2.84	UP	7.30E-05
ENSG00000149418.11	ST14	1.75	UP	7.38E-05
ENSG00000213889.10	PPM1N	1.46	UP	7.67E-05
ENSG00000171631.14	P2RY6	2.20	UP	7.85E-05
ENSG00000189377.9	CXCL17	2.44	UP	8.27E-05
ENSG00000123685.9	BATF3	1.56	UP	8.54E-05
ENSG00000288602.1	C8orf44-SGK3	1.15	UP	8.56E-05
ENSG00000172771.12	EFCAB12	1.53	UP	8.68E-05
ENSG00000198626.17	RYR2	1.03	UP	8.82E-05
ENSG00000133800.9	LYVE1	1.08	UP	8.82E-05
ENSG00000136383.6	ALPK3	1.43	UP	8.90E-05
ENSG00000117519.16	CNN3	-1.20	DOWN	9.04E-05
ENSG00000189157.14	FAM47E	1.31	UP	9.08E-05
ENSG00000179921.15	GPBAR1	1.58	UP	9.20E-05
ENSG00000141542.11	RAB40B	-1.53	DOWN	1.00E-04
ENSG00000119714.11	GPR68	-1.37	DOWN	1.00E-04
ENSG00000109321.11	AREG	1.61	UP	1.01E-04
ENSG00000105202.9	FBL	-1.09	DOWN	1.13E-04
ENSG00000130202.10	NECTIN2	2.14	UP	1.13E-04

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000087116.16	ADAMTS2	2.59	UP	1.17E-04
ENSG00000197980.13	LEKR1	-1.18	DOWN	1.18E-04
ENSG00000175356.13	SCUBE2	1.35	UP	1.19E-04
ENSG00000157017.16	GHRL	1.22	UP	1.23E-04
ENSG00000214655.10	ZSWIM8	1.00	UP	1.23E-04
ENSG00000105516.11	DBP	-1.14	DOWN	1.26E-04
ENSG00000204315.4	FKBPL	1.44	UP	1.27E-04
ENSG00000070915.10	SLC12A3	1.80	UP	1.29E-04
ENSG00000157933.10	SKI	-1.01	DOWN	1.32E-04
ENSG00000168995.13	SIGLEC7	1.09	UP	1.33E-04
ENSG00000131748.16	STARD3	1.04	UP	1.34E-04
ENSG00000219200.11	RNASEK	1.18	UP	1.35E-04
ENSG00000272031.3	ANKRD34A	1.05	UP	1.44E-04
ENSG00000123146.20	ADGRE5	1.19	UP	1.45E-04
ENSG00000124613.8	ZNF391	-1.22	DOWN	1.68E-04
ENSG00000240563.2	L1TD1	1.31	UP	1.84E-04
ENSG00000179604.10	CDC42EP4	1.28	UP	1.85E-04
ENSG00000148468.17	FAM171A1	-1.30	DOWN	1.88E-04
ENSG00000177602.5	HASPIN	-1.54	DOWN	1.89E-04
ENSG00000134202.11	GSTM3	-1.26	DOWN	1.95E-04
ENSG00000102032.13	RENBP	1.82	UP	1.99E-04
ENSG00000105507.3	CABP5	-1.18	DOWN	2.07E-04
ENSG00000197046.12	SIGLEC15	1.39	UP	2.09E-04
ENSG00000049089.15	COL9A2	2.04	UP	2.20E-04
ENSG00000135596.18	MICAL1	1.17	UP	2.22E-04
ENSG00000113749.7	HRH2	1.10	UP	2.22E-04
ENSG00000121318.2	TAS2R10	-1.20	DOWN	2.24E-04
ENSG00000180730.5	SHISA2	-1.83	DOWN	2.27E-04
ENSG00000148303.17	RPL7A	-1.13	DOWN	2.29E-04
ENSG00000130561.17	SAG	1.23	UP	2.30E-04
ENSG00000161640.15	SIGLEC11	2.25	UP	2.35E-04
ENSG00000213512.3	GBP7	1.75	UP	2.40E-04
ENSG00000136160.17	EDNRB	1.31	UP	2.48E-04
ENSG00000160185.15	UBASH3A	-1.02	DOWN	2.56E-04
ENSG00000129354.11	AP1M2	2.15	UP	2.61E-04
ENSG00000196576.15	PLXNB2	1.54	UP	2.68E-04
ENSG00000095739.11	BAMBI	1.17	UP	2.77E-04
ENSG00000141576.16	RNF157	-1.17	DOWN	2.81E-04
ENSG00000206172.8	HBA1	2.22	UP	2.81E-04
ENSG00000111679.17	PTPN6	1.34	UP	2.82E-04

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000185359.13	HGS	1.29	UP	2.87E-04
ENSG00000004660.15	CAMKK1	1.26	UP	3.03E-04
ENSG00000126251.6	GPR42	2.46	UP	3.08E-04
ENSG00000172215.6	CXCR6	-1.04	DOWN	3.16E-04
ENSG00000167173.19	C15orf39	1.29	UP	3.33E-04
ENSG00000184292.7	TACSTD2	1.51	UP	3.43E-04
ENSG00000013364.19	MVP	1.11	UP	3.43E-04
ENSG00000130787.14	HIP1R	-1.32	DOWN	3.47E-04
ENSG00000010327.10	STAB1	1.47	UP	3.49E-04
ENSG00000189013.14	KIR2DL4	1.85	UP	3.77E-04
ENSG00000146411.6	SLC2A12	1.18	UP	3.92E-04
ENSG00000170293.9	CMTM8	-1.06	DOWN	4.05E-04
ENSG00000079393.20	DUSP13	2.33	UP	4.22E-04
ENSG00000166313.19	APBB1	-1.27	DOWN	4.26E-04
ENSG00000008516.17	MMP25	1.02	UP	4.26E-04
ENSG00000110448.11	CD5	-1.16	DOWN	4.32E-04
ENSG00000174514.13	MFSD4A	-1.27	DOWN	4.32E-04
ENSG00000189269.12	DRICH1	1.03	UP	4.39E-04
ENSG00000155265.11	GOLGA7B	-1.03	DOWN	4.43E-04
ENSG00000118804.8	STBD1	1.25	UP	4.59E-04
ENSG00000285938.1	AC072022.2	1.04	UP	4.65E-04
ENSG00000152969.20	JAKMIP1	-1.15	DOWN	4.66E-04
ENSG00000179218.14	CALR	1.00	UP	4.77E-04
ENSG00000105329.10	TGFB1	1.05	UP	4.85E-04
ENSG00000158825.6	CDA	1.17	UP	5.00E-04
ENSG00000086544.3	ITPKC	1.18	UP	5.03E-04
ENSG00000007306.15	CEACAM7	1.91	UP	5.06E-04
ENSG00000099338.23	CATSPERG	1.32	UP	5.10E-04
ENSG00000183579.16	ZNRF3	-1.46	DOWN	5.23E-04
ENSG00000136295.15	TTYH3	1.14	UP	5.28E-04
ENSG00000226288.2	OR52I2	1.36	UP	5.42E-04
ENSG00000106078.19	COBL	1.36	UP	5.42E-04
ENSG00000180891.13	CUEDC1	1.22	UP	5.71E-04
ENSG00000149823.9	VPS51	-1.08	DOWN	5.73E-04
ENSG00000092098.17	RNF31	1.12	UP	5.95E-04
ENSG00000170396.8	ZNF804A	1.30	UP	5.96E-04
ENSG00000140988.16	RPS2	-1.25	DOWN	6.04E-04
ENSG00000278662.5	GOLGA6L10	-1.44	DOWN	6.05E-04
ENSG00000138395.17	CDK15	-1.39	DOWN	6.13E-04
ENSG00000137726.17	FXVD6	1.65	UP	6.25E-04

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000160055.19	TMEM234	1.01	UP	6.38E-04
ENSG00000196535.16	MYO18A	1.12	UP	6.67E-04
ENSG00000278195.2	SSTR3	1.72	UP	6.69E-04
ENSG00000171729.14	TMEM51	2.05	UP	6.96E-04
ENSG00000138031.14	ADCY3	1.05	UP	7.19E-04
ENSG00000204628.12	RACK1	-1.06	DOWN	7.36E-04
ENSG00000129538.14	RNASE1	2.21	UP	7.59E-04
ENSG00000178947.9	SMIM10L2A	-2.08	DOWN	7.68E-04
ENSG00000064666.15	CNN2	1.14	UP	7.71E-04
ENSG00000166211.8	SPIC	1.60	UP	7.83E-04
ENSG00000105976.15	MET	-1.12	DOWN	7.85E-04
ENSG00000166839.17	ANKDD1A	1.30	UP	7.88E-04
ENSG00000123815.12	COQ8B	1.05	UP	8.05E-04
ENSG00000258311.5	AC009779.4	1.69	UP	8.58E-04
ENSG00000164683.18	HEY1	-1.49	DOWN	8.69E-04
ENSG00000203797.11	DDO	1.44	UP	8.81E-04
ENSG00000135929.9	CYP27A1	-1.47	DOWN	8.85E-04
ENSG00000172742.5	OR4D9	1.68	UP	9.03E-04
ENSG00000221996.6	OR52B4	1.56	UP	9.25E-04
ENSG00000112299.8	VNN1	1.12	UP	9.47E-04
ENSG00000129226.14	CD68	2.02	UP	9.52E-04
ENSG00000092051.17	JPH4	1.75	UP	9.55E-04
ENSG00000158714.11	SLAMF8	1.41	UP	9.67E-04
ENSG00000221995.5	TIAF1	1.03	UP	9.71E-04
ENSG00000164283.13	ESM1	-1.31	DOWN	9.80E-04
ENSG00000178404.10	CEP295NL	1.33	UP	9.94E-04
ENSG00000242852.7	ZNF709	-1.02	DOWN	1.04E-03
ENSG00000253598.3	SLC10A5	-1.40	DOWN	1.06E-03
ENSG00000185056.10	C5orf47	1.11	UP	1.07E-03
ENSG00000229314.5	ORM1	-1.68	DOWN	1.10E-03
ENSG00000141441.16	GAREM1	1.56	UP	1.13E-03
ENSG00000105011.9	ASF1B	-1.34	DOWN	1.19E-03
ENSG00000184489.12	PTP4A3	-1.15	DOWN	1.19E-03
ENSG00000181350.12	LRRC75A	-1.02	DOWN	1.19E-03
ENSG00000161381.14	PLXDC1	-1.27	DOWN	1.29E-03
ENSG00000184500.16	PROS1	-1.10	DOWN	1.31E-03
ENSG00000203778.8	FAM229B	-1.11	DOWN	1.31E-03
ENSG00000257065.1	AL049844.1	1.45	UP	1.36E-03
ENSG00000131831.18	RAI2	2.24	UP	1.36E-03
ENSG00000041880.14	PARP3	1.20	UP	1.37E-03

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000204345.1	CD300LD	-2.07	DOWN	1.47E-03
ENSG00000105609.17	LILRB5	2.28	UP	1.51E-03
ENSG00000184361.13	SPATA32	1.82	UP	1.53E-03
ENSG00000171777.16	RASGRP4	1.14	UP	1.54E-03
ENSG00000205810.9	KLRC3	-1.08	DOWN	1.55E-03
ENSG00000169330.9	MINAR1	-1.02	DOWN	1.57E-03
ENSG00000112984.12	KIF20A	-1.05	DOWN	1.58E-03
ENSG00000171596.7	NMUR1	-1.42	DOWN	1.59E-03
ENSG00000102802.10	MEDAG	1.60	UP	1.60E-03
ENSG00000101213.7	PTK6	1.59	UP	1.60E-03
ENSG00000073734.10	ABCB11	1.17	UP	1.62E-03
ENSG00000092421.16	SEMA6A	1.15	UP	1.65E-03
ENSG00000166510.14	CCDC68	1.06	UP	1.68E-03
ENSG00000120738.8	EGR1	1.15	UP	1.77E-03
ENSG00000143036.17	SLC44A3	1.27	UP	1.86E-03
ENSG00000167850.4	CD300C	1.16	UP	1.87E-03
ENSG00000173421.17	CCDC36	2.02	UP	1.88E-03
ENSG00000176076.7	KCNE5	1.40	UP	2.00E-03
ENSG00000100298.15	APOBEC3H	1.29	UP	2.07E-03
ENSG00000168542.16	COL3A1	1.61	UP	2.08E-03
ENSG00000103066.13	PLA2G15	1.26	UP	2.09E-03
ENSG00000102678.7	FGF9	-1.07	DOWN	2.19E-03
ENSG00000286239.1	AC093884.1	1.94	UP	2.19E-03
ENSG00000242265.5	PEG10	-1.15	DOWN	2.22E-03
ENSG00000130487.9	KLHDC7B	1.59	UP	2.22E-03
ENSG00000175505.11	CLCF1	-1.85	DOWN	2.30E-03
ENSG00000146250.7	PRSS35	-1.41	DOWN	2.33E-03
ENSG00000072041.17	SLC6A15	1.29	UP	2.43E-03
ENSG00000243696.5	AC006254.1	1.45	UP	2.48E-03
ENSG00000122861.16	PLAU	1.46	UP	2.61E-03
ENSG00000147117.8	ZNF157	-1.15	DOWN	2.61E-03
ENSG00000142102.16	PGGHG	1.06	UP	2.61E-03
ENSG00000242802.9	AP5Z1	1.13	UP	2.67E-03
ENSG00000141096.6	DPEP3	-1.85	DOWN	2.72E-03
ENSG00000144152.13	FBLN7	-1.46	DOWN	2.75E-03
ENSG00000186417.14	GLDN	1.36	UP	2.76E-03
ENSG00000105499.14	PLA2G4C	1.05	UP	2.78E-03
ENSG00000261150.3	EPPK1	-1.29	DOWN	2.84E-03
ENSG00000137094.14	DNAJB5	-1.17	DOWN	2.86E-03
ENSG00000187715.13	KBTBD12	1.26	UP	2.86E-03

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000285708.1	AC097634.4	1.29	UP	2.86E-03
ENSG00000125449.7	ARMC7	1.24	UP	2.88E-03
ENSG00000182836.10	PLCXD3	1.42	UP	2.89E-03
ENSG00000242732.4	RTL5	1.48	UP	3.07E-03
ENSG00000105717.14	PBX4	-1.60	DOWN	3.08E-03
ENSG00000234719.9	NPIP2	1.51	UP	3.08E-03
ENSG00000132259.13	CNGA4	2.12	UP	3.10E-03
ENSG00000144476.6	ACKR3	-1.02	DOWN	3.11E-03
ENSG00000177807.10	KCNJ10	1.35	UP	3.14E-03
ENSG00000276023.5	DUSP14	-1.04	DOWN	3.16E-03
ENSG00000152760.10	TCTEX1D1	1.12	UP	3.17E-03
ENSG00000178015.5	GPR150	-1.73	DOWN	3.18E-03
ENSG00000205084.11	TMEM231	-1.39	DOWN	3.19E-03
ENSG00000114455.13	HHLA2	-1.19	DOWN	3.28E-03
ENSG00000129048.7	ACKR4	1.16	UP	3.29E-03
ENSG00000161944.16	ASGR2	1.00	UP	3.44E-03
ENSG00000268279.4	AC090004.1	1.18	UP	3.47E-03
ENSG00000285476.1	AC139491.7	-1.14	DOWN	3.52E-03
ENSG00000229894.4	GK3P	1.15	UP	3.58E-03
ENSG00000179593.16	ALOX15B	2.04	UP	3.60E-03
ENSG00000113758.13	DBN1	1.24	UP	3.61E-03
ENSG00000081800.9	SLC13A1	1.38	UP	3.67E-03
ENSG00000164175.15	SLC45A2	1.52	UP	3.73E-03
ENSG00000133107.15	TRPC4	1.50	UP	3.79E-03
ENSG00000111799.21	COL12A1	1.05	UP	3.83E-03
ENSG00000149782.11	PLCB3	1.54	UP	3.84E-03
ENSG00000170190.16	SLC16A5	1.17	UP	3.91E-03
ENSG00000227729.5	RD3L	1.57	UP	3.92E-03
ENSG00000157734.14	SNX22	-1.10	DOWN	3.95E-03
ENSG00000155659.15	VSIG4	1.53	UP	3.95E-03
ENSG00000104142.11	VPS18	1.08	UP	4.02E-03
ENSG00000071242.12	RPS6KA2	-1.12	DOWN	4.19E-03
ENSG00000126010.6	GRPR	-1.51	DOWN	4.30E-03
ENSG00000104856.14	RELB	1.10	UP	4.32E-03
ENSG00000100918.13	REC8	1.09	UP	4.35E-03
ENSG00000102383.14	ZDHHC15	-1.23	DOWN	4.44E-03
ENSG00000177414.13	UBE2U	1.68	UP	4.55E-03
ENSG00000186642.16	PDE2A	1.44	UP	4.56E-03
ENSG00000163472.19	TMEM79	1.27	UP	4.77E-03
ENSG00000137731.14	FXD2	-1.39	DOWN	4.81E-03

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000169064.12	ZBBX	1.25	UP	4.92E-03
ENSG00000162520.15	SYNC	1.08	UP	5.15E-03
ENSG00000144668.12	ITGA9	1.35	UP	5.26E-03
ENSG00000156219.16	ART3	1.46	UP	5.43E-03
ENSG00000173868.11	PHOSPHO1	-1.14	DOWN	5.51E-03
ENSG00000256660.6	CLEC12B	1.12	UP	5.59E-03
ENSG00000204952.3	FBXO47	1.46	UP	5.65E-03
ENSG00000167332.9	OR51E2	1.97	UP	5.72E-03
ENSG00000109472.14	CPE	1.22	UP	5.73E-03
ENSG00000152592.14	DMP1	1.86	UP	5.74E-03
ENSG00000170558.9	CDH2	-1.05	DOWN	5.78E-03
ENSG00000153993.13	SEMA3D	-1.01	DOWN	5.96E-03
ENSG00000206531.10	CD200R1L	-1.25	DOWN	5.96E-03
ENSG00000119608.13	PROX2	-1.29	DOWN	6.01E-03
ENSG00000177494.6	ZBED2	-1.66	DOWN	6.11E-03
ENSG00000261611.6	AC010547.4	-1.01	DOWN	6.22E-03
ENSG00000182168.15	UNC5C	1.25	UP	6.28E-03
ENSG00000125848.10	FLRT3	1.65	UP	6.29E-03
ENSG00000205858.10	LRRC72	1.64	UP	6.40E-03
ENSG00000123500.10	COL10A1	-1.20	DOWN	6.52E-03
ENSG00000160877.6	NACC1	1.18	UP	6.54E-03
ENSG00000100767.17	PAPLN	1.01	UP	7.25E-03
ENSG00000162598.13	C1orf87	1.30	UP	7.27E-03
ENSG00000169291.10	SHE	-1.18	DOWN	7.28E-03
ENSG00000232268.6	OR52I1	1.50	UP	7.57E-03
ENSG00000175489.10	LRRC25	1.09	UP	7.65E-03
ENSG00000167105.8	TMEM92	1.51	UP	7.67E-03
ENSG00000075275.17	CELSR1	-1.03	DOWN	7.67E-03
ENSG00000146904.9	EPHA1	-1.25	DOWN	7.94E-03
ENSG00000166925.9	TSC22D4	1.13	UP	8.06E-03
ENSG00000130768.15	SMPDL3B	1.43	UP	8.27E-03
ENSG00000170790.5	OR10A2	1.69	UP	8.31E-03
ENSG00000154856.13	APCDD1	-1.21	DOWN	8.88E-03
ENSG00000130962.17	PRRG1	1.08	UP	8.91E-03
ENSG00000099203.7	TMED1	1.34	UP	8.93E-03
ENSG00000142185.16	TRPM2	1.38	UP	9.04E-03
ENSG00000206047.2	DEFA1	-1.51	DOWN	9.07E-03
ENSG00000149582.16	TMEM25	-1.22	DOWN	9.09E-03
ENSG00000120337.8	TNFSF18	1.25	UP	9.10E-03
ENSG00000169884.14	WNT10B	-1.16	DOWN	9.19E-03

**S1A Table. Differentially expressed coding transcripts in the contrast Acute and Convalescent.**  
(Continuação)

<b>Gene ID</b>	<b>Gene Name</b>	<b>Log2(FC)</b>	<b>Expression</b>	<b>P-adj</b>
ENSG00000205085.12	FAM71F2	1.10	UP	9.20E-03
ENSG00000115325.13	DOK1	1.06	UP	9.36E-03
ENSG00000160999.10	SH2B2	1.60	UP	9.45E-03
ENSG00000153976.3	HS3ST3A1	1.81	UP	9.51E-03
ENSG00000277639.2	AC007906.2	1.74	UP	9.63E-03
ENSG00000100949.14	RABGGTA	1.33	UP	9.71E-03
ENSG00000109099.15	PMP22	-1.40	DOWN	9.80E-03
ENSG00000186654.21	PRR5	1.13	UP	9.81E-03
ENSG00000121207.12	LRAT	1.27	UP	9.89E-03

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continua)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000232884.9	AF127936.1	4.08	UP	3.96E-73
ENSG00000233785.1	AC131011.2	5.21	UP	6.22E-67
ENSG00000260943.1	LINC02555	4.07	UP	6.00E-57
ENSG00000235192.1	AC009495.3	2.72	UP	1.79E-54
ENSG00000223960.7	CHROMR	2.79	UP	3.11E-54
ENSG00000233030.2	AC243772.2	4.09	UP	7.66E-53
ENSG00000226822.3	LINC02785	2.60	UP	2.48E-52
ENSG00000287181.1	AC107067.3	5.41	UP	7.98E-50
ENSG00000273247.5	AC097376.3	2.37	UP	1.86E-49
ENSG00000253214.2	AC079209.1	3.25	UP	2.13E-47
ENSG00000279296.1	PRAL	3.98	UP	5.09E-47
ENSG00000227502.3	MROCKI	3.98	UP	1.27E-45
ENSG00000287216.1	AC106865.2	4.25	UP	6.90E-44
ENSG00000263766.5	AC025682.2	2.47	UP	3.18E-42
ENSG00000270972.1	AC136475.9	4.47	UP	3.25E-42
ENSG00000286646.1	AL121933.2	2.05	UP	1.01E-40
ENSG00000255328.1	AC136475.5	4.20	UP	8.08E-39
ENSG00000279320.1	AC069528.2	3.04	UP	1.40E-38
ENSG00000231233.1	CFAP58-DT	3.25	UP	2.25E-38
ENSG00000213468.7	FIRRE	2.19	UP	7.04E-38
ENSG00000233070.1	ZFY-AS1	3.40	UP	1.31E-37
ENSG00000237781.3	ADAMTSL4-AS2	3.22	UP	1.13E-36
ENSG00000272491.1	AL109659.2	5.28	UP	2.58E-36
ENSG00000283384.1	AL138694.1	3.81	UP	2.70E-36
ENSG00000228863.8	AL121985.1	3.97	UP	6.62E-35
ENSG00000285492.1	AL356417.3	2.58	UP	2.65E-34
ENSG00000215769.8	ARHGAP27P1- BPTFP1-KPNA2P3	1.32	UP	1.69E-33
ENSG00000253210.2	AC040970.1	2.09	UP	2.60E-32
ENSG00000287188.1	AC068989.1	2.98	UP	3.97E-32
ENSG00000273272.2	U62317.4	2.77	UP	7.77E-32
ENSG00000280739.3	EIF1B-AS1	1.54	UP	1.40E-30
ENSG00000254602.2	AP000662.1	4.36	UP	2.18E-30
ENSG00000233355.7	CHRM3-AS2	-2.03	DOWN	3.07E-30
ENSG00000228318.3	AP001610.2	4.44	UP	6.54E-30
ENSG00000223552.1	CCR5AS	2.16	UP	1.85E-29
ENSG00000259268.2	AC007950.1	3.12	UP	5.30E-29
ENSG00000279236.1	AC064801.2	2.33	UP	5.79E-29
ENSG00000272462.3	U91328.1	1.99	UP	1.91E-28
ENSG00000234506.5	LINC01506	2.19	UP	2.15E-28

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000248489.2	LINC02062	2.57	UP	5.44E-28
ENSG00000228956.8	SATB1-AS1	-1.38	DOWN	9.83E-28
ENSG00000249309.1	AC020703.1	2.30	UP	1.41E-27
ENSG00000251230.6	MIR3945HG	2.94	UP	1.75E-27
ENSG00000257557.2	PPP1R12A-AS1	1.78	UP	3.21E-27
ENSG00000268027.5	AC243960.1	-1.52	DOWN	6.01E-27
ENSG00000230825.2	AC005532.1	2.46	UP	6.71E-27
ENSG00000197536.11	IRF1-AS1	2.26	UP	7.73E-27
ENSG00000250696.5	AC111000.4	-3.23	DOWN	8.04E-27
ENSG00000282851.2	BISPR	1.94	UP	1.25E-26
ENSG00000274536.7	AL034397.3	1.40	UP	1.83E-26
ENSG00000254420.1	AP003086.1	5.02	UP	2.58E-26
ENSG00000179818.14	PCBP1-AS1	1.89	UP	8.90E-26
ENSG00000225470.8	JPX	1.67	UP	1.10E-25
ENSG00000255733.6	IFNG-AS1	-1.60	DOWN	1.19E-25
ENSG00000226004.1	LINC02528	5.00	UP	4.98E-25
ENSG00000243176.6	AC092944.1	1.16	UP	1.04E-24
ENSG00000203999.9	LINC01270	2.60	UP	9.85E-24
ENSG00000224616.3	RTCA-AS1	1.26	UP	1.09E-23
ENSG00000270820.6	AC016727.1	1.49	UP	1.24E-23
ENSG00000223914.4	LINC02471	2.35	UP	1.40E-23
ENSG00000265975.1	AC002091.1	2.62	UP	1.45E-23
ENSG00000285710.1	AC012184.4	3.26	UP	1.88E-23
ENSG00000233154.6	LINC01762	2.05	UP	1.94E-23
ENSG00000250548.7	LINC01303	2.49	UP	2.18E-23
ENSG00000246430.7	LINC00968	2.05	UP	3.71E-23
ENSG00000272316.1	AL021368.2	-1.28	DOWN	4.68E-23
ENSG00000255760.2	LINC02422	2.00	UP	6.33E-23
ENSG00000247199.5	AC011346.1	1.65	UP	9.35E-23
ENSG00000286122.1	AC016074.2	1.60	UP	1.25E-22
ENSG00000247853.2	AC006064.2	1.90	UP	2.22E-22
ENSG00000245060.8	LINC00847	1.59	UP	3.03E-22
ENSG00000237927.1	AL078604.2	2.61	UP	5.05E-22
ENSG00000237943.7	PRKCQ-AS1	-1.34	DOWN	8.44E-22
ENSG00000225964.6	NRIR	3.14	UP	8.55E-22
ENSG00000255355.1	AP000640.2	3.86	UP	1.31E-21
ENSG00000246375.3	PPM1K-DT	3.81	UP	2.03E-21
ENSG00000267745.1	AC060766.7	1.96	UP	2.24E-21
ENSG00000231535.7	LINC00278	1.66	UP	3.20E-21
ENSG00000232021.7	LEF1-AS1	-2.27	DOWN	3.51E-21
ENSG00000286885.1	AL138824.1	1.94	UP	5.65E-21

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000172965.17	MIR4435-2HG	1.39	UP	7.48E-21
ENSG00000235513.2	L3MBTL2-AS1	2.53	UP	9.49E-21
ENSG00000238113.7	LINC01410	2.10	UP	1.84E-20
ENSG00000273133.1	AC116651.1	2.64	UP	2.23E-20
ENSG00000277511.1	AC116407.2	2.81	UP	2.35E-20
ENSG00000274020.4	LINC01138	1.19	UP	2.55E-20
ENSG00000260228.6	AC009119.1	1.33	UP	3.83E-20
ENSG00000287393.1	AL591468.1	4.51	UP	8.36E-20
ENSG00000203804.4	ADAMTSL4-AS1	1.59	UP	1.08E-19
ENSG00000286978.1	AC107067.2	3.89	UP	1.60E-19
ENSG00000250608.2	AC010210.1	1.52	UP	1.99E-19
ENSG00000183784.7	DOCK8-AS1	2.02	UP	2.13E-19
ENSG00000275210.1	AC245884.11	2.34	UP	2.51E-19
ENSG00000245164.8	LINC00861	-1.34	DOWN	3.19E-19
ENSG00000224789.1	AC012363.2	3.61	UP	5.03E-19
ENSG00000280120.1	AC073857.1	-1.40	DOWN	7.44E-19
ENSG00000232774.8	AL355916.1	1.97	UP	7.60E-19
ENSG00000251323.3	LINC02728	2.18	UP	9.79E-19
ENSG00000254288.1	AC087672.2	2.70	UP	1.32E-18
ENSG00000285006.1	AC005280.3	1.73	UP	1.42E-18
ENSG00000222041.11	CYTOR	1.51	UP	1.47E-18
ENSG00000232912.6	RERE-AS1	1.54	UP	1.94E-18
ENSG00000286256.2	AC084871.4	2.52	UP	2.12E-18
ENSG00000279349.1	AC092692.1	1.89	UP	2.79E-18
ENSG00000223387.6	LINC02068	4.45	UP	4.03E-18
ENSG00000272914.1	AL359532.1	2.13	UP	4.46E-18
ENSG00000235532.1	LINC00402	-1.79	DOWN	4.57E-18
ENSG00000233461.6	AL445524.1	1.69	UP	5.21E-18
ENSG00000227017.1	AC007036.1	3.64	UP	6.55E-18
ENSG00000286076.1	AC005050.3	2.78	UP	7.16E-18
ENSG00000281398.4	SNHG4	-1.36	DOWN	7.19E-18
ENSG00000225940.7	C5orf67	2.30	UP	1.15E-17
ENSG00000256433.3	AC005840.2	2.40	UP	1.53E-17
ENSG00000228495.2	LINC01013	-1.76	DOWN	1.88E-17
ENSG00000280734.3	LINC01232	1.47	UP	2.22E-17
ENSG00000229151.2	AC233976.1	-1.85	DOWN	2.39E-17
ENSG00000260711.2	AL121839.2	-1.58	DOWN	2.60E-17
ENSG00000224078.15	SNHG14	-1.19	DOWN	2.78E-17
ENSG00000225889.8	AC012368.1	1.57	UP	4.58E-17
ENSG00000280007.1	AC008079.1	2.39	UP	5.02E-17
ENSG00000267325.2	LINC01415	2.44	UP	9.23E-17

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000285399.3	AC104162.2	1.28	UP	1.18E-16
ENSG00000251072.2	LMNB1-DT	3.06	UP	1.19E-16
ENSG00000226758.1	DISC1-IT1	2.52	UP	1.32E-16
ENSG00000258922.1	AC106028.2	1.51	UP	1.42E-16
ENSG00000281100.1	AC105749.1	1.84	UP	1.57E-16
ENSG00000233184.7	AC093157.1	-1.23	DOWN	2.03E-16
ENSG00000215068.8	AC025171.2	1.23	UP	2.14E-16
ENSG00000286044.1	AP001977.1	2.76	UP	3.00E-16
ENSG00000266604.1	LINC01887	3.48	UP	3.02E-16
ENSG00000261211.1	AL031123.2	2.97	UP	3.52E-16
ENSG00000274184.1	AC011815.2	1.81	UP	4.34E-16
ENSG00000225342.2	LRRK2-DT	1.62	UP	4.71E-16
ENSG00000180769.10	WDFY3-AS2	1.75	UP	8.26E-16
ENSG00000270030.1	AC136475.7	3.08	UP	9.82E-16
ENSG00000272669.1	AL021707.6	2.76	UP	1.07E-15
ENSG00000226950.7	DANCR	-1.40	DOWN	1.10E-15
ENSG00000245556.3	SCAMP1-AS1	1.25	UP	1.19E-15
ENSG00000284882.1	AL359762.1	1.72	UP	1.21E-15
ENSG00000245937.8	LINC01184	-1.01	DOWN	1.28E-15
ENSG00000273320.1	AC007032.1	2.19	UP	1.29E-15
ENSG00000224950.2	AL390066.2	1.56	UP	1.31E-15
ENSG00000278897.1	AC020951.1	-1.16	DOWN	1.84E-15
ENSG00000223799.1	IL10RB-DT	1.95	UP	2.70E-15
ENSG00000284930.1	AC005280.2	1.19	UP	3.96E-15
ENSG00000225411.3	CR786580.1	1.71	UP	4.33E-15
ENSG00000271856.1	LINC01215	-1.45	DOWN	6.34E-15
ENSG00000223525.1	RABGAP1L-IT1	2.34	UP	6.35E-15
ENSG00000247287.3	AL359220.1	-1.21	DOWN	7.19E-15
ENSG00000286330.1	AL353660.1	-1.34	DOWN	8.31E-15
ENSG00000267365.1	KCNJ2-AS1	1.69	UP	8.70E-15
ENSG00000255507.6	UVRAG-DT	2.37	UP	9.01E-15
ENSG00000287263.1	AC008875.3	1.55	UP	1.03E-14
ENSG00000272567.1	AC109347.2	1.98	UP	1.40E-14
ENSG00000260361.1	AC106028.3	2.17	UP	1.40E-14
ENSG00000253522.6	MIR3142HG	-1.46	DOWN	1.61E-14
ENSG00000228107.1	AP000692.1	1.40	UP	1.63E-14
ENSG00000236088.10	COX10-AS1	-1.04	DOWN	2.03E-14
ENSG00000225434.3	LINC01504	1.27	UP	3.74E-14
ENSG00000284669.1	AC092053.4	4.10	UP	3.91E-14
ENSG00000279913.1	AP001962.1	1.54	UP	4.26E-14
ENSG00000229331.1	GK-IT1	1.64	UP	4.42E-14

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000286273.1	AC078816.1	2.88	UP	6.34E-14
ENSG00000206344.7	HCG27	1.20	UP	6.89E-14
ENSG00000224152.1	AC009506.2	1.63	UP	7.04E-14
ENSG00000258867.6	LINC01146	1.42	UP	7.06E-14
ENSG00000212743.2	LINC02656	1.79	UP	7.20E-14
ENSG00000272563.1	AC016745.2	2.56	UP	7.67E-14
ENSG00000258926.2	AL355916.2	2.92	UP	1.14E-13
ENSG00000265666.1	RARA-AS1	1.34	UP	1.15E-13
ENSG00000272941.1	AC083862.2	1.73	UP	1.21E-13
ENSG00000254721.1	AP000879.1	4.04	UP	1.37E-13
ENSG00000206337.12	HCP5	1.15	UP	1.38E-13
ENSG00000272810.1	U91328.3	2.67	UP	1.44E-13
ENSG00000279727.1	LINC02033	1.91	UP	1.79E-13
ENSG00000258777.1	HIF1A-AS1	2.97	UP	1.79E-13
ENSG00000241886.1	AC112496.1	1.72	UP	1.91E-13
ENSG00000251379.1	AC099550.1	1.65	UP	2.13E-13
ENSG00000266088.6	AC004585.1	-1.46	DOWN	2.33E-13
ENSG00000250069.1	AC011379.1	2.18	UP	2.57E-13
ENSG00000248455.6	LINC02217	2.07	UP	3.07E-13
ENSG00000267547.1	AC060766.4	1.72	UP	4.10E-13
ENSG00000261471.1	AC092145.1	1.88	UP	4.17E-13
ENSG00000267152.1	AC093227.1	-1.34	DOWN	4.53E-13
ENSG00000224397.7	SMIM25	1.98	UP	5.19E-13
ENSG00000269821.1	KCNQ1OT1	1.08	UP	5.19E-13
ENSG00000205300.3	AL356414.1	3.23	UP	5.65E-13
ENSG00000261553.5	AL137782.1	-1.27	DOWN	5.78E-13
ENSG00000233214.1	AC002511.2	3.02	UP	6.94E-13
ENSG00000233975.1	LINC02574	3.60	UP	7.03E-13
ENSG00000232931.6	LINC00342	-1.07	DOWN	1.03E-12
ENSG00000279311.1	AC092999.1	2.12	UP	1.10E-12
ENSG00000259005.1	AC005479.1	2.01	UP	1.14E-12
ENSG00000256357.1	AL132708.1	2.47	UP	1.25E-12
ENSG00000246223.9	LINC01550	-1.40	DOWN	1.31E-12
ENSG00000281162.2	LINC01127	1.85	UP	1.56E-12
ENSG00000260296.1	AC095057.3	-1.30	DOWN	1.70E-12
ENSG00000250274.1	AC034199.1	1.89	UP	1.96E-12
ENSG00000251139.2	AC084871.2	2.75	UP	2.54E-12
ENSG00000226067.7	LINC00623	1.41	UP	2.86E-12
ENSG00000214922.9	HLA-F-AS1	1.20	UP	3.21E-12
ENSG00000278970.2	HEIH	1.73	UP	3.51E-12
ENSG00000229425.3	AJ009632.2	1.93	UP	3.81E-12

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000264558.1	AC015674.1	2.55	UP	4.24E-12
ENSG00000223725.6	AC009226.1	-1.99	DOWN	5.09E-12
ENSG00000253438.4	PCAT1	1.00	UP	5.62E-12
ENSG00000287032.1	AC018647.3	1.44	UP	5.78E-12
ENSG00000272054.1	AC007390.2	-1.06	DOWN	6.20E-12
ENSG00000228817.4	BACH1-IT2	1.18	UP	6.28E-12
ENSG00000286153.1	AP000331.1	2.33	UP	8.01E-12
ENSG00000276564.1	AC130650.2	-1.36	DOWN	9.13E-12
ENSG00000235321.1	AC007556.1	2.19	UP	9.96E-12
ENSG00000254325.2	AC018607.1	1.29	UP	1.05E-11
ENSG00000258667.2	HIF1A-AS3	2.36	UP	1.09E-11
ENSG00000236345.1	SCAT8	1.05	UP	1.12E-11
ENSG00000270000.1	AC005479.2	1.88	UP	1.15E-11
ENSG00000232311.1	AL512303.1	1.42	UP	1.16E-11
ENSG00000259363.6	AC090825.1	-1.05	DOWN	1.23E-11
ENSG00000264456.1	AC138207.4	1.41	UP	1.42E-11
ENSG00000255133.2	LINC02721	3.14	UP	1.71E-11
ENSG00000215244.3	LINC02649	1.56	UP	1.81E-11
ENSG00000280270.1	AC068299.2	3.09	UP	1.94E-11
ENSG00000274922.1	AL139384.1	1.18	UP	2.25E-11
ENSG00000271964.1	AC090948.1	-1.43	DOWN	2.45E-11
ENSG00000245904.4	AC025164.2	-1.47	DOWN	2.48E-11
ENSG00000237568.1	AC099063.1	2.46	UP	2.78E-11
ENSG00000255337.1	AP001830.1	2.46	UP	2.93E-11
ENSG00000238045.9	AC009133.1	1.97	UP	3.29E-11
ENSG00000225948.2	LINC02648	-1.38	DOWN	3.38E-11
ENSG00000230438.7	SERPINB9P1	1.39	UP	3.64E-11
ENSG00000237576.2	LINC01888	1.61	UP	3.75E-11
ENSG00000250508.1	LINC02701	2.30	UP	4.74E-11
ENSG00000260368.1	AC027373.1	1.17	UP	4.89E-11
ENSG00000272369.1	AC008035.1	2.07	UP	4.90E-11
ENSG00000271554.1	AL138787.2	2.14	UP	5.18E-11
ENSG00000273972.1	AC068722.2	2.14	UP	5.40E-11
ENSG00000226530.2	AL158055.1	-1.64	DOWN	5.53E-11
ENSG00000249173.6	LINC01093	3.67	UP	6.55E-11
ENSG00000260400.1	AL513534.3	-1.51	DOWN	6.63E-11
ENSG00000272666.1	U62317.1	2.02	UP	6.76E-11
ENSG00000237311.3	AL034397.2	1.96	UP	9.04E-11
ENSG00000249502.3	AC006160.1	1.45	UP	1.12E-10
ENSG00000180712.4	LINC02363	1.75	UP	1.18E-10
ENSG00000249096.7	LINC02362	1.22	UP	1.39E-10

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000270426.1	AC099343.3	1.19	UP	1.41E-10
ENSG00000214708.4	AC116407.1	2.49	UP	1.44E-10
ENSG00000259418.1	AC091117.3	2.15	UP	1.51E-10
ENSG00000237626.2	AL161629.1	2.66	UP	2.23E-10
ENSG00000234883.6	MIR155HG	-1.13	DOWN	2.39E-10
ENSG00000254477.2	AP000640.1	1.20	UP	2.40E-10
ENSG00000254952.1	LINC02705	1.48	UP	2.49E-10
ENSG00000267731.1	AC005332.2	-1.12	DOWN	2.60E-10
ENSG00000272980.4	Z94721.2	-1.28	DOWN	2.78E-10
ENSG00000287131.1	AC096970.1	2.49	UP	2.80E-10
ENSG00000286236.1	AC018755.5	1.54	UP	3.22E-10
ENSG00000251002.8	AC244502.1	1.53	UP	3.28E-10
ENSG00000254396.1	AL355432.1	-2.66	DOWN	3.49E-10
ENSG00000237980.2	LINC02773	2.43	UP	3.79E-10
ENSG00000253736.3	AC022217.4	1.47	UP	3.87E-10
ENSG00000287193.1	AC132938.7	1.73	UP	4.17E-10
ENSG00000287255.1	AC007877.1	1.85	UP	4.38E-10
ENSG00000229140.10	CCDC26	1.38	UP	6.24E-10
ENSG00000231682.1	LINC01891	-1.38	DOWN	6.76E-10
ENSG00000230649.3	AC024084.2	1.21	UP	6.84E-10
ENSG00000205837.7	LINC00487	2.33	UP	7.16E-10
ENSG00000233844.1	KCNQ5-IT1	-1.48	DOWN	7.58E-10
ENSG00000279400.1	AC008957.3	2.14	UP	1.07E-09
ENSG00000287620.1	AC092053.5	2.64	UP	1.18E-09
ENSG00000287510.1	AL137857.1	1.53	UP	1.35E-09
ENSG00000232680.2	AC002511.1	2.55	UP	1.50E-09
ENSG00000232031.1	AL078599.3	1.39	UP	1.52E-09
ENSG00000235903.9	CPB2-AS1	1.23	UP	1.54E-09
ENSG00000283648.1	AC006974.2	2.54	UP	1.58E-09
ENSG00000234076.1	TPRG1-AS1	2.33	UP	1.61E-09
ENSG00000257285.6	AL132780.1	1.72	UP	1.70E-09
ENSG00000271646.1	AC099343.4	1.15	UP	2.67E-09
ENSG00000251131.2	AC025171.3	1.42	UP	2.79E-09
ENSG00000260742.1	AC009962.1	1.48	UP	2.79E-09
ENSG00000243797.6	AC004917.1	2.11	UP	2.80E-09
ENSG00000268170.2	AC073342.2	1.71	UP	2.81E-09
ENSG00000230539.1	AOAH-IT1	1.22	UP	3.18E-09
ENSG00000215533.8	LINC00189	1.97	UP	3.19E-09
ENSG00000276900.1	AC023157.3	1.18	UP	3.44E-09
ENSG00000251442.6	LINC01094	1.27	UP	3.70E-09
ENSG00000250616.2	AC012645.1	-1.35	DOWN	4.67E-09

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000286177.1	AC011462.5	1.44	UP	4.73E-09
ENSG00000255029.2	AC110058.1	2.76	UP	4.75E-09
ENSG00000279227.1	AC009303.4	1.90	UP	5.27E-09
ENSG00000205056.8	LINC02397	-1.27	DOWN	5.33E-09
ENSG00000259536.5	AC091045.2	-1.91	DOWN	6.21E-09
ENSG00000249937.8	LINC02223	2.34	UP	6.23E-09
ENSG00000247982.6	LINC00926	-1.56	DOWN	6.28E-09
ENSG00000264235.6	AP005329.1	1.16	UP	6.40E-09
ENSG00000287100.1	AL078600.1	1.29	UP	6.76E-09
ENSG00000285108.1	AC103718.1	2.24	UP	7.05E-09
ENSG00000234756.1	LINC02621	3.03	UP	7.12E-09
ENSG00000278231.1	AL133342.1	1.20	UP	7.24E-09
ENSG00000280248.1	AC124319.3	2.28	UP	7.40E-09
ENSG00000254362.1	AC011726.3	1.60	UP	7.86E-09
ENSG00000256262.1	USP30-AS1	1.39	UP	8.41E-09
ENSG00000237505.8	PKN2-AS1	2.07	UP	9.11E-09
ENSG00000230789.1	ARHGAP26-IT1	1.10	UP	1.04E-08
ENSG00000287875.1	AC068193.1	1.29	UP	1.06E-08
ENSG00000272498.1	AC090948.2	-1.42	DOWN	1.17E-08
ENSG00000215424.10	MCM3AP-AS1	-1.19	DOWN	1.18E-08
ENSG00000270659.1	AC079610.1	-1.23	DOWN	1.21E-08
ENSG00000203497.2	PDCD4-AS1	1.66	UP	1.24E-08
ENSG00000229852.4	AC019205.1	-1.20	DOWN	1.27E-08
ENSG00000275278.1	AC012150.2	1.47	UP	1.34E-08
ENSG00000246273.8	SBF2-AS1	-1.11	DOWN	1.39E-08
ENSG00000272558.1	U91328.2	2.74	UP	1.43E-08
ENSG00000234998.1	AC244453.3	2.65	UP	1.44E-08
ENSG00000253838.1	AC007991.2	3.09	UP	1.84E-08
ENSG00000286162.2	AL162253.2	1.46	UP	1.87E-08
ENSG00000225731.1	AP001627.1	2.85	UP	1.91E-08
ENSG00000274015.2	AL136038.7	-1.31	DOWN	1.91E-08
ENSG00000226312.7	CFLAR-AS1	1.65	UP	1.94E-08
ENSG00000197301.7	HMGA2-AS1	1.52	UP	2.06E-08
ENSG00000273038.2	AL365203.2	-1.10	DOWN	2.13E-08
ENSG00000279513.1	AL157902.2	-1.28	DOWN	2.17E-08
ENSG00000269951.1	AC090181.2	-1.37	DOWN	2.25E-08
ENSG00000230735.1	AC093423.2	-1.22	DOWN	2.26E-08
ENSG00000227945.1	AL590006.1	-2.08	DOWN	2.33E-08
ENSG00000227082.3	LINC02798	1.73	UP	2.38E-08
ENSG00000264672.6	SEPTIN4-AS1	2.10	UP	2.43E-08
ENSG00000257433.6	AC004241.1	1.01	UP	2.49E-08

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000278668.1	AC005899.8	1.64	UP	2.88E-08
ENSG00000271734.1	Z98200.2	1.23	UP	3.16E-08
ENSG00000259182.5	AC019254.1	2.56	UP	3.34E-08
ENSG00000256448.5	AP000763.3	1.09	UP	3.58E-08
ENSG00000287549.1	AC092268.2	2.38	UP	3.58E-08
ENSG00000287367.1	AC016583.2	1.65	UP	3.74E-08
ENSG00000266389.1	AC002091.2	1.71	UP	3.76E-08
ENSG00000254649.1	AP003086.2	3.25	UP	4.64E-08
ENSG00000226891.9	LINC01359	1.04	UP	5.19E-08
ENSG00000215196.5	BASP1-AS1	1.94	UP	5.36E-08
ENSG00000283064.1	AL353759.1	1.57	UP	5.37E-08
ENSG00000253986.1	AC104561.3	1.92	UP	5.82E-08
ENSG00000256582.1	LINC02390	-1.34	DOWN	6.33E-08
ENSG00000254211.6	LINC01485	1.76	UP	6.48E-08
ENSG00000237188.5	AC242426.2	1.58	UP	7.84E-08
ENSG00000269952.1	AL117336.1	1.57	UP	8.11E-08
ENSG00000261997.1	AC007336.1	1.20	UP	8.45E-08
ENSG00000256803.1	AC024224.2	1.94	UP	8.53E-08
ENSG00000287644.1	AC080112.5	2.12	UP	9.34E-08
ENSG00000256427.2	AC010175.1	-1.68	DOWN	9.52E-08
ENSG00000286458.1	AC083870.1	-1.42	DOWN	9.53E-08
ENSG00000249667.1	LINC01259	-1.67	DOWN	9.65E-08
ENSG00000245080.7	MIR3150BHG	2.08	UP	9.88E-08
ENSG00000272777.1	AC019131.2	-1.25	DOWN	9.97E-08
ENSG00000181908.5	LINC02724	1.60	UP	1.06E-07
ENSG00000259375.1	AC087286.3	1.92	UP	1.07E-07
ENSG00000215765.3	AC245128.1	2.72	UP	1.08E-07
ENSG00000288562.1	AL049198.1	1.81	UP	1.10E-07
ENSG00000240859.3	AC093627.4	1.14	UP	1.16E-07
ENSG00000278972.1	AC015920.1	-1.39	DOWN	1.21E-07
ENSG00000231528.3	FAM225A	2.59	UP	1.27E-07
ENSG00000226777.7	FAM30A	-1.00	DOWN	1.33E-07
ENSG00000267711.1	AC060766.6	1.64	UP	1.50E-07
ENSG00000272842.1	AL391834.1	-1.52	DOWN	1.53E-07
ENSG00000272338.2	AC067838.1	-1.42	DOWN	1.56E-07
ENSG00000270681.1	AC095055.1	-1.69	DOWN	1.63E-07
ENSG00000234389.1	AC007278.1	1.99	UP	1.65E-07
ENSG00000277548.1	AC018926.3	1.04	UP	1.69E-07
ENSG00000287485.1	AL451166.1	2.13	UP	1.74E-07
ENSG00000228906.1	AL353804.1	1.60	UP	1.79E-07
ENSG00000272144.1	AC025171.4	1.03	UP	1.84E-07

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000234553.1	AC022431.1	2.30	UP	1.93E-07
ENSG00000224418.1	STK24-AS1	1.20	UP	1.95E-07
ENSG00000287733.1	AC083862.3	1.20	UP	1.97E-07
ENSG00000257258.2	AC012150.1	1.49	UP	1.98E-07
ENSG00000241490.1	AC093010.2	-1.26	DOWN	1.99E-07
ENSG00000253983.3	AC087627.1	2.13	UP	2.06E-07
ENSG00000251259.1	AC004069.1	1.07	UP	2.20E-07
ENSG00000224666.3	ETV7-AS1	2.68	UP	2.34E-07
ENSG00000275846.1	AL513548.3	-1.21	DOWN	2.36E-07
ENSG00000233338.1	TLR8-AS1	2.22	UP	2.36E-07
ENSG00000280832.1	GSEC	1.66	UP	2.67E-07
ENSG00000228363.2	AC015971.1	-1.44	DOWN	2.68E-07
ENSG00000270105.1	AC136475.8	3.16	UP	2.91E-07
ENSG00000279267.1	AL078621.3	-1.19	DOWN	3.41E-07
ENSG00000260517.3	AC009093.2	-1.18	DOWN	3.50E-07
ENSG00000258511.1	LINC02295	-1.96	DOWN	3.76E-07
ENSG00000205537.2	AC121338.1	1.68	UP	3.96E-07
ENSG00000246898.1	LINC00920	-1.40	DOWN	4.03E-07
ENSG00000279463.1	AL159972.1	-1.37	DOWN	4.17E-07
ENSG00000229056.2	HECW2-AS1	-1.48	DOWN	4.31E-07
ENSG00000272918.1	AC005070.3	-1.02	DOWN	5.48E-07
ENSG00000249771.2	AC108210.1	1.18	UP	5.73E-07
ENSG00000260528.5	FAM157C	1.30	UP	5.77E-07
ENSG00000258479.6	LINC00640	1.65	UP	5.84E-07
ENSG00000284977.2	AL160272.1	1.07	UP	6.45E-07
ENSG00000214870.9	AC004540.1	1.65	UP	6.49E-07
ENSG00000251867.4	AC009812.1	-1.37	DOWN	6.60E-07
ENSG00000278090.3	LUNAR1	-1.79	DOWN	6.62E-07
ENSG00000274173.1	AL035661.1	1.82	UP	6.91E-07
ENSG00000244479.7	OR2A1-AS1	-1.11	DOWN	6.93E-07
ENSG00000246548.3	LINC02288	2.10	UP	7.30E-07
ENSG00000285994.1	AL731559.1	-1.28	DOWN	7.87E-07
ENSG00000261754.2	AC008555.1	-1.23	DOWN	8.54E-07
ENSG00000233230.1	AC079807.1	1.03	UP	8.80E-07
ENSG00000259994.1	AL353796.1	-1.05	DOWN	9.09E-07
ENSG00000260398.1	AC068700.1	-1.39	DOWN	9.18E-07
ENSG00000223466.2	LINC01825	-1.25	DOWN	9.22E-07
ENSG00000288542.1	AL133318.1	-1.42	DOWN	1.00E-06
ENSG00000230454.1	U73166.1	1.89	UP	1.06E-06
ENSG00000287201.1	AC009682.1	-1.10	DOWN	1.06E-06
ENSG00000240143.1	AL023653.1	1.33	UP	1.11E-06

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000260911.2	AC135050.3	1.62	UP	1.25E-06
ENSG00000254928.1	AP001372.3	1.88	UP	1.27E-06
ENSG00000273445.1	AC133644.2	1.16	UP	1.28E-06
ENSG00000233672.9	RNASEH2B-AS1	1.32	UP	1.35E-06
ENSG00000253924.2	AC103831.1	-1.10	DOWN	1.50E-06
ENSG00000280129.1	AL132780.5	1.02	UP	1.51E-06
ENSG00000226337.3	TMEM252-DT	1.57	UP	1.55E-06
ENSG00000261487.1	AC135048.1	1.32	UP	1.64E-06
ENSG00000277246.1	AL157762.1	1.12	UP	1.67E-06
ENSG00000277763.1	AL138995.1	1.06	UP	1.71E-06
ENSG00000236525.1	AC007278.2	1.65	UP	1.82E-06
ENSG00000278962.1	AC092645.1	-1.51	DOWN	2.08E-06
ENSG00000203801.8	LINC00222	1.47	UP	2.15E-06
ENSG00000273076.1	AL021707.7	2.15	UP	2.18E-06
ENSG00000286721.1	AC010623.1	-1.19	DOWN	2.19E-06
ENSG00000260923.7	LINC02193	1.65	UP	2.31E-06
ENSG00000273004.1	AL078644.2	1.74	UP	2.39E-06
ENSG00000238005.4	AL391832.2	1.33	UP	2.45E-06
ENSG00000280190.1	AC027279.4	-1.79	DOWN	2.64E-06
ENSG00000259319.1	AF111167.2	1.20	UP	2.69E-06
ENSG00000265907.2	AP000919.2	1.13	UP	2.82E-06
ENSG00000267904.1	AC024075.1	-1.36	DOWN	2.96E-06
ENSG00000272501.1	AL662844.4	1.10	UP	2.97E-06
ENSG00000286536.1	AL591506.1	1.37	UP	2.99E-06
ENSG00000233029.3	AC244453.2	1.95	UP	3.34E-06
ENSG00000260197.1	AC010889.1	-1.02	DOWN	3.57E-06
ENSG00000249252.5	C1QTNF7-AS1	1.44	UP	3.74E-06
ENSG00000227517.7	LINC01483	1.43	UP	4.12E-06
ENSG00000246016.2	LINC01513	1.52	UP	4.13E-06
ENSG00000260249.3	AC007608.3	2.11	UP	4.25E-06
ENSG00000282572.2	AC215522.2	1.48	UP	4.44E-06
ENSG00000234997.2	AC016745.1	1.84	UP	4.52E-06
ENSG00000240219.1	AL512306.2	1.39	UP	4.93E-06
ENSG00000236337.1	FMR1-IT1	1.21	UP	5.31E-06
ENSG00000266049.1	AP001011.2	1.48	UP	5.48E-06
ENSG00000259296.1	AC020892.2	2.15	UP	5.59E-06
ENSG00000272625.1	AP000919.4	1.10	UP	5.59E-06
ENSG00000287480.1	AL158832.2	1.77	UP	5.88E-06
ENSG00000245105.4	A2M-AS1	-1.23	DOWN	5.96E-06
ENSG00000266371.1	AC079915.1	1.48	UP	6.07E-06
ENSG00000261996.1	AC004706.1	-1.57	DOWN	6.12E-06

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000270120.1	AC007728.3	1.34	UP	6.76E-06
ENSG00000257764.2	AC020656.1	1.25	UP	7.49E-06
ENSG00000283743.2	Z84466.1	1.52	UP	7.60E-06
ENSG00000259376.1	AC090907.1	2.49	UP	7.82E-06
ENSG00000273265.1	CNNM3-DT	-1.28	DOWN	7.84E-06
ENSG00000234614.1	C2CD4D-AS1	-1.17	DOWN	7.93E-06
ENSG00000215458.8	AATBC	1.42	UP	8.03E-06
ENSG00000231105.2	ECE1-AS1	1.99	UP	8.20E-06
ENSG00000273196.1	AC062037.3	1.61	UP	9.21E-06
ENSG00000272288.6	AL451165.2	1.05	UP	9.47E-06
ENSG00000269925.1	Z98884.2	1.01	UP	9.84E-06
ENSG00000237101.1	AC092809.5	2.07	UP	9.90E-06
ENSG00000286511.1	Z95118.2	1.40	UP	9.94E-06
ENSG00000280276.1	AC009229.4	2.13	UP	1.04E-05
ENSG00000286633.1	AL160400.1	1.73	UP	1.04E-05
ENSG00000286965.1	AC108066.2	-1.14	DOWN	1.06E-05
ENSG00000276115.1	AC026356.2	-1.47	DOWN	1.09E-05
ENSG00000246174.9	KCTD21-AS1	-1.52	DOWN	1.09E-05
ENSG00000283286.1	AC093277.1	2.16	UP	1.09E-05
ENSG00000260188.1	AC002464.1	1.33	UP	1.18E-05
ENSG00000261218.5	AC099524.1	1.06	UP	1.21E-05
ENSG00000269220.1	LINC00528	1.17	UP	1.22E-05
ENSG00000204054.14	LINC00963	1.00	UP	1.23E-05
ENSG00000278740.1	AC005332.7	-1.02	DOWN	1.25E-05
ENSG00000273369.1	AC096586.2	-1.38	DOWN	1.37E-05
ENSG00000286545.1	AC092645.2	-1.48	DOWN	1.39E-05
ENSG00000243055.1	GK-AS1	1.96	UP	1.46E-05
ENSG00000285647.1	AL671883.3	2.79	UP	1.49E-05
ENSG00000285933.1	AP003498.3	-2.82	DOWN	1.50E-05
ENSG00000254231.3	AC103760.1	-1.17	DOWN	1.50E-05
ENSG00000230257.5	NFE4	1.16	UP	1.62E-05
ENSG00000273951.1	AL031667.3	-1.55	DOWN	1.71E-05
ENSG00000239265.5	CLRN1-AS1	2.35	UP	1.77E-05
ENSG00000258101.2	AC010173.1	1.34	UP	1.79E-05
ENSG00000266385.1	AC005899.6	1.87	UP	1.95E-05
ENSG00000270755.1	AL136141.1	2.43	UP	2.00E-05
ENSG00000204934.10	ATP6V0E2-AS1	-1.69	DOWN	2.21E-05
ENSG00000249993.1	BFSP2-AS1	-2.04	DOWN	2.31E-05
ENSG00000232063.2	AL691447.2	1.43	UP	2.32E-05
ENSG00000285535.2	AC021683.5	-1.32	DOWN	2.42E-05
ENSG00000249988.1	AC092546.1	-1.74	DOWN	2.47E-05

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000257275.6	AL139020.1	-1.17	DOWN	2.49E-05
ENSG00000286089.1	AC095057.4	-1.77	DOWN	2.50E-05
ENSG00000286797.1	AC009315.1	-1.79	DOWN	2.63E-05
ENSG00000235576.1	LINC01871	-1.20	DOWN	2.66E-05
ENSG00000231160.10	KLF3-AS1	-1.04	DOWN	2.79E-05
ENSG00000224356.5	AL356966.1	-1.14	DOWN	2.85E-05
ENSG00000227354.7	RBM26-AS1	-1.03	DOWN	2.87E-05
ENSG00000272529.1	AC090948.3	-1.18	DOWN	3.00E-05
ENSG00000273812.3	BX640514.2	1.50	UP	3.14E-05
ENSG00000225806.8	AL121917.1	-1.05	DOWN	3.15E-05
ENSG00000287778.1	AC006230.1	-1.16	DOWN	3.18E-05
ENSG00000253115.1	AC087672.1	1.95	UP	3.23E-05
ENSG00000280407.2	AC132872.4	2.72	UP	3.26E-05
ENSG00000241860.7	AL627309.5	1.24	UP	3.42E-05
ENSG00000265401.1	AC093484.3	1.43	UP	3.42E-05
ENSG00000279821.1	AC145098.2	1.79	UP	3.47E-05
ENSG00000286533.1	AL078604.4	2.11	UP	3.51E-05
ENSG00000240758.2	AC010655.2	-2.39	DOWN	3.54E-05
ENSG00000286375.1	AL512590.3	2.51	UP	3.75E-05
ENSG00000283897.2	AC011416.3	-1.43	DOWN	3.77E-05
ENSG00000248810.2	LINC02432	1.10	UP	3.77E-05
ENSG00000279481.1	AC104791.2	-1.26	DOWN	3.83E-05
ENSG00000286207.1	AC012443.2	1.15	UP	3.91E-05
ENSG00000281969.1	AL592158.1	1.74	UP	4.04E-05
ENSG00000287771.1	AC007271.1	1.27	UP	4.05E-05
ENSG00000243179.1	AC110769.1	1.34	UP	4.17E-05
ENSG00000286671.1	AC025253.2	-1.67	DOWN	4.48E-05
ENSG00000287665.1	AC092428.1	1.69	UP	4.49E-05
ENSG00000260000.2	AL133338.1	-1.03	DOWN	4.49E-05
ENSG00000232316.2	LINC02518	1.74	UP	4.60E-05
ENSG00000240527.1	AL365273.1	1.18	UP	4.70E-05
ENSG00000278861.1	AC117503.2	-1.61	DOWN	4.75E-05
ENSG00000287167.1	AL133313.1	2.70	UP	4.88E-05
ENSG00000276007.1	AC079414.3	-1.01	DOWN	4.96E-05
ENSG00000187904.3	AC097382.1	1.57	UP	5.02E-05
ENSG00000263627.1	PPP4R1-AS1	1.49	UP	5.18E-05
ENSG00000253532.1	AC107909.1	1.35	UP	5.22E-05
ENSG00000232656.8	IDI2-AS1	1.43	UP	5.38E-05
ENSG00000287736.1	AF305872.2	2.16	UP	5.51E-05
ENSG00000254054.3	AC087273.2	1.52	UP	5.83E-05
ENSG00000232504.5	ST3GAL5-AS1	1.39	UP	5.85E-05

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000270638.1	AL023806.1	-1.13	DOWN	5.86E-05
ENSG00000274964.1	AC026356.1	-1.12	DOWN	6.26E-05
ENSG00000234902.6	AC007879.3	-1.56	DOWN	6.26E-05
ENSG00000275582.1	AL031670.1	2.02	UP	6.40E-05
ENSG00000271109.2	AC008555.4	-1.10	DOWN	6.97E-05
ENSG00000244198.7	ARHGEF35-AS1	-1.07	DOWN	7.15E-05
ENSG00000237054.9	PRMT5-AS1	1.65	UP	7.22E-05
ENSG00000287030.1	AC107032.3	1.84	UP	7.30E-05
ENSG00000241657.1	TRBV11-2	-1.43	DOWN	7.36E-05
ENSG00000231858.5	AC067945.3	1.79	UP	7.47E-05
ENSG00000260816.2	AC027279.1	-1.31	DOWN	7.50E-05
ENSG00000254791.1	FAR1-IT1	1.18	UP	7.52E-05
ENSG00000272371.1	AL591167.1	-1.63	DOWN	7.60E-05
ENSG00000223776.5	LGALS8-AS1	2.11	UP	7.66E-05
ENSG00000288049.1	AC010889.2	-1.09	DOWN	7.70E-05
ENSG00000279491.1	AP003733.3	1.16	UP	7.75E-05
ENSG00000279511.1	AL356274.2	1.85	UP	7.76E-05
ENSG00000277969.1	AC006449.7	1.30	UP	7.88E-05
ENSG00000259544.1	AC021739.4	1.60	UP	8.07E-05
ENSG00000272909.1	AL122035.2	-1.09	DOWN	8.15E-05
ENSG00000224490.5	TTC21B-AS1	1.88	UP	8.31E-05
ENSG00000273112.1	AL590385.2	1.10	UP	8.42E-05
ENSG00000286940.1	AL645933.4	1.43	UP	8.70E-05
ENSG00000254554.1	AC080023.1	2.09	UP	8.97E-05
ENSG00000245954.8	LINC02273	-1.30	DOWN	9.11E-05
ENSG00000256948.1	AC026369.3	1.67	UP	9.12E-05
ENSG00000233559.2	LINC00513	1.83	UP	1.00E-04
ENSG00000240710.1	AL512306.3	1.19	UP	1.01E-04
ENSG00000279891.1	AC022498.2	1.25	UP	1.02E-04
ENSG00000287989.1	AL450352.1	-1.10	DOWN	1.10E-04
ENSG00000251034.2	AC087854.1	-1.00	DOWN	1.12E-04
ENSG00000257715.1	AC007298.1	1.07	UP	1.13E-04
ENSG00000260337.4	AC091544.4	1.86	UP	1.14E-04
ENSG00000230149.2	AL021707.3	2.63	UP	1.15E-04
ENSG00000122043.11	LINC00544	-1.31	DOWN	1.22E-04
ENSG00000278727.1	AC000403.1	1.16	UP	1.24E-04
ENSG00000272742.1	AC135457.1	1.35	UP	1.26E-04
ENSG00000286194.1	AC138207.9	1.10	UP	1.27E-04
ENSG00000224429.8	LINC00539	-1.25	DOWN	1.27E-04
ENSG00000276317.1	AL357033.3	1.34	UP	1.27E-04
ENSG00000236469.1	AC007881.2	2.03	UP	1.33E-04

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000272990.1	AC084036.1	-1.13	DOWN	1.36E-04
ENSG00000257052.1	AP003721.4	1.21	UP	1.39E-04
ENSG00000277496.1	AL357033.4	1.44	UP	1.39E-04
ENSG00000250348.1	AC113404.1	-1.63	DOWN	1.45E-04
ENSG00000225450.1	AL021707.1	1.91	UP	1.55E-04
ENSG00000287200.1	AC022506.2	1.51	UP	1.57E-04
ENSG00000243273.1	AC020636.1	1.72	UP	1.65E-04
ENSG00000273002.1	AL355388.1	1.03	UP	1.79E-04
ENSG00000226012.1	AP001434.1	1.91	UP	1.80E-04
ENSG00000251393.4	AC005280.1	1.15	UP	1.80E-04
ENSG00000224649.1	AF124730.2	2.16	UP	1.81E-04
ENSG00000231621.1	ANKRD44-AS1	-1.25	DOWN	1.86E-04
ENSG00000280064.1	AC130304.1	1.42	UP	1.86E-04
ENSG00000267632.1	AC067852.3	1.30	UP	1.92E-04
ENSG00000267058.1	AC006213.2	-1.09	DOWN	1.92E-04
ENSG00000280033.1	AC116407.4	1.45	UP	2.00E-04
ENSG00000254119.5	LINC02842	1.52	UP	2.01E-04
ENSG00000228526.7	MIR34AHG	1.56	UP	2.08E-04
ENSG00000276116.2	FUT8-AS1	-1.10	DOWN	2.13E-04
ENSG00000259062.2	ACTN1-AS1	1.36	UP	2.14E-04
ENSG00000287935.1	AC136297.1	1.28	UP	2.20E-04
ENSG00000259293.1	LIPC-AS1	1.66	UP	2.22E-04
ENSG00000272858.1	Z93930.3	-1.39	DOWN	2.23E-04
ENSG00000264575.1	LINC00526	-1.39	DOWN	2.26E-04
ENSG00000260317.1	AC009812.4	-1.05	DOWN	2.31E-04
ENSG00000233730.1	LINC01765	1.06	UP	2.35E-04
ENSG00000228329.3	LINC01890	1.80	UP	2.44E-04
ENSG00000237310.2	AC008267.5	-1.36	DOWN	2.48E-04
ENSG00000261737.1	AL049597.2	1.06	UP	2.50E-04
ENSG00000260992.1	DOCK9-DT	-1.64	DOWN	2.58E-04
ENSG00000228043.5	AC114763.1	1.01	UP	2.61E-04
ENSG00000258325.2	ITFG2-AS1	-1.28	DOWN	2.62E-04
ENSG00000276957.1	AL158063.1	-1.01	DOWN	2.63E-04
ENSG00000232184.1	AL662889.1	-1.11	DOWN	2.63E-04
ENSG00000279425.1	AC092279.3	-1.00	DOWN	2.66E-04
ENSG00000226089.2	AL122017.1	1.50	UP	2.71E-04
ENSG00000278864.1	AC055811.4	-1.13	DOWN	2.73E-04
ENSG00000227591.5	HSD11B1-AS1	1.27	UP	2.84E-04
ENSG00000273348.1	AC027449.1	-1.20	DOWN	2.88E-04
ENSG00000286171.1	AC073140.2	-2.03	DOWN	2.95E-04
ENSG00000272468.1	AL021807.1	1.39	UP	2.96E-04

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000231680.1	LINC02723	1.31	UP	2.97E-04
ENSG00000229017.7	LINC01277	1.05	UP	2.98E-04
ENSG00000213600.3	U73169.1	1.18	UP	3.04E-04
ENSG00000278983.1	AC048380.2	1.54	UP	3.07E-04
ENSG00000233610.1	LINC00462	1.64	UP	3.16E-04
ENSG00000274275.1	AC009831.3	-1.22	DOWN	3.19E-04
ENSG00000264659.2	AC064805.2	1.02	UP	3.19E-04
ENSG00000270933.1	AC010719.1	-1.23	DOWN	3.27E-04
ENSG00000233875.1	AL592078.1	1.36	UP	3.39E-04
ENSG00000259321.1	AL136295.2	1.14	UP	3.49E-04
ENSG00000226853.3	AC010894.2	1.37	UP	3.52E-04
ENSG00000260329.1	AC007541.1	-1.07	DOWN	3.62E-04
ENSG00000261267.1	AC026470.2	2.26	UP	3.63E-04
ENSG00000284606.1	AC105233.5	-1.33	DOWN	3.63E-04
ENSG00000236140.1	AC245014.1	-2.26	DOWN	3.72E-04
ENSG00000261135.1	AL137802.2	-2.19	DOWN	3.87E-04
ENSG00000204584.1	AC027801.1	1.26	UP	3.95E-04
ENSG00000275888.1	AC132872.3	2.14	UP	3.99E-04
ENSG00000204625.10	HCG9	1.64	UP	4.11E-04
ENSG00000261117.1	AC009486.1	2.32	UP	4.26E-04
ENSG00000267452.3	LINC02073	-1.64	DOWN	4.49E-04
ENSG00000238009.6	AL627309.1	1.29	UP	4.52E-04
ENSG00000276071.1	AC074138.1	-1.11	DOWN	4.84E-04
ENSG00000257303.2	AC073896.2	-1.13	DOWN	5.12E-04
ENSG00000282508.2	LINC01002	1.14	UP	5.14E-04
ENSG00000257681.1	AC025265.1	1.40	UP	5.31E-04
ENSG00000233056.2	ERVH48-1	-2.02	DOWN	5.39E-04
ENSG00000272465.1	AL031768.1	1.34	UP	5.62E-04
ENSG00000286782.1	AL355377.3	1.04	UP	5.66E-04
ENSG00000254789.3	AC073172.1	1.64	UP	5.68E-04
ENSG00000287299.1	AC012459.1	1.23	UP	5.71E-04
ENSG00000251584.2	AC096751.2	1.25	UP	5.72E-04
ENSG00000215374.6	FAM66B	-1.26	DOWN	5.81E-04
ENSG00000226571.2	AL592429.2	-1.02	DOWN	5.93E-04
ENSG00000267598.1	AC011446.2	1.19	UP	5.97E-04
ENSG00000267270.6	PARD6G-AS1	1.36	UP	5.98E-04
ENSG00000287092.1	AL589693.1	-1.20	DOWN	6.04E-04
ENSG00000285374.1	AL359762.2	1.61	UP	6.10E-04
ENSG00000286127.1	AP000553.8	1.23	UP	6.44E-04
ENSG00000265845.2	AC024267.5	1.34	UP	6.58E-04
ENSG00000233569.2	AL161630.1	1.90	UP	6.76E-04

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000235621.9	LINC00494	-1.09	DOWN	6.86E-04
ENSG00000261889.1	AC108134.2	1.85	UP	7.16E-04
ENSG00000272308.1	AC104113.1	-1.65	DOWN	7.19E-04
ENSG00000286975.1	AP005136.4	1.11	UP	7.42E-04
ENSG00000226383.7	LINC01876	-1.08	DOWN	7.43E-04
ENSG00000223711.1	AC069213.1	-1.36	DOWN	7.45E-04
ENSG00000253535.5	AC120193.1	-1.04	DOWN	7.47E-04
ENSG00000253559.1	OSGEPL1-AS1	-1.34	DOWN	7.57E-04
ENSG00000234290.2	AC116366.2	1.01	UP	7.64E-04
ENSG00000272516.1	AL158211.4	-1.23	DOWN	7.78E-04
ENSG00000229160.1	AC009229.2	2.35	UP	7.91E-04
ENSG00000255097.1	AP006259.1	1.18	UP	7.96E-04
ENSG00000285159.1	AL627422.2	-2.20	DOWN	8.02E-04
ENSG00000234293.1	BACH1-IT3	1.05	UP	8.06E-04
ENSG00000279294.1	AC092135.1	1.50	UP	8.07E-04
ENSG00000259687.2	LINC01220	1.03	UP	8.14E-04
ENSG00000230013.2	CT70	1.80	UP	8.38E-04
ENSG00000258082.1	AL391832.3	1.05	UP	8.50E-04
ENSG00000273305.1	AC009237.15	-1.35	DOWN	8.51E-04
ENSG00000272010.1	AC100814.2	-1.11	DOWN	8.62E-04
ENSG00000279665.1	AC012100.3	1.24	UP	8.73E-04
ENSG00000229388.1	LINC01715	-1.39	DOWN	8.86E-04
ENSG00000267128.2	RNF157-AS1	-1.53	DOWN	9.08E-04
ENSG00000249532.5	MIR302CHG	1.55	UP	9.12E-04
ENSG00000279066.1	HEXD-IT1	2.19	UP	9.26E-04
ENSG00000260823.1	AC026461.3	2.21	UP	9.37E-04
ENSG00000233834.6	AC005083.1	-1.21	DOWN	9.49E-04
ENSG00000279476.1	AC092139.3	1.12	UP	9.60E-04
ENSG00000225632.1	AL161644.1	-2.03	DOWN	9.68E-04
ENSG00000223697.3	AF230666.1	1.36	UP	1.01E-03
ENSG00000272851.1	AC096772.2	1.25	UP	1.01E-03
ENSG00000254829.1	AP003032.2	2.31	UP	1.02E-03
ENSG00000227045.1	AL589765.1	1.31	UP	1.03E-03
ENSG00000287418.1	AC013439.2	1.72	UP	1.04E-03
ENSG00000230896.1	AL604028.1	-1.32	DOWN	1.08E-03
ENSG00000286084.2	AL096794.1	-1.27	DOWN	1.08E-03
ENSG00000279554.1	AC130448.2	1.01	UP	1.08E-03
ENSG00000287077.1	AL157893.2	1.74	UP	1.09E-03
ENSG00000267174.5	AC011472.2	1.33	UP	1.09E-03
ENSG00000274105.1	AC084824.4	-1.01	DOWN	1.09E-03
ENSG00000247317.3	LY6E-DT	1.38	UP	1.10E-03

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000276476.3	AL136962.1	-1.13	DOWN	1.12E-03
ENSG00000228655.7	AC079793.1	1.32	UP	1.13E-03
ENSG00000280099.1	AL603750.1	-1.48	DOWN	1.14E-03
ENSG00000265206.5	AC004687.1	1.45	UP	1.14E-03
ENSG00000285761.1	AL645939.6	1.59	UP	1.16E-03
ENSG00000233755.1	AL050344.1	2.16	UP	1.18E-03
ENSG00000287863.1	AL139801.1	1.47	UP	1.20E-03
ENSG00000280119.1	AC093642.2	-1.26	DOWN	1.24E-03
ENSG00000230753.6	ZNF341-AS1	1.80	UP	1.32E-03
ENSG00000285554.1	AC242988.2	1.14	UP	1.33E-03
ENSG00000280167.1	AP000943.3	1.05	UP	1.40E-03
ENSG00000273118.1	AC093865.1	-1.18	DOWN	1.41E-03
ENSG00000270147.1	AC068620.2	-1.16	DOWN	1.42E-03
ENSG00000243960.1	AL390195.2	-1.16	DOWN	1.44E-03
ENSG00000272609.1	AC016252.1	2.22	UP	1.47E-03
ENSG00000251161.4	AC020661.1	2.33	UP	1.48E-03
ENSG00000234238.2	AC022498.1	1.33	UP	1.56E-03
ENSG00000277310.1	AC090246.1	1.54	UP	1.59E-03
ENSG00000272638.1	AC006027.1	1.40	UP	1.66E-03
ENSG00000258666.1	AL157871.4	2.16	UP	1.67E-03
ENSG00000274859.1	AC131238.1	1.82	UP	1.67E-03
ENSG00000272211.1	AC114760.2	1.56	UP	1.67E-03
ENSG00000277449.1	CEBPB-AS1	1.19	UP	1.69E-03
ENSG00000272716.1	AL121658.1	1.26	UP	1.76E-03
ENSG00000273314.1	AC005229.4	1.04	UP	1.78E-03
ENSG00000204860.5	FAM201A	-1.50	DOWN	1.80E-03
ENSG00000259088.1	AL137779.2	1.27	UP	1.84E-03
ENSG00000279989.1	AC011815.3	1.48	UP	1.85E-03
ENSG00000286118.1	AC234031.1	1.19	UP	1.85E-03
ENSG00000224388.1	BACE2-IT1	-1.98	DOWN	1.87E-03
ENSG00000261251.1	Z97055.2	-1.15	DOWN	1.87E-03
ENSG00000231412.2	AC005392.2	1.79	UP	2.01E-03
ENSG00000253190.4	AC084082.1	1.18	UP	2.07E-03
ENSG00000276968.1	AL158196.1	-1.28	DOWN	2.10E-03
ENSG00000230492.1	AL049651.1	1.32	UP	2.10E-03
ENSG00000272382.1	AC025171.5	1.64	UP	2.12E-03
ENSG00000228719.1	AL022313.2	1.93	UP	2.17E-03
ENSG00000279199.1	AC068669.1	1.06	UP	2.19E-03
ENSG00000283209.1	AC106858.1	1.40	UP	2.21E-03
ENSG00000231039.2	AL355303.1	2.14	UP	2.23E-03
ENSG00000271659.1	AL161729.4	-1.90	DOWN	2.26E-03

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000272583.1	AL592494.2	-1.02	DOWN	2.40E-03
ENSG00000270321.2	AC007953.2	1.70	UP	2.40E-03
ENSG00000260594.1	AC099313.1	2.22	UP	2.51E-03
ENSG00000267212.1	AC018761.3	1.37	UP	2.52E-03
ENSG00000253358.1	AC087439.1	1.54	UP	2.55E-03
ENSG00000269927.1	AC004817.3	1.69	UP	2.59E-03
ENSG00000272824.1	AC245100.7	1.52	UP	2.68E-03
ENSG00000257400.1	AC023161.1	1.57	UP	2.70E-03
ENSG00000256073.3	URB1-AS1	-1.25	DOWN	2.71E-03
ENSG00000281852.1	LINC00891	-1.54	DOWN	2.72E-03
ENSG00000260448.6	LCMT1-AS1	1.05	UP	2.75E-03
ENSG00000278948.1	AL031587.5	1.21	UP	2.79E-03
ENSG00000283108.1	AC011451.3	-1.27	DOWN	2.88E-03
ENSG00000258760.1	AL355076.2	-1.41	DOWN	2.92E-03
ENSG00000226904.1	AL353608.2	1.14	UP	2.94E-03
ENSG00000272130.1	AC091946.2	-1.17	DOWN	2.98E-03
ENSG00000263069.6	RNF213-AS1	1.67	UP	3.11E-03
ENSG00000275532.1	AC006449.2	2.12	UP	3.13E-03
ENSG00000254571.1	AL358937.1	2.01	UP	3.20E-03
ENSG00000214548.18	MEG3	1.19	UP	3.20E-03
ENSG00000261083.3	LINC02516	1.39	UP	3.31E-03
ENSG00000286507.1	AC004947.3	1.34	UP	3.31E-03
ENSG00000273055.1	AC005046.2	1.43	UP	3.45E-03
ENSG00000256249.1	AC026333.3	1.35	UP	3.49E-03
ENSG00000274719.1	AC012653.2	1.90	UP	3.53E-03
ENSG00000284825.1	AL121935.1	-1.32	DOWN	3.57E-03
ENSG00000236501.6	AC074286.1	1.18	UP	3.67E-03
ENSG00000285117.1	AC068724.5	-1.36	DOWN	3.74E-03
ENSG00000220925.2	IGBP1-AS2	1.81	UP	3.78E-03
ENSG00000228950.1	AC023137.2	-1.30	DOWN	3.79E-03
ENSG00000228274.4	AL021707.2	-1.95	DOWN	3.89E-03
ENSG00000230569.1	AC114763.2	2.08	UP	3.93E-03
ENSG00000266680.1	AL135905.1	1.05	UP	3.98E-03
ENSG00000278765.1	AC004477.3	-1.31	DOWN	4.01E-03
ENSG00000254865.1	AC100763.1	1.95	UP	4.03E-03
ENSG00000287344.1	AC079304.1	1.69	UP	4.16E-03
ENSG00000224969.1	AL645608.1	1.59	UP	4.19E-03
ENSG00000288582.2	NABP1-OT1	1.56	UP	4.22E-03
ENSG00000231329.8	AL031772.1	1.40	UP	4.23E-03
ENSG00000287065.1	AP005209.2	1.64	UP	4.24E-03
ENSG00000273399.2	AL159169.3	-1.29	DOWN	4.25E-03

S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.

(Continuação)

Gene ID	Gene Name	Log2(FC)	Expression	P-adj
ENSG00000278869.1	BX539320.1	1.62	UP	4.34E-03
ENSG00000287613.1	AC069549.2	1.40	UP	4.39E-03
ENSG00000272540.1	AL662797.2	1.02	UP	4.46E-03
ENSG00000227292.1	AC009229.1	2.11	UP	4.56E-03
ENSG00000260423.2	LINC02367	1.23	UP	4.59E-03
ENSG00000231880.2	KF459542.1	-1.75	DOWN	4.70E-03
ENSG00000272236.1	AL645939.5	1.47	UP	4.82E-03
ENSG00000254802.1	AC022182.2	1.07	UP	4.84E-03
ENSG00000257925.1	AC008083.2	-1.83	DOWN	4.85E-03
ENSG00000280384.1	FP325332.1	-1.13	DOWN	4.85E-03
ENSG00000246731.3	AC100786.1	1.17	UP	4.93E-03
ENSG00000231187.3	AL356056.2	1.14	UP	4.96E-03
ENSG00000181798.3	LINC00471	-1.65	DOWN	5.27E-03
ENSG00000235119.1	AL138895.1	1.05	UP	5.46E-03
ENSG00000240012.1	SLC9A9-AS1	-1.15	DOWN	5.50E-03
ENSG00000136315.4	AL355922.1	1.14	UP	5.53E-03
ENSG00000231896.1	AC019185.1	1.93	UP	5.61E-03
ENSG00000274215.1	AC106028.4	1.70	UP	5.65E-03
ENSG00000255418.6	LINC02718	-1.10	DOWN	5.81E-03
ENSG00000278192.1	AL118505.1	1.76	UP	5.86E-03
ENSG00000226869.6	LHFPL3-AS1	1.02	UP	5.94E-03
ENSG00000254248.1	AC068189.1	1.87	UP	5.97E-03
ENSG00000231426.7	FILNC1	1.10	UP	6.13E-03
ENSG00000273306.1	AC018690.1	-1.08	DOWN	6.19E-03
ENSG00000286616.1	AL008730.1	1.28	UP	6.65E-03
ENSG00000244926.7	ALKBH3-AS1	1.47	UP	6.66E-03
ENSG00000286043.1	AC091214.1	1.60	UP	6.67E-03
ENSG00000228587.1	AL049748.1	1.98	UP	6.79E-03
ENSG00000288007.1	AC092803.4	1.51	UP	6.80E-03
ENSG00000255655.1	AC007570.1	1.32	UP	6.87E-03
ENSG00000231612.1	AC104462.1	-1.65	DOWN	7.05E-03
ENSG00000224292.1	AF196972.1	-1.04	DOWN	7.23E-03
ENSG00000234484.1	AL032821.1	1.62	UP	7.30E-03
ENSG00000254444.1	AC022762.1	1.32	UP	7.37E-03
ENSG00000253618.1	GRPEL2-AS1	-1.60	DOWN	7.41E-03
ENSG00000280721.1	LINC01943	1.29	UP	7.52E-03
ENSG00000286828.1	AC008883.3	-1.06	DOWN	7.75E-03
ENSG00000224137.1	LINC01857	-1.14	DOWN	7.88E-03
ENSG00000271821.1	AL662844.3	1.53	UP	7.91E-03
ENSG00000256209.2	AC073578.1	1.91	UP	7.97E-03
ENSG00000287547.1	AC234644.2	-1.54	DOWN	8.07E-03

**S1B Table. Differentially expressed lncRNAs in the contrast Acute and Convalescent.**

(Continuação)

<b>Gene ID</b>	<b>Gene Name</b>	<b>Log2(FC)</b>	<b>Expression</b>	<b>P-adj</b>
ENSG00000277301.1	AL034550.2	-1.51	DOWN	8.07E-03
ENSG00000286887.1	AL355881.2	-1.13	DOWN	8.08E-03
ENSG00000188525.4	AC010969.1	1.92	UP	8.22E-03
ENSG00000228126.1	FALEC	-1.54	DOWN	8.29E-03
ENSG00000287625.1	AC022210.2	-1.30	DOWN	8.37E-03
ENSG00000258035.2	AC123567.2	1.21	UP	8.39E-03
ENSG00000224091.1	AC104389.2	1.03	UP	8.46E-03
ENSG00000259704.2	AC124248.1	1.48	UP	8.70E-03
ENSG00000249159.6	AC091965.1	-1.59	DOWN	8.93E-03
ENSG00000287012.1	AC108667.3	1.66	UP	8.96E-03
ENSG00000275995.1	AC109809.1	-1.70	DOWN	9.07E-03
ENSG00000279390.1	AF127577.6	1.55	UP	9.41E-03
ENSG00000253139.1	AC013644.1	1.46	UP	9.54E-03
ENSG00000287682.1	AC020651.2	1.49	UP	9.55E-03
ENSG00000253720.2	AC022973.3	1.64	UP	9.78E-03
ENSG00000253554.7	LINC01414	1.59	UP	9.82E-03
ENSG00000257725.1	LINC02399	-1.40	DOWN	9.83E-03
ENSG00000242288.9	AC022400.3	-1.58	DOWN	9.86E-03
ENSG00000232353.5	AC026320.1	1.94	UP	9.96E-03

**S2 Table. LncRNA-mRNA *cis* interactions according to FEELnc.**

LncRNA ID	LncRNA Name	mRNA ID	mRNA Name	Correlation	P-adj	Distance	Location
ENSG00000270426.1	AC099343.3	ENSG00000168310.11	IRF2	0.95392325	2.75109E-08	0	intronic
ENSG00000273247.5	AC097376.3	ENSG00000172007.7	RAB33B	0.97414099	4.53815E-05	37975	upstream
ENSG00000232021.7	LEF1-AS1	ENSG00000138795.10	LEF1	0.95983511	1.60176E-12	9987	upstream
ENSG00000267547.1	AC060766.4	ENSG00000172123.12	SLFN12	0.96129598	1.54974E-08	6687	downstream
ENSG00000241886.1	AC112496.1	ENSG00000198814.12	GK	0.95703973	2.40198E-10	2145	downstream
ENSG00000272567.1	AC109347.2	ENSG00000145365.11	TIFA	0.95356442	4.55663E-09	1221	downstream
ENSG00000270120.1	AC007728.3	ENSG00000167207.13	NOD2	0.95264826	1.74064E-06	2053	downstream
ENSG00000267745.1	AC060766.7	ENSG00000172123.12	SLFN12	0.99285348	9.57641E-07	1292	downstream
ENSG00000233785.1	AC131011.2	ENSG00000130066.16	SAT1	0.96566088	1.59191E-07	217	upstream

**S3 Table. LncRNA-mRNA *trans* interactions with potential of ligation according to LncTar.**

(Continua)

LncRNA ID	LncRNA Name	mRNA ID	mRNA Name	ndG	Correlation	P-adj
ENSG00000179818.14	PCBP1-AS1	ENSG00000138433.16	CIR1	-0.1066	0.96465315	0.002780623
ENSG00000179818.14	PCBP1-AS1	ENSG00000182957.16	SPATA13	-0.1113	0.95427244	2.75363E-07
ENSG00000179818.14	PCBP1-AS1	ENSG00000132475.10	H3-3B	-0.1066	0.95018736	1.19078E-11
ENSG00000179818.14	PCBP1-AS1	ENSG00000102524.11	TNFSF13B	-0.1125	0.95125948	2.31351E-06
ENSG00000179818.14	PCBP1-AS1	ENSG00000155313.15	USP25	-0.1065	0.95525058	3.86854E-10
ENSG00000179818.14	PCBP1-AS1	ENSG00000137842.7	TMEM62	-0.1392	0.95043282	0.001264815
ENSG00000179818.14	PCBP1-AS1	ENSG00000070190.13	DAPP1	-0.1194	0.9597573	8.40706E-09
ENSG00000179818.14	PCBP1-AS1	ENSG00000102921.8	N4BP1	-0.1102	0.95703761	2.16764E-06
ENSG00000179818.14	PCBP1-AS1	ENSG00000138646.9	HERC5	-0.1043	0.95565486	1.17525E-05
ENSG00000179818.14	PCBP1-AS1	ENSG00000181381.13	DDX60L	-0.1066	0.95744804	4.60321E-07
ENSG00000179818.14	PCBP1-AS1	ENSG00000107864.15	CPEB3	-0.1173	0.95136525	0.000102892
ENSG00000179818.14	PCBP1-AS1	ENSG00000147050.15	KDM6A	-0.1057	0.9653016	0.000133598
ENSG00000179818.14	PCBP1-AS1	ENSG00000114127.10	XRN1	-0.102	0.95824617	2.04678E-07
ENSG00000179818.14	PCBP1-AS1	ENSG00000198604.11	BAZ1A	-0.1057	0.95936314	3.79571E-09
ENSG00000179818.14	PCBP1-AS1	ENSG00000120217.14	CD274	-0.139	0.96244448	0.002254382
ENSG00000179818.14	PCBP1-AS1	ENSG00000154305.18	MIA3	-0.1022	0.95319929	1.2638E-05
ENSG00000197536.11	IRF1-AS1	ENSG00000111331.13	OAS3	-0.1816	0.95957105	2.91331E-05
ENSG00000197536.11	IRF1-AS1	ENSG00000140464.20	PML	-0.1002	0.95530695	1.81936E-05
ENSG00000197536.11	IRF1-AS1	ENSG00000102921.8	N4BP1	-0.1867	0.95319607	3.15583E-09
ENSG00000197536.11	IRF1-AS1	ENSG00000185722.18	ANKFY1	-0.1146	0.9581783	0.000422944
ENSG00000197536.11	IRF1-AS1	ENSG00000172493.21	AFF1	-0.1191	0.9700451	2.5946E-08
ENSG00000203804.4	ADAMTSL4-AS1	ENSG00000168026.18	TTC21A	-0.1009	0.95142646	1.00476E-05
ENSG00000203804.4	ADAMTSL4-AS1	ENSG00000135148.12	TRAFD1	-0.1072	0.95281351	9.48767E-07
ENSG00000203804.4	ADAMTSL4-AS1	ENSG00000133943.20	DGLUCY	-0.1064	0.9531197	0.000310434

**S3 Table. LncRNA-mRNA *trans* interactions with potential of ligation according to LncTar.**

(Continuação)

LncRNA ID	LncRNA Name	mRNA ID	mRNA Name	ndG	Correlation	P-adj
ENSG00000203804.4	ADAMTSL4-AS1	ENSG00000140464.20	PML	-0.1098	0.96490091	0.000931465
ENSG00000203804.4	ADAMTSL4-AS1	ENSG00000173821.19	RNF213	-0.1001	0.95540775	1.06476E-06
ENSG00000206337.12	HCP5	ENSG00000168003.16	SLC3A2	-0.1632	0.95288648	1.14537E-12
ENSG00000206337.12	HCP5	ENSG00000122122.10	SASH3	-0.1037	0.95097398	4.07692E-11
ENSG00000206337.12	HCP5	ENSG00000101160.14	CTSZ	-0.1222	0.95312722	2.95557E-10
ENSG00000213468.7	FIRRE	ENSG00000106617.15	PRKAG2	-0.1024	0.96836915	1.65119E-10
ENSG00000213468.7	FIRRE	ENSG00000112773.16	TENT5A	-0.1162	0.9518734	3.58805E-08
ENSG00000213468.7	FIRRE	ENSG00000134321.12	RSAD2	-0.1052	0.9518734	5.72571E-06
ENSG00000213468.7	FIRRE	ENSG00000123130.17	ACOT9	-0.1036	0.96040957	6.02916E-09
ENSG00000213468.7	FIRRE	ENSG00000196141.14	SPATS2L	-0.1028	0.95326835	1.38148E-05
ENSG00000215068.8	AC025171.2	ENSG00000171943.12	SRGAP2C	-0.1237	0.95417478	0.008839816
ENSG00000215068.8	AC025171.2	ENSG00000138688.15	KIAA1109	-0.1062	0.95504955	4.38961E-11
ENSG00000215068.8	AC025171.2	ENSG00000105939.13	ZC3HAV1	-0.1037	0.95940482	8.27668E-09
ENSG00000215068.8	AC025171.2	ENSG0000010539.11	ZNF200	-0.1017	0.96157506	5.43509E-08
ENSG00000215068.8	AC025171.2	ENSG00000152242.11	C18orf25	-0.1136	0.95204799	1.6149E-11
ENSG00000215769.8	ARHGAP27P1-BPTFP1-KPNA2P3	ENSG00000141664.10	ZCCHC2	-0.1178	0.95999637	5.64318E-09
ENSG00000222041.11	CYTOR	ENSG00000135148.12	TRAFD1	-0.1011	0.9514047	2.28934E-05
ENSG00000222041.11	CYTOR	ENSG00000107099.15	DOCK8	-0.115	0.95266275	6.89062E-16
ENSG00000222041.11	CYTOR	ENSG00000184014.8	DENND5A	-0.1159	0.95604846	4.51553E-13
ENSG00000222041.11	CYTOR	ENSG00000133812.15	SBF2	-0.1389	0.95225082	5.47304E-13
ENSG00000223960.7	CHROMR	ENSG00000116977.18	LGALS8	-0.1601	0.95104852	6.43069E-10
ENSG00000223960.7	CHROMR	ENSG00000134326.11	CMPK2	-0.128	0.96905665	6.91121E-06
ENSG00000223960.7	CHROMR	ENSG00000134321.12	RSAD2	-0.1602	0.98340065	6.57471E-06
ENSG00000223960.7	CHROMR	ENSG00000055332.18	EIF2AK2	-0.1106	0.9645594	5.67242E-07
ENSG00000223960.7	CHROMR	ENSG00000138035.15	PNPT1	-0.136	0.96672163	0.000122826

**S3 Table. LncRNA-mRNA *trans* interactions with potential of ligation according to LncTar.**

(Continuação)

LncRNA ID	LncRNA Name	mRNA ID	mRNA Name	ndG	Correlation	P-adj
ENSG00000223960.7	CHROMR	ENSG00000123609.11	NMI	-0.1104	0.96687527	1.23683E-08
ENSG00000223960.7	CHROMR	ENSG00000163840.10	DTX3L	-0.1715	0.95103034	6.16071E-09
ENSG00000223960.7	CHROMR	ENSG00000138642.15	HERC6	-0.173	0.95279297	2.38561E-05
ENSG00000223960.7	CHROMR	ENSG00000198087.7	CD2AP	-0.1554	0.95854433	6.42295E-08
ENSG00000223960.7	CHROMR	ENSG00000112773.16	TENT5A	-0.1024	0.96803904	5.31743E-07
ENSG00000223960.7	CHROMR	ENSG00000111912.20	NCOA7	-0.1233	0.95760774	1.96824E-05
ENSG00000223960.7	CHROMR	ENSG00000122643.22	NT5C3A	-0.1008	0.95849104	4.46422E-06
ENSG00000223960.7	CHROMR	ENSG00000059378.13	PARP12	-0.1266	0.96873411	7.65973E-05
ENSG00000223960.7	CHROMR	ENSG00000086065.14	CHMP5	-0.1162	0.9677956	2.73062E-07
ENSG00000223960.7	CHROMR	ENSG00000152558.15	TMEM123	-0.1468	0.95169033	5.81349E-09
ENSG00000223960.7	CHROMR	ENSG00000111224.14	PARP11	-0.1023	0.95368564	0.000519841
ENSG00000223960.7	CHROMR	ENSG00000182957.16	SPATA13	-0.1032	0.95333202	3.93159E-10
ENSG00000223960.7	CHROMR	ENSG00000120690.16	ELF1	-0.1059	0.97699926	1.15827E-10
ENSG00000223960.7	CHROMR	ENSG00000136147.18	PHF11	-0.145	0.96782723	4.67146E-07
ENSG00000223960.7	CHROMR	ENSG00000067221.14	STOML1	-0.1098	0.96081257	6.23544E-07
ENSG00000223960.7	CHROMR	ENSG00000121281.13	ADCY7	-0.1011	0.95832578	2.45616E-06
ENSG00000223960.7	CHROMR	ENSG00000125148.7	MT2A	-0.1031	0.96040508	1.72795E-06
ENSG00000223960.7	CHROMR	ENSG00000157601.14	MX1	-0.122	0.95697844	2.41725E-06
ENSG00000223960.7	CHROMR	ENSG00000147050.15	KDM6A	-0.1207	0.97125849	1.46696E-07
ENSG00000223960.7	CHROMR	ENSG00000138496.16	PARP9	-0.1023	0.95988963	1.8431E-08
ENSG00000223960.7	CHROMR	ENSG00000133106.14	EPSTI1	-0.1088	0.96790153	1.66386E-07
ENSG00000223960.7	CHROMR	ENSG00000010539.11	ZNF200	-0.1021	0.96021958	0.000143781
ENSG00000223960.7	CHROMR	ENSG00000117475.14	BLZF1	-0.1088	0.95430443	3.5876E-07
ENSG00000223960.7	CHROMR	ENSG00000121858.11	TNFSF10	-0.1146	0.97497998	2.58492E-06

**S3 Table. LncRNA-mRNA *trans* interactions with potential of ligation according to LncTar.**

(Continuação)

LncRNA ID	LncRNA Name	mRNA ID	mRNA Name	ndG	Correlation	P-adj
ENSG00000223960.7	CHROMR	ENSG00000070190.13	DAPP1	-0.1576	0.96310907	8.04341E-10
ENSG00000223960.7	CHROMR	ENSG00000173221.14	GLRX	-0.1535	0.95506383	4.24533E-08
ENSG00000223960.7	CHROMR	ENSG00000111911.7	HINT3	-0.1227	0.96228999	3.29206E-06
ENSG00000223960.7	CHROMR	ENSG00000013374.16	NUB1	-0.1648	0.95269119	1.73702E-05
ENSG00000223960.7	CHROMR	ENSG00000132256.19	TRIM5	-0.1127	0.97203451	0.000751834
ENSG00000223960.7	CHROMR	ENSG00000132530.17	XAF1	-0.1344	0.95217709	1.94286E-07
ENSG00000223960.7	CHROMR	ENSG00000125779.22	PANK2	-0.1048	0.96277635	6.78151E-06
ENSG00000223960.7	CHROMR	ENSG00000123130.17	ACOT9	-0.1389	0.96525817	2.0811E-05
ENSG00000223960.7	CHROMR	ENSG00000120280.6	CXorf21	-0.1405	0.9810804	8.03204E-07
ENSG00000223960.7	CHROMR	ENSG00000177409.12	SAMD9L	-0.2231	0.96229562	2.38128E-07
ENSG00000223960.7	CHROMR	ENSG00000135363.12	LMO2	-0.1813	0.97828967	0.000621127
ENSG00000223960.7	CHROMR	ENSG00000067066.17	SP100	-0.1003	0.96219059	4.24499E-11
ENSG00000223960.7	CHROMR	ENSG00000112367.11	FIG4	-0.1077	0.95164466	3.82379E-05
ENSG00000223960.7	CHROMR	ENSG00000162654.9	GBP4	-0.1103	0.9640017	3.43133E-06
ENSG00000223960.7	CHROMR	ENSG00000119917.14	IFIT3	-0.1587	0.97949187	2.3548E-06
ENSG00000224078.15	SNHG14	ENSG00000173611.18	SCAI	-0.1163	0.95287263	2.65867E-13
ENSG00000224078.15	SNHG14	ENSG00000149970.16	CNKSR2	-0.1053	0.96131784	1.31585E-13
ENSG00000224078.15	SNHG14	ENSG00000150907.10	FOXO1	-0.1251	0.95648195	1.93123E-05
ENSG00000224789.1	AC012363.2	ENSG00000168394.11	TAP1	-0.1004	0.95551005	1.57953E-08
ENSG00000224789.1	AC012363.2	ENSG00000149131.16	SERPING1	-0.1113	0.96288733	0.000322742
ENSG00000224789.1	AC012363.2	ENSG00000135148.12	TRAFD1	-0.1045	0.96956437	9.84532E-09
ENSG00000224789.1	AC012363.2	ENSG00000173821.19	RNF213	-0.1147	0.95494715	7.17964E-07
ENSG00000225342.2	LRRK2-DT	ENSG00000163512.14	AZI2	-0.1249	0.95421101	0.000382546
ENSG00000225342.2	LRRK2-DT	ENSG00000122643.22	NT5C3A	-0.1041	0.97316796	1.11413E-05
ENSG00000225342.2	LRRK2-DT	ENSG00000062716.13	VMP1	-0.1562	0.96147147	4.84691E-15

**S3 Table. LncRNA-mRNA *trans* interactions with potential of ligation according to LncTar.**

(Continuação)

LncRNA ID	LncRNA Name	mRNA ID	mRNA Name	ndG	Correlation	P-adj
ENSG00000225342.2	LRRK2-DT	ENSG00000198160.14	MIER1	-0.1106	0.9719614	7.02493E-12
ENSG00000225342.2	LRRK2-DT	ENSG00000143384.13	MCL1	-0.1369	0.95533307	6.791E-16
ENSG00000225342.2	LRRK2-DT	ENSG00000116977.18	LGALS8	-0.115	0.95885787	3.99635E-05
ENSG00000225342.2	LRRK2-DT	ENSG00000134326.11	CMPK2	-0.1802	0.95839194	7.11454E-05
ENSG00000225342.2	LRRK2-DT	ENSG00000055332.18	EIF2AK2	-0.1432	0.95121587	4.1187E-06
ENSG00000225342.2	LRRK2-DT	ENSG00000143889.16	HNRNPLL	-0.182	0.9537074	0.005583379
ENSG00000225342.2	LRRK2-DT	ENSG00000138069.18	RAB1A	-0.1456	0.95349219	0.000843008
ENSG00000225342.2	LRRK2-DT	ENSG00000144118.14	RALB	-0.144	0.954034	2.3097E-06
ENSG00000225342.2	LRRK2-DT	ENSG00000123609.11	NMI	-0.1101	0.95339192	2.4522E-06
ENSG00000225342.2	LRRK2-DT	ENSG00000138434.17	ITPRID2	-0.1931	0.96988286	4.49962E-08
ENSG00000225342.2	LRRK2-DT	ENSG00000144848.11	ATG3	-0.1565	0.96831811	2.04444E-06
ENSG00000225342.2	LRRK2-DT	ENSG00000188313.13	PLSCR1	-0.1142	0.95629171	1.02899E-06
ENSG00000225342.2	LRRK2-DT	ENSG00000082996.19	RNF13	-0.1172	0.95406901	2.63961E-11
ENSG00000225342.2	LRRK2-DT	ENSG00000114450.10	GNB4	-0.1214	0.97141528	4.17279E-08
ENSG00000225342.2	LRRK2-DT	ENSG00000174749.6	FAM241A	-0.1671	0.95569386	0.000905207
ENSG00000225342.2	LRRK2-DT	ENSG00000164096.13	C4orf3	-0.1469	0.96672142	2.46776E-08
ENSG00000225342.2	LRRK2-DT	ENSG00000172007.7	RAB33B	-0.1162	0.97724688	0.002322647
ENSG00000225342.2	LRRK2-DT	ENSG00000181381.13	DDX60L	-0.1246	0.96661874	5.45505E-07
ENSG00000225342.2	LRRK2-DT	ENSG00000137414.6	FAM8A1	-0.1129	0.98243832	7.36147E-09
ENSG00000225342.2	LRRK2-DT	ENSG00000198087.7	CD2AP	-0.1196	0.95912561	6.65152E-06
ENSG00000225342.2	LRRK2-DT	ENSG00000135535.17	CD164	-0.1003	0.95534651	3.35046E-12
ENSG00000225342.2	LRRK2-DT	ENSG00000106392.11	C1GALT1	-0.2084	0.95907875	2.56417E-07
ENSG00000225342.2	LRRK2-DT	ENSG00000105835.12	NAMPT	-0.1002	0.95980843	2.1768E-11
ENSG00000225342.2	LRRK2-DT	ENSG00000096968.14	JAK2	-0.1385	0.95548942	4.63811E-08
ENSG00000225342.2	LRRK2-DT	ENSG00000086065.14	CHMP5	-0.1169	0.96228844	1.08961E-05

**S3 Table. LncRNA-mRNA *trans* interactions with potential of ligation according to LncTar.**

(Continuação)

LncRNA ID	LncRNA Name	mRNA ID	mRNA Name	ndG	Correlation	P-adj
ENSG00000225342.2	LRRK2-DT	ENSG0000026103.22	FAS	-0.1388	0.95743476	3.45628E-05
ENSG00000225342.2	LRRK2-DT	ENSG00000138190.17	EXOC6	-0.1317	0.9616306	8.64334E-05
ENSG00000225342.2	LRRK2-DT	ENSG00000155629.15	PIK3AP1	-0.1525	0.96745924	3.0295E-08
ENSG00000225342.2	LRRK2-DT	ENSG00000152558.15	TMEM123	-0.1805	0.96730954	9.17599E-09
ENSG00000225342.2	LRRK2-DT	ENSG00000183735.10	TBK1	-0.1705	0.96572974	2.68235E-06
ENSG00000225342.2	LRRK2-DT	ENSG00000059758.8	CDK17	-0.1529	0.96376427	6.06212E-08
ENSG00000225342.2	LRRK2-DT	ENSG00000182957.16	SPATA13	-0.1142	0.95451889	4.81693E-06
ENSG00000225342.2	LRRK2-DT	ENSG00000136147.18	PHF11	-0.1304	0.97450017	0.002493474
ENSG00000225342.2	LRRK2-DT	ENSG00000102524.11	TNFSF13B	-0.1405	0.97539384	3.23139E-06
ENSG00000225342.2	LRRK2-DT	ENSG00000198604.11	BAZ1A	-0.1737	0.95230879	8.27297E-09
ENSG00000225342.2	LRRK2-DT	ENSG00000137842.7	TMEM62	-0.2567	0.96084996	1.70422E-05
ENSG00000225342.2	LRRK2-DT	ENSG00000185947.15	ZNF267	-0.1092	0.97079625	3.35363E-11
ENSG00000225342.2	LRRK2-DT	ENSG00000126858.18	RHOT1	-0.11	0.96566399	3.83427E-08
ENSG00000225342.2	LRRK2-DT	ENSG00000132475.10	H3-3B	-0.1198	0.96071051	1.86057E-11
ENSG00000225342.2	LRRK2-DT	ENSG00000101596.16	SMCHD1	-0.1459	0.96522571	2.09978E-12
ENSG00000225342.2	LRRK2-DT	ENSG00000155313.15	USP25	-0.1811	0.97091241	1.41464E-09
ENSG00000225342.2	LRRK2-DT	ENSG00000068366.20	ACSL4	-0.1079	0.95550323	1.33656E-11
ENSG00000225342.2	LRRK2-DT	ENSG00000102081.15	FMR1	-0.1779	0.96143556	1.25006E-07
ENSG00000225470.8	JPX	ENSG00000117010.17	ZNF684	-0.1204	0.95716402	1.41049E-05
ENSG00000225470.8	JPX	ENSG00000134326.11	CMPK2	-0.1193	0.97654018	0.000782654
ENSG00000225470.8	JPX	ENSG00000055332.18	EIF2AK2	-0.4404	0.97291466	3.49326E-05
ENSG00000225470.8	JPX	ENSG00000123609.11	NMI	-0.2079	0.95432635	0.000545164
ENSG00000225470.8	JPX	ENSG00000082996.19	RNF13	-0.1007	0.95433375	1.3065E-09
ENSG00000225470.8	JPX	ENSG00000114450.10	GNB4	-0.1736	0.95507695	6.11462E-06
ENSG00000225470.8	JPX	ENSG00000137414.6	FAM8A1	-0.1016	0.97552753	9.59223E-08

**S3 Table. LncRNA-mRNA *trans* interactions with potential of ligation according to LncTar.**

(Continuação)

LncRNA ID	LncRNA Name	mRNA ID	mRNA Name	ndG	Correlation	P-adj
ENSG00000225470.8	JPX	ENSG00000112773.16	TENT5A	-0.1128	0.96202417	0.005526817
ENSG00000225470.8	JPX	ENSG00000111912.20	NCOA7	-0.101	0.9715097	0.001289457
ENSG00000225470.8	JPX	ENSG00000132256.19	TRIM5	-0.1585	0.97113064	0.009543807
ENSG00000225470.8	JPX	ENSG00000111224.14	PARP11	-0.1492	0.98203003	0.007788722
ENSG00000225470.8	JPX	ENSG00000059758.8	CDK17	-0.1272	0.98028552	7.77085E-05
ENSG00000225470.8	JPX	ENSG00000139618.15	BRCA2	-0.1198	0.96867257	0.009503112
ENSG00000225470.8	JPX	ENSG00000102524.11	TNFSF13B	-0.1137	0.97331371	9.28281E-06
ENSG00000225470.8	JPX	ENSG00000125148.7	MT2A	-0.1121	0.95747849	5.22521E-11
ENSG00000225470.8	JPX	ENSG00000101596.16	SMCHD1	-0.1698	0.98350932	2.93772E-12
ENSG00000225470.8	JPX	ENSG00000155313.15	USP25	-0.1425	0.98115528	1.05099E-07
ENSG00000225470.8	JPX	ENSG00000102081.15	FMR1	-0.2048	0.96745603	0.000646375
ENSG00000225470.8	JPX	ENSG00000198160.14	MIER1	-0.1275	0.96675476	9.65841E-10
ENSG00000225470.8	JPX	ENSG00000197121.15	PGAP1	-0.1683	0.96269877	8.69023E-05
ENSG00000225470.8	JPX	ENSG00000122643.22	NT5C3A	-0.1102	0.9709601	3.02478E-05
ENSG00000225470.8	JPX	ENSG00000106617.15	PRKAG2	-0.1704	0.95315394	2.22464E-06
ENSG00000225470.8	JPX	ENSG00000152558.15	TMEM123	-0.1681	0.97598007	1.5532E-08
ENSG00000225470.8	JPX	ENSG00000138434.17	ITPRID2	-0.1283	0.97435852	1.35346E-05
ENSG00000225470.8	JPX	ENSG00000137842.7	TMEM62	-0.1035	0.97796226	5.99231E-08
ENSG00000225470.8	JPX	ENSG00000132475.10	H3-3B	-0.1051	0.95945062	7.80198E-11
ENSG00000225470.8	JPX	ENSG00000162654.9	GBP4	-0.1072	0.95412945	0.004491383
ENSG00000225470.8	JPX	ENSG00000171943.12	SRGAP2C	-0.1396	0.95392604	3.93545E-08
ENSG00000225470.8	JPX	ENSG00000121858.11	TNFSF10	-0.1061	0.96344411	5.57636E-06
ENSG00000225470.8	JPX	ENSG00000070190.13	DAPP1	-0.1356	0.96400208	1.17045E-06
ENSG00000225470.8	JPX	ENSG00000067221.14	STOML1	-0.1317	0.95323999	3.75012E-11
ENSG00000225470.8	JPX	ENSG00000101347.10	SAMHD1	-0.1057	0.95021666	2.34096E-07

**S3 Table. LncRNA-mRNA *trans* interactions with potential of ligation according to LncTar.**

(Continuação)

LncRNA ID	LncRNA Name	mRNA ID	mRNA Name	ndG	Correlation	P-adj
ENSG00000225470.8	JPX	ENSG00000106392.11	C1GALT1	-0.1822	0.965847	1.59295E-05
ENSG00000225470.8	JPX	ENSG00000133106.14	EPSTI1	-0.1066	0.95445228	3.87548E-05
ENSG00000225470.8	JPX	ENSG00000126858.18	RHOT1	-0.1651	0.9542619	0.001366042
ENSG00000225470.8	JPX	ENSG00000136560.14	TANK	-0.1703	0.9811412	5.01539E-07
ENSG00000225470.8	JPX	ENSG00000137628.17	DDX60	-0.2273	0.96364901	3.46723E-07
ENSG00000225470.8	JPX	ENSG00000187231.14	SESTD1	-0.1858	0.97567329	0.005425029
ENSG00000225470.8	JPX	ENSG00000138246.17	DNAJC13	-0.1571	0.95515946	0.000216029
ENSG00000225470.8	JPX	ENSG00000188313.13	PLSCR1	-0.2451	0.95691606	3.43589E-06
ENSG00000225470.8	JPX	ENSG00000181381.13	DDX60L	-0.148	0.98264607	9.20735E-07
ENSG00000225470.8	JPX	ENSG00000135535.17	CD164	-0.1052	0.95447228	2.58481E-11
ENSG00000225470.8	JPX	ENSG00000112367.11	FIG4	-0.1213	0.95644636	0.000662219
ENSG00000225470.8	JPX	ENSG00000134321.12	RSAD2	-0.105	0.96444403	1.12376E-05
ENSG00000225470.8	JPX	ENSG00000198087.7	CD2AP	-0.1023	0.96164422	0.000764092
ENSG00000225470.8	JPX	ENSG00000114127.10	XRN1	-0.1043	0.95827993	9.70128E-07
ENSG00000225470.8	JPX	ENSG00000140396.13	NCOA2	-0.1034	0.9624063	3.05001E-06
ENSG00000225470.8	JPX	ENSG00000165185.14	KIAA1958	-0.1446	0.96949802	4.1062E-07
ENSG00000225470.8	JPX	ENSG00000152778.9	IFIT5	-0.1088	0.96686249	8.74393E-06
ENSG00000225470.8	JPX	ENSG00000102218.6	RP2	-0.1593	0.95188048	6.11128E-07
ENSG00000225470.8	JPX	ENSG00000067066.17	SP100	-0.1467	0.95779417	1.17307E-08
ENSG00000225470.8	JPX	ENSG00000143384.13	MCL1	-0.109	0.95162826	1.18117E-15
ENSG00000225470.8	JPX	ENSG00000010539.11	ZNF200	-0.115	0.95203317	0.005910108
ENSG00000225470.8	JPX	ENSG00000137965.11	IFI44	-0.1037	0.95369742	3.30676E-06
ENSG00000225470.8	JPX	ENSG00000163565.18	IFI16	-0.1053	0.96152362	6.59662E-07
ENSG00000225470.8	JPX	ENSG00000177409.12	SAMD9L	-0.1149	0.97715791	5.37643E-07
ENSG00000225470.8	JPX	ENSG00000155629.15	PIK3AP1	-0.1036	0.96941142	2.20422E-07

**S3 Table. LncRNA-mRNA *trans* interactions with potential of ligation according to LncTar.**

(Continuação)

LncRNA ID	LncRNA Name	mRNA ID	mRNA Name	ndG	Correlation	P-adj
ENSG00000225889.8	AC012368.1	ENSG00000105939.13	ZC3HAV1	-0.1991	0.95741656	8.76099E-09
ENSG00000228956.8	SATB1-AS1	ENSG00000117602.12	RCAN3	-0.1728	0.95636355	0.005045118
ENSG00000228956.8	SATB1-AS1	ENSG00000152495.11	CAMK4	-0.1257	0.96825486	1.04155E-08
ENSG00000228956.8	SATB1-AS1	ENSG00000181690.8	PLAG1	-0.1234	0.96916294	3.08216E-07
ENSG00000228956.8	SATB1-AS1	ENSG00000173611.18	SCAI	-0.1013	0.97201495	4.68596E-05
ENSG00000228956.8	SATB1-AS1	ENSG00000149311.18	ATM	-0.1389	0.95114839	1.2799E-17
ENSG00000228956.8	SATB1-AS1	ENSG00000127334.11	DYRK2	-0.1398	0.95939275	8.39871E-12
ENSG00000231233.1	CFAP58-DT	ENSG00000106617.15	PRKAG2	-0.1076	0.95192189	6.58415E-07
ENSG00000231535.7	LINC00278	ENSG00000156500.15	FAM122C	-0.1199	0.96160514	1.18229E-08
ENSG00000231535.7	LINC00278	ENSG00000172493.21	AFF1	-0.1006	0.95162962	2.31836E-06
ENSG00000231535.7	LINC00278	ENSG00000155313.15	USP25	-0.1038	0.95838793	2.73369E-10
ENSG00000231535.7	LINC00278	ENSG00000102081.15	FMR1	-0.1004	0.95638366	3.22439E-09
ENSG00000231535.7	LINC00278	ENSG00000181381.13	DDX60L	-0.1612	0.96259115	4.46204E-07
ENSG00000231535.7	LINC00278	ENSG00000115267.8	IFIH1	-0.1094	0.96566083	8.61127E-06
ENSG00000231535.7	LINC00278	ENSG00000138688.15	KIAA1109	-0.1137	0.97597869	1.70257E-10
ENSG00000231535.7	LINC00278	ENSG00000111911.7	HINT3	-0.1108	0.95545987	0.003431407
ENSG00000231535.7	LINC00278	ENSG00000125148.7	MT2A	-0.118	0.9644944	6.93625E-10
ENSG00000231535.7	LINC00278	ENSG00000103121.9	CMC2	-0.1583	0.95202564	0.000687815
ENSG00000232021.7	LEF1-AS1	ENSG00000138795.10	LEF1	-0.3698	0.95983511	1.49638E-12
ENSG00000232021.7	LEF1-AS1	ENSG00000117602.12	RCAN3	-0.1339	0.95993135	7.31602E-12
ENSG00000232021.7	LEF1-AS1	ENSG00000091409.15	ITGA6	-0.1125	0.96683878	1.46587E-13
ENSG00000232021.7	LEF1-AS1	ENSG00000152495.11	CAMK4	-0.1837	0.95332936	7.01491E-13
ENSG00000233070.1	ZFY-AS1	ENSG00000163666.10	HESX1	-0.1205	0.97510151	0.000386241
ENSG00000233070.1	ZFY-AS1	ENSG00000101608.12	MYL12A	-0.1654	0.95634846	4.6301E-14
ENSG00000233355.7	CHRM3-AS2	ENSG00000152495.11	CAMK4	-0.1019	0.96147059	5.63293E-10

**S3 Table. LncRNA-mRNA *trans* interactions with potential of ligation according to LncTar.**

(Continuação)

LncRNA ID	LncRNA Name	mRNA ID	mRNA Name	ndG	Correlation	P-adj
ENSG00000233355.7	CHRM3-AS2	ENSG00000171817.17	ZNF540	-0.1161	0.95232812	7.30214E-06
ENSG00000233355.7	CHRM3-AS2	ENSG00000149311.18	ATM	-0.1205	0.95686308	9.52233E-18
ENSG00000233785.1	AC131011.2	ENSG00000196141.14	SPATS2L	-0.1121	0.95681365	5.56186E-06
ENSG00000233785.1	AC131011.2	ENSG00000138496.16	PARP9	-0.1086	0.95255932	6.62567E-09
ENSG00000233785.1	AC131011.2	ENSG00000102897.10	LYRM1	-0.3876	0.96020629	3.74501E-11
ENSG00000234506.5	LINC01506	ENSG00000067066.17	SP100	-0.1042	0.95641919	5.36427E-11
ENSG00000234506.5	LINC01506	ENSG00000101608.12	MYL12A	-0.1606	0.96133701	2.55284E-13
ENSG00000234506.5	LINC01506	ENSG00000134321.12	RSAD2	-0.1802	0.97044855	6.7313E-06
ENSG00000234506.5	LINC01506	ENSG00000138646.9	HERC5	-0.1198	0.95092499	8.35862E-06
ENSG00000234506.5	LINC01506	ENSG00000152778.9	IFIT5	-0.1068	0.95606843	3.96292E-07
ENSG00000234506.5	LINC01506	ENSG00000196954.14	CASP4	-0.1276	0.95290402	1.27239E-09
ENSG00000236337.1	FMR1-IT1	ENSG00000154305.18	MIA3	-0.1051	0.95164272	5.41128E-13
ENSG00000237781.3	ADAMTSL4-AS2	ENSG00000168394.11	TAP1	-0.1157	0.96327353	1.07802E-08
ENSG00000237781.3	ADAMTSL4-AS2	ENSG00000100342.21	APOL1	-0.103	0.95422383	2.97311E-06
ENSG00000245164.8	LINC00861	ENSG00000118420.17	UBE3D	-0.1583	0.95241102	4.89996E-13
ENSG00000245937.8	LINC01184	ENSG00000033867.16	SLC4A7	-0.1803	0.95353734	8.61456E-13
ENSG00000257433.6	AC004241.1	ENSG00000124222.22	STX16	-0.1183	0.95042741	1.23445E-09
ENSG00000263766.5	AC025682.2	ENSG00000059378.13	PARP12	-0.1001	0.96941653	9.34099E-08
ENSG00000263766.5	AC025682.2	ENSG00000169871.13	TRIM56	-0.1104	0.95054141	2.25403E-12
ENSG00000263766.5	AC025682.2	ENSG00000132530.17	XAF1	-0.1048	0.95295135	6.24813E-08
ENSG00000263766.5	AC025682.2	ENSG00000141664.10	ZCCHC2	-0.1036	0.9511156	2.41036E-09
ENSG00000263766.5	AC025682.2	ENSG00000124256.15	ZBP1	-0.5867	0.9533828	3.9123E-06
ENSG00000263766.5	AC025682.2	ENSG00000123130.17	ACOT9	-0.121	0.95601023	2.23961E-09
ENSG00000267547.1	AC060766.4	ENSG00000115339.14	GALNT3	-0.1585	0.95130039	1.46245E-09
ENSG00000267745.1	AC060766.7	ENSG00000082996.19	RNF13	-0.1283	0.95299437	2.75211E-13

**S3 Table. LncRNA-mRNA *trans* interactions with potential of ligation according to LncTar.**

(Continuação)

LncRNA ID	LncRNA Name	mRNA ID	mRNA Name	ndG	Correlation	P-adj
ENSG00000267745.1	AC060766.7	ENSG00000137842.7	TMEM62	-0.1238	0.9548269	0.000105482
ENSG00000268027.5	AC243960.1	ENSG00000181163.13	NPM1	-0.1393	0.95150601	1.06859E-17
ENSG00000270426.1	AC099343.3	ENSG00000124222.22	STX16	-0.1188	0.96906275	9.29458E-09
ENSG00000270972.1	AC136475.9	ENSG00000142687.18	KIAA0319L	-0.156	0.95637267	1.57354E-07
ENSG00000270972.1	AC136475.9	ENSG00000124256.15	ZBP1	-0.1029	0.962065	1.04456E-06
ENSG00000273247.5	AC097376.3	ENSG00000097033.14	SH3GLB1	-0.1165	0.95049184	2.4359E-13
ENSG00000273247.5	AC097376.3	ENSG00000116977.18	LGALS8	-0.1099	0.95761688	3.09206E-07
ENSG00000273247.5	AC097376.3	ENSG00000134326.11	CMPK2	-0.1258	0.9741369	2.28804E-05
ENSG00000273247.5	AC097376.3	ENSG00000055332.18	EIF2AK2	-0.1388	0.96039404	1.60727E-06
ENSG00000273247.5	AC097376.3	ENSG00000136560.14	TANK	-0.1577	0.97170718	6.04909E-09
ENSG00000273247.5	AC097376.3	ENSG00000115339.14	GALNT3	-0.221	0.96876786	0.000386292
ENSG00000273247.5	AC097376.3	ENSG00000138434.17	ITPRID2	-0.151	0.96039282	3.83684E-09
ENSG00000273247.5	AC097376.3	ENSG00000163512.14	AZI2	-0.115	0.96621711	4.29579E-06
ENSG00000273247.5	AC097376.3	ENSG00000163746.11	PLSCR2	-0.1282	0.95916242	2.98477E-07
ENSG00000273247.5	AC097376.3	ENSG00000188313.13	PLSCR1	-0.1168	0.97431796	5.97559E-07
ENSG00000273247.5	AC097376.3	ENSG00000181381.13	DDX60L	-0.1346	0.95345131	4.26595E-07
ENSG00000273247.5	AC097376.3	ENSG00000137414.6	FAM8A1	-0.1008	0.95899211	2.3383E-09
ENSG00000273247.5	AC097376.3	ENSG00000112773.16	TENT5A	-0.1187	0.95251852	6.2629E-06
ENSG00000273247.5	AC097376.3	ENSG00000135535.17	CD164	-0.1372	0.96345371	1.37757E-12
ENSG00000273247.5	AC097376.3	ENSG00000122643.22	NT5C3A	-0.1391	0.95212442	7.09331E-06
ENSG00000273247.5	AC097376.3	ENSG00000096968.14	JAK2	-0.1651	0.95958757	2.40453E-08
ENSG00000273247.5	AC097376.3	ENSG00000086065.14	CHMP5	-0.1248	0.95680612	1.90606E-06
ENSG00000273247.5	AC097376.3	ENSG00000152558.15	TMEM123	-0.1839	0.9725592	7.33446E-09
ENSG00000273247.5	AC097376.3	ENSG00000183735.10	TBK1	-0.1687	0.95358764	7.36036E-09
ENSG00000273247.5	AC097376.3	ENSG00000136147.18	PHF11	-0.1212	0.95419779	5.66896E-05

**S3 Table. LncRNA-mRNA *trans* interactions with potential of ligation according to LncTar.**

(Continuação)

LncRNA ID	LncRNA Name	mRNA ID	mRNA Name	ndG	Correlation	P-adj
ENSG00000273247.5	AC097376.3	ENSG00000185947.15	ZNF267	-0.1179	0.9608562	2.74082E-12
ENSG00000273247.5	AC097376.3	ENSG00000123728.10	RAP2C	-0.1212	0.95238411	8.60114E-08
ENSG00000273247.5	AC097376.3	ENSG00000062716.13	VMP1	-0.1335	0.95889744	1.1874E-15
ENSG00000273247.5	AC097376.3	ENSG00000198160.14	MIER1	-0.1695	0.96312005	9.11321E-13
ENSG00000273247.5	AC097376.3	ENSG00000138069.18	RAB1A	-0.1109	0.97231789	2.0472E-06
ENSG00000273247.5	AC097376.3	ENSG00000172007.7	RAB33B	-0.3362	0.97414099	4.50677E-05
ENSG00000273247.5	AC097376.3	ENSG00000106829.19	TLE4	-0.1013	0.95652389	1.51965E-05
ENSG00000273247.5	AC097376.3	ENSG00000174021.11	GNG5	-0.1451	0.96755714	0.001195319
ENSG00000273247.5	AC097376.3	ENSG00000163565.18	IFI16	-0.1678	0.96038998	7.0641E-08
ENSG00000273247.5	AC097376.3	ENSG00000067066.17	SP100	-0.2011	0.95395314	1.72537E-10
ENSG00000273247.5	AC097376.3	ENSG00000138246.17	DNAJC13	-0.1295	0.96256526	6.21787E-09
ENSG00000273247.5	AC097376.3	ENSG00000138646.9	HERC5	-0.1647	0.95643069	1.07437E-05
ENSG00000273247.5	AC097376.3	ENSG00000145365.11	TIFA	-0.1392	0.95876552	0.003693826
ENSG00000273247.5	AC097376.3	ENSG00000112419.14	PHACTR2	-0.102	0.95034406	0.000176493
ENSG00000273247.5	AC097376.3	ENSG00000107864.15	CPEB3	-0.1065	0.9640236	0.000519164
ENSG00000273247.5	AC097376.3	ENSG00000155629.15	PIK3AP1	-0.2046	0.97611596	1.32486E-08
ENSG00000273247.5	AC097376.3	ENSG00000115267.8	IFIH1	-0.1241	0.95325181	7.46222E-06
ENSG00000273247.5	AC097376.3	ENSG00000173221.14	GLRX	-0.1031	0.95110367	4.54254E-06
ENSG00000273247.5	AC097376.3	ENSG00000111912.20	NCOA7	-0.225	0.96531616	5.79343E-05
ENSG00000273247.5	AC097376.3	ENSG00000137575.12	SDCBP	-0.1062	0.95852958	1.15186E-14
ENSG00000273247.5	AC097376.3	ENSG00000154589.7	LY96	-0.1007	0.95438809	0.000169926
ENSG00000273247.5	AC097376.3	ENSG00000152778.9	IFIT5	-0.1186	0.96467709	7.62266E-07
ENSG00000273247.5	AC097376.3	ENSG00000108984.15	MAP2K6	-0.1202	0.95614924	3.85667E-05
ENSG00000274020.4	LINC01138	ENSG00000142687.18	KIAA0319L	-0.1022	0.95979632	0.002866273
ENSG00000274020.4	LINC01138	ENSG00000172183.15	ISG20	-0.1064	0.96352653	2.70475E-05

**S3 Table. LncRNA-mRNA *trans* interactions with potential of ligation according to LncTar.**

(Continuação)

LncRNA ID	LncRNA Name	mRNA ID	mRNA Name	ndG	Correlation	P-adj
ENSG00000274020.4	LINC01138	ENSG00000183486.13	MX2	-0.1104	0.95803146	2.34545E-07
ENSG00000274020.4	LINC01138	ENSG00000135148.12	TRAFD1	-0.1122	0.9571003	1.09065E-05
ENSG00000274020.4	LINC01138	ENSG00000140464.20	PML	-0.1075	0.97136613	7.43963E-08
ENSG00000274020.4	LINC01138	ENSG00000059378.13	PARP12	-0.1789	0.96024552	2.16944E-06
ENSG00000274020.4	LINC01138	ENSG00000136816.16	TOR1B	-0.106	0.96158285	0.000120846
ENSG00000274020.4	LINC01138	ENSG00000156587.16	UBE2L6	-0.1446	0.96007347	0.000122325
ENSG00000274020.4	LINC01138	ENSG00000166900.17	STX3	-0.1019	0.95357535	6.38448E-11
ENSG00000274020.4	LINC01138	ENSG00000168404.13	MLKL	-0.1211	0.95052272	1.90683E-06
ENSG00000274020.4	LINC01138	ENSG00000185722.18	ANKFY1	-0.1913	0.97507622	1.24638E-06
ENSG00000274020.4	LINC01138	ENSG00000108771.13	DHX58	-0.1085	0.95213211	2.65427E-05
ENSG00000274020.4	LINC01138	ENSG00000108424.10	KPNB1	-0.1398	0.95985777	1.03846E-08
ENSG00000274020.4	LINC01138	ENSG00000173821.19	RNF213	-0.1081	0.95832089	1.36321E-06
ENSG00000274020.4	LINC01138	ENSG00000125826.21	RBCK1	-0.1095	0.9527044	2.71411E-05
ENSG00000277511.1	AC116407.2	ENSG00000055332.18	EIF2AK2	-0.2198	0.96675757	1.66369E-07
ENSG00000277511.1	AC116407.2	ENSG00000138035.15	PNPT1	-0.1097	0.95326709	7.32837E-07
ENSG00000277511.1	AC116407.2	ENSG00000138385.16	SSB	-0.1719	0.95457574	2.96676E-12
ENSG00000277511.1	AC116407.2	ENSG00000163512.14	AZI2	-0.1262	0.97400465	1.29711E-11
ENSG00000277511.1	AC116407.2	ENSG00000188313.13	PLSCR1	-0.2564	0.95109796	1.69361E-07
ENSG00000277511.1	AC116407.2	ENSG00000114450.10	GNB4	-0.1154	0.95141086	2.43033E-11
ENSG00000277511.1	AC116407.2	ENSG00000172007.7	RAB33B	-0.1165	0.96253819	4.87442E-10
ENSG00000277511.1	AC116407.2	ENSG00000112773.16	TENT5A	-0.1583	0.95549263	2.50113E-08
ENSG00000277511.1	AC116407.2	ENSG00000111911.7	HINT3	-0.1373	0.95304199	3.66219E-10
ENSG00000277511.1	AC116407.2	ENSG00000177409.12	SAMD9L	-0.1099	0.96802149	1.86145E-07
ENSG00000277511.1	AC116407.2	ENSG00000152558.15	TMEM123	-0.175	0.97928307	4.27349E-09
ENSG00000277511.1	AC116407.2	ENSG00000136147.18	PHF11	-0.1058	0.96687328	1.03108E-09

**S3 Table. LncRNA-mRNA *trans* interactions with potential of ligation according to LncTar.**

(Continuação)

LncRNA ID	LncRNA Name	mRNA ID	mRNA Name	ndG	Correlation	P-adj
ENSG00000277511.1	AC116407.2	ENSG00000140280.14	LYSMD2	-0.1136	0.9587725	7.59382E-09
ENSG00000277511.1	AC116407.2	ENSG00000185947.15	ZNF267	-0.149	0.95118818	9.1335E-15
ENSG00000277511.1	AC116407.2	ENSG00000103121.9	CMC2	-0.1074	0.96199564	7.03697E-09
ENSG00000277511.1	AC116407.2	ENSG00000132530.17	XAF1	-0.1067	0.95241004	6.13902E-08
ENSG00000277511.1	AC116407.2	ENSG00000102081.15	FMR1	-0.1342	0.95073289	8.07105E-14
ENSG00000282851.2	BISPR	ENSG00000135114.12	OASL	-0.1024	0.96887076	2.02667E-05
ENSG00000283384.1	AL138694.1	ENSG00000196141.14	SPATS2L	-0.183	0.95216356	5.58492E-06
ENSG00000285399.3	AC104162.2	ENSG00000013374.16	NUB1	-0.1631	0.9660603	2.24964E-07
ENSG00000285399.3	AC104162.2	ENSG00000055332.18	EIF2AK2	-0.1951	0.96687073	3.08669E-07
ENSG00000285399.3	AC104162.2	ENSG00000182957.16	SPATA13	-0.127	0.96267485	1.28687E-11
ENSG00000285399.3	AC104162.2	ENSG00000067221.14	STOML1	-0.1038	0.96730605	3.66497E-11
ENSG00000285399.3	AC104162.2	ENSG00000101347.10	SAMHD1	-0.1635	0.95778386	8.93069E-12
ENSG00000285399.3	AC104162.2	ENSG00000155313.15	USP25	-0.158	0.95927857	8.18157E-12
ENSG00000285399.3	AC104162.2	ENSG00000168310.11	IRF2	-0.1119	0.96547209	5.89206E-06
ENSG00000285399.3	AC104162.2	ENSG00000059758.8	CDK17	-0.2308	0.95039682	6.10357E-12
ENSG00000285399.3	AC104162.2	ENSG00000136147.18	PHF11	-0.1933	0.96376094	1.83787E-08
ENSG00000285399.3	AC104162.2	ENSG00000168404.13	MLKL	-0.1037	0.95811232	2.27292E-06
ENSG00000285399.3	AC104162.2	ENSG00000124222.22	STX16	-0.1172	0.95692448	8.34668E-07
ENSG00000285399.3	AC104162.2	ENSG00000162946.23	DISC1	-0.1064	0.95692256	4.61455E-05
ENSG00000285399.3	AC104162.2	ENSG00000134326.11	CMPK2	-0.1123	0.95048058	3.40217E-06
ENSG00000285399.3	AC104162.2	ENSG00000059728.11	MXD1	-0.1122	0.95259072	7.52172E-12
ENSG00000285399.3	AC104162.2	ENSG00000067066.17	SP100	-0.1188	0.95995929	1.92436E-11
ENSG00000285399.3	AC104162.2	ENSG00000163840.10	DTX3L	-0.1022	0.95055054	1.72026E-09
ENSG00000285399.3	AC104162.2	ENSG00000173193.15	PARP14	-0.1045	0.95995681	2.33222E-08
ENSG00000285399.3	AC104162.2	ENSG00000181381.13	DDX60L	-0.1046	0.96361873	2.91958E-07

**S3 Table. LncRNA-mRNA *trans* interactions with potential of ligation according to LncTar.**

(Continuação)

LncRNA ID	LncRNA Name	mRNA ID	mRNA Name	ndG	Correlation	P-adj
ENSG00000285399.3	AC104162.2	ENSG00000059378.13	PARP12	-0.1144	0.95332617	2.25196E-06
ENSG00000285399.3	AC104162.2	ENSG00000140464.20	PML	-0.1362	0.95843333	4.00135E-07
ENSG00000285399.3	AC104162.2	ENSG00000010539.11	ZNF200	-0.1292	0.9745201	1.86227E-07
ENSG00000285399.3	AC104162.2	ENSG00000102921.8	N4BP1	-0.1071	0.96130779	5.18834E-10
ENSG00000285399.3	AC104162.2	ENSG00000185722.18	ANKFY1	-0.1213	0.95007833	1.48282E-06
ENSG00000285399.3	AC104162.2	ENSG00000102081.15	FMR1	-0.1144	0.95271458	8.44738E-13
ENSG00000285399.3	AC104162.2	ENSG00000172493.21	AFF1	-0.1199	0.95164523	7.46098E-09
ENSG00000285399.3	AC104162.2	ENSG00000105939.13	ZC3HAV1	-0.1439	0.9675195	1.10668E-08
ENSG00000285399.3	AC104162.2	ENSG00000102524.11	TNFSF13B	-0.119	0.95403361	8.75141E-07
ENSG00000285399.3	AC104162.2	ENSG00000198604.11	BAZ1A	-0.1356	0.95800836	3.57448E-10
ENSG00000287393.1	AL591468.1	ENSG00000156500.15	FAM122C	-0.3282	0.9738199	7.84963E-09

**S4 Table. Top 5 KEGG pathways ranked according to the highest ratio between our significant target mRNAs and the total of genes in the pathway.**

<b>KEGG Pathway</b>	<b>KEGG Size</b>	<b>% Genes</b>	<b>mRNAs</b>
RIG-I-like receptor signaling pathway	68	7.35	AZI2; TBK1; TANK; IFIH1; DHX58
Viral life cycle - HIV-1	56	7.14	MX1; TRIM5; SAMHD1; MX2
Influenza A	163	6.75	OAS3; PML; RSAD2; EIF2AK2; MX1; TNFSF10; JAK2; FAS; TBK1; IFIH1; MX2
SNARE interactions in vesicular transport	31	6.45	STX16; STX3
Mucin type O-glycan biosynthesis	33	6.06	C1GALT1; GALNT3

**S5 Table. Interferon Stimulated Genes according to Interferome Database and KEGG pathways related to them.**

(Continua)

Ensembl ID	Gene Name	Gene Type	Log2(FC)	P-adj
ENSG00000223960	CHROMR	lncRNA	2.794990775	3.10605E-54
ENSG00000225342	LRRK2-DT	lncRNA	1.622759073	4.70923E-16
ENSG00000123130	ACOT9	protein_coding	2.199420893	1.99904E-45
ENSG00000068366	ACSL4	protein_coding	1.182697835	3.50018E-11
ENSG00000172493	AFF1	protein_coding	1.567474388	7.57528E-14
ENSG00000185722	ANKFY1	protein_coding	1.840630551	1.78477E-35
ENSG00000100342	APOL1	protein_coding	2.435006433	6.20155E-22
ENSG00000144848	ATG3	protein_coding	1.266510456	5.6092E-12
ENSG00000149311	ATM	protein_coding	-1.193112485	4.84468E-40
ENSG00000163512	AZI2	protein_coding	1.665314643	2.30143E-27
ENSG00000198604	BAZ1A	protein_coding	1.508041884	1.38767E-14
ENSG00000117475	BLZF1	protein_coding	1.892239087	2.21542E-36
ENSG00000139618	BRCA2	protein_coding	2.144660501	5.32929E-29
ENSG00000133943	DGLUCY	protein_coding	1.450057986	8.20599E-15
ENSG00000106392	C1GALT1	protein_coding	1.571605381	1.43303E-15
ENSG00000164096	C4orf3	protein_coding	1.393142573	2.02357E-15
ENSG00000174749	FAM241A	protein_coding	1.426317491	8.51914E-12
ENSG00000197536	IRF1-AS1	lncRNA	2.26352049	7.73123E-27
ENSG00000196954	CASP4	protein_coding	2.040789287	2.63821E-33
ENSG00000135535	CD164	protein_coding	1.381367105	1.42274E-18
ENSG00000120217	CD274	protein_coding	3.527100936	2.74135E-19
ENSG00000198087	CD2AP	protein_coding	1.934142045	3.59539E-22
ENSG00000059758	CDK17	protein_coding	1.280783873	3.09702E-14
ENSG00000086065	CHMP5	protein_coding	2.465485344	9.63401E-31
ENSG00000138433	CIR1	protein_coding	1.509544345	8.62464E-24
ENSG00000103121	CMC2	protein_coding	1.729149379	8.84101E-27
ENSG00000134326	CMPK2	protein_coding	3.718987415	2.20533E-23
ENSG00000107864	CPEB3	protein_coding	1.854285389	3.85126E-28
ENSG00000120280	CXorf21	protein_coding	2.089143025	1.01768E-37
ENSG00000070190	DAPP1	protein_coding	1.634200531	1.04427E-19
ENSG00000137628	DDX60	protein_coding	2.682343395	6.65306E-29
ENSG00000181381	DDX60L	protein_coding	2.823889605	1.04145E-21
ENSG00000184014	DENND5A	protein_coding	1.182599833	8.78046E-19
ENSG00000108771	DHX58	protein_coding	3.665604684	2.95119E-52
ENSG00000162946	DISC1	protein_coding	1.865620325	1.5578E-22
ENSG00000107099	DOCK8	protein_coding	1.162487178	4.67086E-25
ENSG00000163840	DTX3L	protein_coding	2.095099594	5.61417E-33
ENSG00000127334	DYRK2	protein_coding	-1.393677866	2.70331E-40
ENSG00000055332	EIF2AK2	protein_coding	2.930499428	5.93676E-33
ENSG00000120690	ELF1	protein_coding	1.809911846	7.35788E-37

**S5 Table. Interferon Stimulated Genes according to Interferome Database and KEGG pathways related to them.**

(Continuação)

Ensembl ID	Gene Name	Gene Type	Log2(FC)	P-adj
ENSG00000133106	EPST11	protein_coding	2.716617571	4.22767E-30
ENSG00000156500	FAM122C	protein_coding	1.523652115	7.10701E-14
ENSG00000112773	TENT5A	protein_coding	2.361000961	5.05096E-35
ENSG00000026103	FAS	protein_coding	1.557897294	2.07754E-10
ENSG00000112367	FIG4	protein_coding	1.131578664	2.23092E-17
ENSG00000150907	FOXO1	protein_coding	-1.26111231	1.4743E-24
ENSG00000115339	GALNT3	protein_coding	1.899704813	1.69537E-24
ENSG00000162654	GBP4	protein_coding	2.508987835	7.25589E-18
ENSG00000198814	GK	protein_coding	1.486716422	1.80292E-10
ENSG00000173221	GLRX	protein_coding	1.955392131	4.05203E-37
ENSG00000114450	GNB4	protein_coding	1.426878947	4.46564E-13
ENSG00000206337	HCP5	lncRNA	1.147123343	1.37643E-13
ENSG00000138646	HERC5	protein_coding	3.811705738	1.53079E-23
ENSG00000138642	HERC6	protein_coding	3.01496903	1.7617E-49
ENSG00000163666	HESX1	protein_coding	5.638879065	1.82091E-39
ENSG00000111911	HINT3	protein_coding	1.768849043	5.59658E-25
ENSG00000143889	HNRNPLL	protein_coding	2.086083196	7.96261E-20
ENSG00000163565	IFI16	protein_coding	2.434164418	7.25903E-30
ENSG00000137965	IFI44	protein_coding	3.398961832	1.79991E-21
ENSG00000115267	IFIH1	protein_coding	3.257282509	4.77189E-31
ENSG00000119917	IFIT3	protein_coding	4.046274201	2.41084E-32
ENSG00000152778	IFIT5	protein_coding	2.910781753	6.87887E-32
ENSG00000168310	IRF2	protein_coding	1.260530899	3.24763E-16
ENSG00000172183	ISG20	protein_coding	2.180835467	2.75715E-29
ENSG00000091409	ITGA6	protein_coding	-1.590064755	4.09833E-34
ENSG00000096968	JAK2	protein_coding	2.049644154	1.26295E-26
ENSG00000138688	KIAA1109	protein_coding	1.620077581	3.36318E-24
ENSG00000108424	KPNB1	protein_coding	2.228402566	7.97364E-43
ENSG00000116977	LGALS8	protein_coding	1.475203462	8.54029E-32
ENSG00000222041	CYTOR	lncRNA	1.510796203	1.47188E-18
ENSG00000135363	LMO2	protein_coding	2.135854074	3.51028E-33
ENSG00000154589	LY96	protein_coding	1.999137893	1.9495E-19
ENSG00000102897	LYRM1	protein_coding	1.671385053	1.4346E-30
ENSG00000140280	LYSMD2	protein_coding	1.832031252	9.26824E-22
ENSG00000108984	MAP2K6	protein_coding	2.265184984	1.02464E-45
ENSG00000143384	MCL1	protein_coding	1.108054167	2.18561E-15
ENSG00000154305	MIA3	protein_coding	1.206054569	1.49612E-12
ENSG00000168404	MLKL	protein_coding	1.638149704	3.08701E-17
ENSG00000125148	MT2A	protein_coding	3.998377546	3.63136E-36
ENSG00000157601	MX1	protein_coding	3.718928483	7.18363E-31

**S5 Table. Interferon Stimulated Genes according to Interferome Database and KEGG pathways related to them.**

(Continuação)

Ensembl ID	Gene Name	Gene Type	Log2(FC)	P-adj
ENSG00000183486	MX2	protein_coding	2.666102565	6.32873E-43
ENSG00000059728	MXD1	protein_coding	1.608666828	1.49957E-21
ENSG00000101608	MYL12A	protein_coding	1.465607938	3.58629E-31
ENSG00000102921	N4BP1	protein_coding	1.583732285	1.79926E-20
ENSG00000105835	NAMPT	protein_coding	1.511610806	8.36266E-13
ENSG00000111912	NCOA7	protein_coding	3.49887718	3.36924E-49
ENSG00000123609	NMI	protein_coding	1.974149435	4.80475E-24
ENSG00000167207	NOD2	protein_coding	1.372427225	1.0688E-09
ENSG00000181163	NPM1	protein_coding	-1.145832328	6.67829E-39
ENSG00000122643	NT5C3A	protein_coding	3.156317859	4.23592E-25
ENSG00000013374	NUB1	protein_coding	1.823874899	3.3819E-19
ENSG00000111331	OAS3	protein_coding	3.97396377	1.0504E-28
ENSG00000135114	OASL	protein_coding	3.797343593	1.22094E-41
ENSG00000125779	PANK2	protein_coding	1.134352789	4.65955E-16
ENSG00000111224	PARP11	protein_coding	2.066113423	1.27259E-29
ENSG00000059378	PARP12	protein_coding	2.793357538	2.39323E-47
ENSG00000173193	PARP14	protein_coding	2.111384903	2.37602E-16
ENSG00000138496	PARP9	protein_coding	2.532371409	9.00143E-29
ENSG00000197121	PGAP1	protein_coding	2.29018994	4.31105E-24
ENSG00000112419	PHACTR2	protein_coding	2.017074706	2.8121E-26
ENSG00000136147	PHF11	protein_coding	1.944947572	6.79773E-26
ENSG00000155629	PIK3AP1	protein_coding	2.107054877	1.9061E-26
ENSG00000188313	PLSCR1	protein_coding	3.13975629	1.37901E-27
ENSG00000163746	PLSCR2	protein_coding	3.187469608	2.72851E-35
ENSG00000140464	PML	protein_coding	2.757651956	6.32214E-30
ENSG00000138035	PNPT1	protein_coding	2.607830624	4.95129E-28
ENSG00000106617	PRKAG2	protein_coding	1.46743396	1.24541E-28
ENSG00000138069	RAB1A	protein_coding	1.285102445	2.5987E-24
ENSG00000144118	RALB	protein_coding	1.555955883	1.18887E-15
ENSG00000123728	RAP2C	protein_coding	1.224415741	2.91849E-29
ENSG00000125826	RBCK1	protein_coding	1.888384192	2.02919E-21
ENSG00000117602	RCAN3	protein_coding	-1.772558504	1.49872E-35
ENSG00000173821	RNF213	protein_coding	2.765648394	1.89993E-36
ENSG00000102218	RP2	protein_coding	1.254055957	4.98028E-16
ENSG00000134321	RSAD2	protein_coding	3.997301937	3.5158E-15
ENSG00000177409	SAMD9L	protein_coding	2.703203171	2.48156E-16
ENSG00000101347	SAMHD1	protein_coding	1.384133442	8.83881E-15
ENSG00000122122	SASH3	protein_coding	1.390059775	3.5891E-12
ENSG00000130066	SAT1	protein_coding	2.792497579	8.2967E-39
ENSG00000149131	SERPING1	protein_coding	3.720795513	1.50895E-23

**S5 Table. Interferon Stimulated Genes according to Interferome Database and KEGG pathways related to them.**

(Continuação)

Ensembl ID	Gene Name	Gene Type	Log2(FC)	P-adj
ENSG00000187231	SESTD1	protein_coding	1.428657617	7.64922E-21
ENSG00000168003	SLC3A2	protein_coding	2.309928839	4.7892E-33
ENSG00000033867	SLC4A7	protein_coding	-1.197976328	1.54898E-25
ENSG00000172123	SLFN12	protein_coding	1.953458346	3.11157E-21
ENSG00000101596	SMCHD1	protein_coding	1.453299487	2.00694E-18
ENSG00000067066	SP100	protein_coding	1.737834739	1.54746E-31
ENSG00000182957	SPATA13	protein_coding	1.401839438	3.3789E-21
ENSG00000196141	SPATS2L	protein_coding	4.944520611	3.63088E-57
ENSG00000171943	SRGAP2C	protein_coding	2.031372756	1.01449E-24
ENSG00000138385	SSB	protein_coding	1.269496146	5.41252E-12
ENSG00000138434	ITPRID2	protein_coding	1.505251537	6.06901E-19
ENSG00000067221	STOML1	protein_coding	3.343825961	5.20951E-37
ENSG00000166900	STX3	protein_coding	1.434201333	1.33442E-18
ENSG00000136560	TANK	protein_coding	1.708529392	5.55849E-23
ENSG00000168394	TAP1	protein_coding	2.22064884	2.17225E-24
ENSG00000183735	TBK1	protein_coding	1.083241551	1.77162E-14
ENSG00000145365	TIFA	protein_coding	1.975370199	2.78513E-23
ENSG00000106829	TLE4	protein_coding	1.234846889	2.46686E-19
ENSG00000152558	TMEM123	protein_coding	2.211305778	5.48477E-28
ENSG00000137842	TMEM62	protein_coding	1.463025919	1.50613E-25
ENSG00000121858	TNFSF10	protein_coding	3.018876174	2.82122E-19
ENSG00000102524	TNFSF13B	protein_coding	2.612010726	2.48089E-16
ENSG00000136816	TOR1B	protein_coding	2.771957944	1.17642E-39
ENSG00000135148	TRAFD1	protein_coding	2.026483213	5.14205E-27
ENSG00000132256	TRIM5	protein_coding	2.40356094	1.90657E-31
ENSG00000169871	TRIM56	protein_coding	1.372410388	4.36909E-26
ENSG00000168026	TTC21A	protein_coding	3.004145462	3.77348E-37
ENSG00000156587	UBE2L6	protein_coding	2.627917197	1.93759E-29
ENSG00000118420	UBE3D	protein_coding	-1.16291157	5.46708E-17
ENSG00000155313	USP25	protein_coding	1.415111156	3.45873E-18
ENSG00000062716	VMP1	protein_coding	1.051591722	5.23232E-15
ENSG00000132530	XAF1	protein_coding	3.1437212	2.91032E-27
ENSG00000114127	XRN1	protein_coding	1.869648351	6.5832E-15
ENSG00000124256	ZBP1	protein_coding	3.211607527	1.37971E-51
ENSG00000105939	ZC3HAV1	protein_coding	1.760662087	2.65746E-20
ENSG00000141664	ZCCHC2	protein_coding	2.313952517	1.40731E-44
ENSG00000233070	ZFY-AS1	lncRNA	3.403027738	1.30542E-37
ENSG00000010539	ZNF200	protein_coding	1.660284137	1.76545E-20
ENSG00000185947	ZNF267	protein_coding	1.136584388	5.61859E-12
ENSG00000117010	ZNF684	protein_coding	3.354524873	5.56087E-42

## ANEXO A - Normas da Revista PLOS Neglected Tropical Diseases

# Submission Guidelines

## About the Journal

*PLOS Neglected Tropical Diseases* publishes original research articles of importance to the NTDs community and the wider health community. We will consider manuscripts of any length; we encourage the submission of both substantial full-length bodies of work and shorter manuscripts that report novel findings that might be based on a more limited range of experiments.

The writing style should be concise and accessible, avoiding jargon so that the paper is understandable for readers outside a specialty or those whose first language is not English. Editors will make suggestions for how to achieve this, as well as suggestions for cuts or additions that could be made to the article to strengthen the argument. Our aim is to make the editorial process rigorous and consistent, but not intrusive or overbearing. Authors are encouraged to use their own voice and to decide how best to present their ideas, results, and conclusions.

## About the Journal

*PLOS Neglected Tropical Diseases* is committed to the highest ethical standards in medical research. Accordingly, we ask authors to provide specific information regarding ethical treatment of research participants, patient consent, patient privacy, protocols, authorship, and competing interests. We also ask that reports of certain specific types of studies adhere to generally accepted standards. Our requirements are based on the [Uniform Requirements for Manuscripts Submitted to Biomedical Journals](#), issued by the International Committee for Medical Journal Editors.

### Related information for authors

- [PLOS Writing Center](#)
- [Submission system](#)
- [Journal scope and publication criteria](#)
- [Getting started guide](#)
- [Guidelines for other article types](#)
- [Guidelines for revisions](#)
- [Publication fees](#)

## Style and Format

When you first submit to the journal, providing you include all the necessary information needed for editorial assessment and review, we will not ask you to make any formatting changes. During resubmission, we may ask you to meet formatting requirements.

<b>File format</b>	<p>Manuscript files can be in the following formats: DOC, DOCX, RTF or PDF. Microsoft Word documents should not be locked or protected.</p> <p>LaTeX manuscripts must be submitted as PDFs. <a href="#">Read the LaTeX guidelines.</a></p>
<b>Length</b>	<p>Manuscripts can be any length. There are no restrictions on word count, number of figures, or amount of supporting information.</p> <p>We encourage you to present and discuss your findings concisely.</p>
<b>Font</b>	<p>Use a standard font size and any standard font, except for the font named “Symbol”. To add symbols to the manuscript, use the Insert → Symbol function in your word processor or paste in the appropriate Unicode character.</p>
<b>Headings</b>	<p>Limit manuscript sections and sub-sections to 3 heading levels. Make sure heading levels are clearly indicated in the manuscript text.</p>
<b>Layout and spacing</b>	<p>Manuscript text should be double-spaced.</p> <p>Do not format text in multiple columns.</p>
<b>Page and line numbers</b>	<p>Include page numbers and line numbers in the manuscript file. Use continuous line numbers (do not restart the numbering on each page).</p>
<b>Tables</b>	<p>Insert tables immediately after the first paragraph in which they are cited.</p>
<b>Supporting Information</b>	<p>Upload Supporting Information (SI) files separately.</p>
<b>Footnotes</b>	<p>Footnotes are not permitted. If your manuscript contains footnotes, move the information into the main text or the reference list, depending on the content.</p>
<b>Language</b>	<p>Manuscripts must be submitted in English.</p> <p>You may submit translations of the manuscript or abstract as supporting information. <a href="#">Read the supporting information guidelines.</a></p>
<b>Abbreviations</b>	<p>Define abbreviations upon first appearance in the text.</p> <p>Do not use non-standard abbreviations unless they appear at least three times in the text.</p> <p>Keep abbreviations to a minimum.</p>

**Reference style**

PLOS uses “Vancouver” style, as outlined in the [ICMJE sample references](#).  
[See reference formatting examples and additional instructions below.](#)

**Equations**

We recommend using MathType for display and inline equations, as it will provide the most reliable outcome. If this is not possible, Equation Editor or Microsoft's Insert→Equation function is acceptable.

Avoid using MathType, Equation Editor, or the Insert→Equation function to insert single variables (e.g., “ $a^2 + b^2 = c^2$ ”), Greek or other symbols (e.g.,  $\beta$ ,  $\Delta$ , or ‘[prime]’), or mathematical operators (e.g.,  $\times$ ,  $\geq$ , or  $\pm$ ) in running text. Wherever possible, insert single symbols as normal text with the correct Unicode (hex) values.

Do not use MathType, Equation Editor, or the Insert→Equation function for only a portion of an equation. Rather, ensure that the entire equation is included. Equations should not contain a mix of different equation tools. Avoid “hybrid” inline or display equations, in which part is text and part is MathType, or part is MathType and part is Equation Editor.

**Nomenclature** Use correct and established nomenclature wherever possible.

<i>Units of measurement</i>	Use SI units. If you do not use these exclusively, provide the SI value in parentheses after each value. <a href="#">Read more about SI units.</a>
<i>Drugs</i>	Provide the Recommended International Non-Proprietary Name (rINN). Write in italics (e.g., <i>Homo sapiens</i> ). Write out in full the genus and species, both in the title of the manuscript and at the first mention of an organism in a paper. After first mention, the first letter of the genus name followed by the full species name may be used (e.g., <i>H. sapiens</i> ).
<i>Species names</i>	Write in italics. Use the recommended name by consulting the appropriate genetic nomenclature database (e.g., <a href="#">HUGO</a> for human genes). It is sometimes advisable to indicate the synonyms for the gene the first time it appears in the text. Gene prefixes such as those used for oncogenes or cellular localization should be shown in roman typeface (e.g., v-fes, c-MYC).
<i>Genes, mutations, genotypes, and alleles</i>	
<i>Allergens</i>	The systematic allergen nomenclature of the World Health Organization/International Union of Immunological Societies (WHO/IUIS) Allergen Nomenclature Sub-committee should be used for manuscripts that include the description or use of allergenic proteins. For manuscripts describing new allergens, the systematic name of the allergen should be approved by the WHO/IUIS Allergen Nomenclature Sub-Committee prior to manuscript publication. Examples of the systematic allergen nomenclature can be found at the <a href="#">WHO/IUIS Allergen Nomenclature site</a> .

### Copyediting manuscripts

Prior to submission, authors who believe their manuscripts would benefit from in-depth professional copyediting are encouraged to use language-editing and copyediting services. Obtaining this service is the responsibility of the author and should be done before initial submission. These services can be found on the web using search terms like “scientific editing service” or “manuscript editing service”.

*Note that if your manuscript is accepted, PLOS will not perform a detailed copyediting step. Therefore, please carefully review your manuscript, paying special attention to spelling, punctuation, and grammar, as well as scientific content.*

## Manuscript Organization

Most manuscripts should be organized as follows. Instructions for each element appear below.

- Title
- Authors and Affiliations
- Abstract
- Author Summary
- Introduction
- Methods
- Results
- Discussion
- Acknowledgments
- References
- Supporting information Captions

Uniformity in format facilitates the experience of readers and users of the journal. To provide flexibility, however, the Results and Discussion can be combined into one Results/Discussion section.



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## Parts of a Submission

### Title

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

Title	Length	Guidelines	Examples
<b>Full title</b>	250 characters	Specific, concise, and comprehensible to readers outside the field	descriptive, and readers Impact of cigarette smoke exposure on innate immunity: <i>A Caenorhabditis elegans</i> model Solar drinking water disinfection (SODIS) to reduce childhood diarrhoea in rural Bolivia: A cluster-randomized, controlled trial
<b>Short title</b>	70 characters	State the topic of the study	Cigarette smoke exposure and innate immunity SODIS and childhood diarrhoea

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 list

### Authorship

### requirements

All authors must meet the criteria for authorship as outlined in the [authorship policy](#). Those who contributed to the work but do not meet the criteria for authorship can be mentioned in the Acknowledgments. [Read more about Acknowledgments.](#)

The corresponding author must provide an ORCID iD at the time of submission by entering it in the user profile in the submission system. [Read more about ORCID.](#)

### 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:

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- 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.

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Author names will be published exactly as they appear in the manuscript file. Please double-check the information carefully to make sure it is correct.

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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.

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### How to select a new corresponding author in Editorial Manager

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If a manuscript is submitted on behalf of a consortium or group, include its name in the manuscript byline. Do not add it to the author list in the submission system. You may include the full list of members in the Acknowledgments or in a supporting information file.

PubMed only indexes individual consortium or group author members listed in the article byline. If included, these individuals must qualify for authorship according to our [criteria](#).

[Read the group authorship policy.](#)

## Author contributions

Provide at minimum one contribution for each author in the submission system. Use the CRediT taxonomy to describe each contribution. [Read the policy and the full list of roles.](#)

Contributions will be published with the final article, and they should accurately reflect contributions to the work. The submitting author is responsible for completing this information at submission, and we expect that all authors will have reviewed, discussed, and agreed to their individual contributions ahead of this time.

*PLOS Neglected Tropical Diseases* will contact all authors by email at submission to ensure that they are aware of the submission.

## Cover letter

Upload a cover letter as a separate file in the online system.

The cover letter should address the following questions:

- Why is this manuscript suitable for publication in *PLOS Neglected Tropical Diseases*?

- Why will your study inspire the NTDs community, and how will it drive the understanding of NTD pathobiology, epidemiology, prevention, treatment, control, or policy?

The cover letter will only be available to the editor and the journal staff.

## Title page

The title, authors, and affiliations should all be included on a title page as the first page of the manuscript file.



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## 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.

The Abstract is conceptually divided into the following three sections with these headings: Background, Methodology/Principal Findings, and Conclusions/Significance.

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.

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		<a href="#">Life in Hot Carbon Monoxide: The Complete Genome Sequence of Carboxydothemus hydrogenoformans Z-2901</a>

## 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.

This section should also include a section with descriptions of any statistical methods employed. These should conform to the [criteria outlined by the Uniform Requirements](#), as follows:

*Describe statistical methods with enough detail to enable a knowledgeable reader with access to the original data to judge its appropriateness for the study and to verify the reported results. When possible, quantify findings and present them with appropriate indicators of measurement error or uncertainty (such as confidence intervals). Avoid relying solely on statistical hypothesis testing, such as P values, which fail to convey important information about effect size and precision of estimates. References for the design of the study and statistical methods should be to standard works when possible (with pages stated). Define statistical terms, abbreviations, and most symbols. Specify the statistical software package(s) and versions used. Distinguish prespecified from exploratory analyses, including subgroup analyses.*

Submit detailed protocols for newer or less established methods. Well-established protocols may simply be referenced. Protocol documents for clinical trials, observational studies, and other **non-laboratory** investigations may be uploaded as supporting information.

We recommend and encourage you to deposit **laboratory protocols** in [protocols.io](https://protocols.io), where protocols can be assigned their own persistent digital object identifiers (DOIs).

To include a link to a protocol in your article:

1. Describe your step-by-step protocol on protocols.io
2. Select **Get DOI** to issue your protocol a persistent digital object identifier (DOI)
3. Include the DOI link in the Methods section of your manuscript using the following format provided by protocols.io:  
[http://dx.doi.org/10.17504/protocols.io.\[PROTOCOL DOI\]](http://dx.doi.org/10.17504/protocols.io.[PROTOCOL DOI])

At this stage, your protocol is only visible to those with the link. This allows editors and reviewers to consult your protocol when evaluating the manuscript. You can make your protocols public at any time by selecting **Publish** on the protocols.io site. Any referenced protocol(s) will automatically be made public when your article is published.

*PLOS ONE* offers an option for publishing peer-reviewed Lab Protocol articles, which describe protocols hosted on protocols.io articles. Read more [information on Lab Protocol articles](#).

## 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).

For more information on how best to provide data, read our [policy on data availability](#). PLOS does not accept references to “data not shown.”

As outlined in the [Uniform Requirements](#), authors that present statistical data in the Results section should do the following:

*Give numeric results not only as derivatives (for example, percentages) but also as the absolute numbers from which the derivatives were calculated, and specify the statistical significance attached to them, if any. Restrict tables and figures to those needed to explain the argument of the paper and to assess supporting data. Use graphs as an alternative to tables with many entries; do not duplicate data in graphs and tables. Avoid nontechnical uses of technical terms in statistics, such as “random” (which implies a randomizing device), “normal,” “significant,” “correlations,” and “sample.”*

## 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.

PLOS journals publicly acknowledge the indispensable efforts of our editors and reviewers on an annual basis. To ensure equitable recognition and avoid any appearance of partiality, do not include editors or peer reviewers—named or unnamed—in the Acknowledgments.

Do not include funding sources in the Acknowledgments or anywhere else in the manuscript file. Funding information should only be entered in the financial disclosure section of the submission system.

## References

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

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

Do not cite the following sources in the reference list:

- Unavailable and unpublished work, including manuscripts that have been submitted but not yet accepted (e.g., “unpublished work,” “data not shown”). Instead, include those data as supplementary material or deposit the data in a publicly available database.
- 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.

Ensure that your reference list includes full and current bibliography details for every cited work at the time of your article’s submission (and publication, if accepted). If cited work is corrected, retracted, or marked with an expression of concern before your article is published, and if you feel it is appropriate to cite the work even in light of the post-publication notice, include in your manuscript citations and full references for both the affected article and the post-publication notice. Email the journal office if you have questions.

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.

Do not include citations in abstracts.

Make sure the parts of the manuscript are in the correct order *before* ordering the citations.

### Formatting references

Because all references will be linked electronically as much as possible to the papers they cite, proper formatting of references is crucial.

PLOS uses the reference style outlined by the International Committee of Medical Journal Editors (ICMJE), also referred to as the “Vancouver” style. Example formats are listed below. Additional examples are in the [ICMJE sample references](#).

A reference management tool, EndNote, offers a current [style file](#) that can assist you with the formatting of your references. If you have problems with any reference management program, please contact the source company's technical support.

Source	Format
Published articles	<p>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 (<i>Ailuropoda melanoleuca</i>). <i>Genet Mol Res</i>. 2011;10: 1576-1588.</p> <p>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. <i>Mol Immunol</i>. 2014 Nov 22. pii: S0161-5890(14)00313-7. doi: 10.1016/j.molimm.2014.11.005.</p> <p>Note: A DOI number for the full-text article is acceptable as an alternative to or in addition to traditional volume and page numbers. When providing a DOI, adhere to the format in the example above with both the label and full DOI included at the end of the reference (doi: 10.1016/j.molimm.2014.11.005). Do not provide a shortened DOI or the URL.</p>
Accepted, unpublished articles	Same as published articles, but substitute “Forthcoming” for page numbers or DOI.
Online articles	Huynen MMTE, Martens P, Hilderlink HBM. The health impacts of globalisation: a conceptual framework. <i>Global Health</i> . 2005;1: 14. Available from: <a href="http://www.globalizationandhealth.com/content/1/1/14">http://www.globalizationandhealth.com/content/1/1/14</a>
Books	Bates B. <i>Bargaining for life: A social history of tuberculosis</i> . 1st ed. Philadelphia: University of Pennsylvania Press; 1992.
Book chapters	Hansen B. New York City epidemics and history for the public. In: Harden VA, Risse GB, editors. <i>AIDS and the historian</i> . Bethesda: National Institutes of Health; 1991. pp. 21-28.
Deposited articles (preprints, e-prints, or arXiv)	<p>Krick T, Shub DA, Verstraete N, Ferreiro DU, Alonso LG, Shub M, et al. Amino acid metabolism conflicts with protein diversity. arXiv:1403.3301v1 [Preprint]. 2014 [cited 2014 March 17]. Available from: <a href="https://128.84.21.199/abs/1403.3301v1">https://128.84.21.199/abs/1403.3301v1</a></p> <p>Kording KP, Mensh B. Ten simple rules for structuring papers. <i>BioRxiv</i> [Preprint]. 2016 bioRxiv 088278 [posted 2016 Nov 28; revised 2016 Dec 14; revised 2016 Dec 15; cited 2017 Feb 9]: [12 p.]. Available from: <a href="https://www.biorxiv.org/content/10.1101/088278v5">https://www.biorxiv.org/content/10.1101/088278v5</a> doi: 10.1101/088278</p>

Published media (print or online newspapers and magazine articles)	Fountain H. For Already Vulnerable Penguins, Study Finds Climate Change Is Another Danger. The New York Times. 2014 Jan 29 [Cited March 17]. Available from: <a href="http://www.nytimes.com/2014/01/30/science/earth/climate-change-taking-toll-on-penguins-study-finds.html">http://www.nytimes.com/2014/01/30/science/earth/climate-change-taking-toll-on-penguins-study-finds.html</a>
New (blogs, written works)	Allen L. Announcing PLOS Blogs. 2010 Sep 1 [cited 17 March 2014]. webIn: PLOS Blogs [Internet]. San Francisco: PLOS 2006 - . [about 2 sites, or other screens]. Available from: <a href="http://blogs.plos.org/plos/2010/09/announcing-plos-blogs/">http://blogs.plos.org/plos/2010/09/announcing-plos-blogs/</a> .
Masters' theses doctoral dissertations	Wells A. Exploring the development of the independent, electronic, or scholarly journal. M.Sc. Thesis, The University of Sheffield. 1999. Available from: <a href="http://cuminCAD.scix.net/cgi-bin/works/Show?2e09">http://cuminCAD.scix.net/cgi-bin/works/Show?2e09</a>
Databases and repositories (Figshare, arXiv)	Roberts SB. QPX Genome Browser Feature Tracks; 2013 [cited 2013 Oct 5]. Database: figshare [Internet]. Available from: <a href="http://figshare.com/articles/QPX_Genome_Browser_Feature_Tracks/701214">http://figshare.com/articles/QPX_Genome_Browser_Feature_Tracks/701214</a>
Multimedia (videos, movies, or TV shows)	Hitchcock A, producer and director. Rear Window [Film]; 1954. Los Angeles: MGM.

Journal name abbreviations should be those found in the [National Center for Biotechnology Information \(NCBI\) databases](#).

## Supporting information

Authors can submit essential supporting files and multimedia files along with their manuscripts. All supporting information will be subject to peer review. All file types can be submitted, but files must be smaller than 20 MB in size.

Authors may use almost any description as the item name for a supporting information file as long as it contains an "S" and number. For example, "S1 Appendix" and "S2 Appendix," "S1 Table" and "S2 Table," and so forth.

Supporting information files are published exactly as provided, and are not copyedited.

### Supporting information captions

List supporting information captions at the end of the manuscript file. Do not submit captions in a separate file.

The file number and name are required in a caption, and we highly recommend including a one-line title as well. You may also include a legend in your caption, but it is not required.

## Example caption

**S1 Text. Title is strongly recommended.** Legend is optional.

### In-text citations

We recommend that you cite supporting information in the manuscript text, but this is not a requirement. If you cite supporting information in the text, citations do not need to be in numerical order.

Read the [supporting information guidelines](#) for more details about submitting supporting information and multimedia files.

## 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.

Cite figures in ascending numeric order at first appearance in the manuscript file.

[Read the guidelines for figures.](#)

### Figure captions

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:

- A figure label with Arabic numerals, and "Figure" abbreviated to "Fig" (e.g. Fig 1, Fig 2, Fig 3, etc). Match the label of your figure with the name of the file uploaded at submission (e.g. a figure citation of "Fig 1" must refer to a figure file named "Fig1.tif").
- A concise, descriptive title

The caption may also include a legend as needed.

[Read more about figure captions.](#)

### Tables

Cite tables in ascending numeric order upon first appearance in the manuscript file.

Place each table in your manuscript file directly after the paragraph in which it is first cited (read order). Do not submit your tables in separate files.

Tables require a label (e.g., "Table 1") and brief descriptive title to be placed above the table. Place legends, footnotes, and other text below the table.

[Read the guidelines for tables.](#)

## Data reporting

All data and related metadata underlying the findings reported in a submitted manuscript should be deposited in an appropriate public repository, unless already provided as part of the submitted article.

### [Read our policy on data availability.](#)

Repositories may be either subject-specific (where these exist) and accept specific types of structured data, or generalist repositories that accept multiple data types. We recommend that authors select repositories appropriate to their field. Repositories may be subject-specific (e.g., GenBank for sequences and PDB for structures), general, or institutional, as long as DOIs or accession numbers are provided and the data are at least as open as CC BY. Authors are encouraged to select repositories that meet accepted criteria as trustworthy digital repositories, such as criteria of the Centre for Research Libraries or Data Seal of Approval. Large, international databases are more likely to persist than small, local ones.

### [See our list of recommended repositories.](#)

To support data sharing and author compliance of the PLOS data policy, we have integrated our submission process with a select set of data repositories. The list is neither representative nor exhaustive of the suitable repositories available to authors. Current repository integration partners include [Dryad](#) and [FlowRepository](#). Please contact [data@plos.org](mailto:data@plos.org) to make recommendations for further partnerships.

Instructions for PLOS submissions with data deposited in an integration partner repository:

- Deposit data in the integrated repository of choice.
- Once deposition is final and complete, the repository will provide you with a dataset DOI (provisional) and private URL for reviewers to gain access to the data.
- Enter the given data DOI into the full Data Availability Statement, which is requested in the Additional Information section of the PLOS submission form. Then provide the URL passcode in the Attach Files section.

If you have any questions, please [email us](#).

## Accession numbers

All appropriate data sets, images, and information should be deposited in an appropriate public repository. [See our list of recommended repositories.](#)

Accession numbers (and version numbers, if appropriate) should be provided in the Data Availability Statement. Accession numbers or a citation to the DOI should also be provided when the data set is mentioned within the manuscript.

In some cases authors may not be able to obtain accession numbers or DOIs until the manuscript is accepted; in these cases, the authors must provide these numbers at acceptance. In all other cases, these numbers must be provided at full submission.

## Identifiers

As much as possible, please provide accession numbers or identifiers for all entities such as genes, proteins, mutants, diseases, etc., for which there is an entry in a public database, for example:

- [Ensembl](#)
- [Entrez Gene](#)
- [FlyBase](#)
- [InterPro](#)
- [Mouse Genome Database \(MGD\)](#)
- [Online Mendelian Inheritance in Man \(OMIM\)](#)
- [PubChem](#)

Identifiers should be provided in parentheses after the entity on first use.

## Small and macromolecule crystal data

Manuscripts reporting new and unpublished three-dimensional structures must include sufficient supporting data and detailed descriptions of the methodologies used to allow the reproduction and validation of the structures. All novel structures must have been deposited in a community endorsed database prior to submission (please see our list of [recommended repositories](#)).

### Small molecule single crystal data

Authors reporting X-Ray crystallographic structures of small organic, metal-organic, and inorganic molecules must deposit their data with the Cambridge Crystallographic Data Centre (CCDC), the Inorganic Crystal Structure Database (ICSD), or similar community databases providing a recognized validation functionality. Authors are also required to include the relevant structure reference numbers within the main text (e.g. the CCDC ID number), as well as the crystallographic information files (.cif format) as Supplementary Information, along with the checkCIF validation reports that can be obtained via the International Union of Crystallography (IUCr).

### Macromolecular structures

Authors reporting novel macromolecular structures must have deposited their data prior to submission with the Worldwide Protein Data Bank (wwPDB), the Biological Magnetic Resonance Data Bank (BMRB), the Electron Microscopy Data Bank (EMDB), or other community databases providing a recognized validation functionality. Authors must include the structure reference numbers within the main text and submit as Supplementary Information the official validation reports from these databases.

## Striking image

You can upload a visually striking image alongside your submission, which we may use to showcase your article through PLOS' online channels. We choose the monthly issue image from the striking images submitted with articles scheduled for publication.

## Submission Criteria

- Choose an image that represents the article in a striking and eye-catching way.
- It can be derived from a figure or supporting information file from the paper, and it may be a cropped portion of an image or the entire image.
- Alternatively, you can create or source an image, as long as it adheres to our CC BY license.
- High resolution: between 300-600 dpi
- Single panel
- Ideally avoid added details like text, scale bars, and arrows.

## How to Submit

1. Submit your striking image to the submission system using the file type “Striking Image”.
2. Upload a separate file with the corresponding caption.

If no striking image is uploaded, a member of the journal team will choose an appropriate image, which may be a figure from the submission or a separately sourced CC BY image.

Striking images should not contain potentially identifying images of people. [Read our policy on identifying information.](#)

[The PLOS licenses and copyright policy](#) also applies to striking images.

## Additional Information Requested at Submission

### Financial Disclosure Statement

This information should describe sources of funding that have supported the work. If your manuscript is published, your statement will appear in the Funding section of the article.

Include your statement in the Financial Disclosure section of the initial submission form.

The statement should include:

- Specific grant numbers
- Initials of authors who received each award
- URLs to sponsors' websites

Also state whether any sponsors or funders (other than the named authors) played any role in:

- Study design
- Data collection and analysis
- Decision to publish
- Preparation of the manuscript

If they had no role in the research, include this sentence: “The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.”

If the study was unfunded, include this sentence as the Financial Disclosure statement: “The author(s) received no specific funding for this work.”

[Read our policy on disclosure of funding sources.](#)

## Competing interests

The corresponding author is asked at submission to declare, on behalf of all authors, whether there are any financial, personal, or professional interests that could be construed to have influenced the work.

Any relevant competing interests of authors must be available to editors and reviewers during the review process and will be stated in published articles.

[Read our policy on competing interests.](#)

## Related manuscripts

When submitting a manuscript, all authors are asked to indicate that they do not have a related or duplicate manuscript under consideration (or accepted) for publication elsewhere. If related work has been or will be submitted elsewhere or is in press elsewhere, then a copy must be uploaded with the article submitted to PLOS. Reviewers will be asked to comment on the overlap between related submissions.

Read our policies on [related manuscripts](#).

## Preprints

PLOS encourages authors to post preprints to accelerate the dissemination of research. Posting a manuscript on a preprint server does not impact consideration of the manuscript at any PLOS journal.

Authors posting preprints on [bioRxiv](#) or [medRxiv](#) can choose to concurrently submit their manuscripts to relevant PLOS journals through the direct transfer service.

Authors submitting manuscripts in the life and health sciences to *PLOS Neglected Tropical Diseases* may choose to have PLOS forward their submission to bioRxiv or medRxiv, depending on the scope of the paper, for consideration for posting as a preprint.

[Read more about preprints.](#)

[Learn how to post a preprint to bioRxiv or medRxiv at PLOS Neglected Tropical Diseases.](#)

## Reviewer and editor suggestions

We ask authors to suggest suitable editors and at least four potential reviewers when submitting their manuscript. Bear in mind any potential competing interests when making these suggestions. It is not appropriate to suggest recent collaborators or other researchers at your institution. See our [policy on competing interests](#) for more information.

## Guidelines for Specific Study Types

Study design, reporting, and analyses are assessed against all relevant research and methodological technique standards held by the community. Guidelines for specific study types are outlined below.

### Human and animal research

All research involving humans and animals must have been approved by the authors' institutional review board or equivalent committee(s), and that board must be named by the authors in the manuscript. For research involving human participants, informed consent must have been obtained (or the reason for lack of consent explained, e.g. the data were analyzed anonymously) and all clinical investigation must have been conducted according to the principles expressed in the [Declaration of Helsinki](#). It must be stated in the Methods section of the paper whether informed consent was written or oral. If informed consent was oral, it must be stated in the paper: (a) why written consent could not be obtained, (b) that the IRB approved the use of oral consent, and (c) how oral consent was documented.

Authors should be able to submit, upon request, a statement from the research ethics committee or institutional review board indicating approval of the research. We also encourage authors to submit a sample of a patient consent form, and may require submission on particular occasions.

All animal work must have been conducted according to relevant national and international guidelines. In accordance with the recommendations of the Weatherall report, [The use of non-human primates in research](#), we specifically require authors to include details of animal welfare and steps taken to ameliorate suffering in all work involving non-human primates. The institution that approved the study must be named, and it must be stated in the paper that the study was conducted adhering to the institution's guidelines for animal husbandry.

### Patient privacy and informed consent for publication

Our human participant policy conforms to the [Uniform Requirements](#) of the International Committee of Medical Journal Editors:

*Patients have a right to privacy that should not be infringed without informed consent. Identifying information should not be published in written descriptions, photographs, and pedigrees unless the information is essential for scientific purposes and the patient (or parent or guardian) gives written informed consent for publication. Informed consent for this purpose requires that the patient be shown the manuscript to be published. Complete anonymity is difficult to achieve, and informed consent for publication should be obtained if there is any doubt. If data are changed to protect anonymity, authors should provide assurance that alterations of the data do not distort scientific meaning. When informed consent has been obtained it should be indicated in the published article.*

For papers that include identifying information, or potentially identifying information, authors must download the *Consent Form for Publication in a PLOS Journal* (below), which the patient, parent, or guardian must sign once they have read the paper and been informed about the terms of the PLOS content license.

Once authors have obtained the signed consent form, it should be filed securely in the patient's case notes and the manuscript submitted to PLOS should include this

statement indicating that specific consent for publication was obtained: “The patients in this manuscript have given written informed consent (as outlined in the PLOS consent form) to publication of their case details.”



**Download the PLOS consent form (PDF):**

- [English](#)
- [French](#)
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- [Spanish](#)
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## Clinical trials

PLOS follows the [World Health Organization’s \(WHO\) definition of a clinical trial](#):

*A clinical trial is any research study that prospectively assigns human participants or groups of humans to one or more health-related interventions to evaluate the effects on health outcomes [...] Interventions include but are not restricted to drugs, cells and other biological products, surgical procedures, radiologic procedures, devices, behavioural treatments, process-of-care changes, preventive care, etc.*

### Registering Clinical Trials

All clinical trials submitted to PLOS journals must be entered in a publicly accessible registry approved by the WHO or ICMJE. [See the list of approved registries.](#)

PLOS journals consider prospective trial registration (that is, registration before participant enrollment has begun) to be best publication practice, as recommended by the ICMJE. Clinical trials that began to enroll participants before ICMJE recommendations took effect on July 1, 2005 may be retrospectively registered.

More information about trial registration, including the WHO definition of a clinical trial, is in the [ICMJE FAQ](#).

*PLOS Neglected Tropical Diseases* is unlikely to publish clinical trials that are not prospectively registered. We recognize, however, that in rare cases late registration may occur for exceptional reasons that merit consideration. Authors seeking evaluation by *PLOS Neglected Tropical Diseases* of a non-prospectively registered clinical trial must provide a compelling reason for lack of prospective registration.

In addition, as for all PLOS journals, authors wishing to submit a clinical trial that was not publicly registered before participant enrollment began must register the trial retrospectively in a publicly accessible registry. They must also:

- Register all related clinical trials and confirm they have done so in the Methods section
- Explain in the Methods the specific reasons for failing to register before participant enrollment

- Confirm that future trials will be registered prospectively

PLOS journal editors may decline to further consider any clinical trial for which, in the editor's judgment, absence of prospective registration raises concerns of selective publication or selective reporting of research outcomes.

PLOS supports the public disclosure of all clinical trial results, as mandated, for example, by the 2007 FDA Amendments Act. Prior disclosure of results on a clinical trial registry site will not affect consideration.

## Required Documentation

Clinical trial reports must adhere to the relevant reporting guidelines for their study design, such as [CONSORT](#) for randomized controlled trials, [TREND](#) for non-randomized trials, and other specialized guidelines as appropriate.

For all clinical trial submissions, authors must include the following:

- Registration details (reported in the Methods section and in the submission form)
- CONSORT checklist or relevant reporting guideline (uploaded as supporting information)
- CONSORT flow diagram (uploaded as Fig 1)
- Trial protocol (uploaded as supporting information)
- Details of prior approval for human subjects research by an institutional review board (IRB) or equivalent ethics committee(s)

The submission will not be considered if documentation is not provided. The checklist, flow diagram, and protocol will be published with the article if the manuscript is accepted.

The manuscript file must include the following information:

- An explanation of any deviation from the trial protocol
- Description of informed consent obtained from participants
- Any information on statistical methods or participants not indicated in the CONSORT documentation

## Systematic reviews and meta-analyses

Submissions with systematic reviews and meta-analyses are considered research articles. Submit these manuscripts with the "Research Article" type in the submission system.

Reports of systematic reviews and meta-analyses must adhere to the [PRISMA Statement](#) or alternative guidelines appropriate to the study design, and include the completed checklist and flow diagram to accompany the main text. Authors must complete the appropriate reporting checklist not only with page references, but also with sufficient text excerpted from the manuscript to explain how they accomplished all applicable items.

Download blank templates of the checklist and flow diagram from the [EQUATOR web site](#).

Abstracts should follow PRISMA for Abstracts, using the PLOS abstract format. Authors must also state within the Methods section of their paper whether a protocol exists for their systematic review, and if so, provide a copy of the protocol as supporting information.

The journal supports the prospective registration of systematic reviews. Authors whose systematic review was prospectively registered (e.g., in a registry such as [PROSPERO](#)) should provide the registry number in their abstract. Registry details and protocols will be made available to editors and reviewers, and included with the paper if the report is ultimately published.

## Diagnostic studies

Reports of studies of diagnostic accuracy must adhere to the [STARD requirements](#) or alternative guidelines appropriate to the study design (see the [EQUATOR web site](#)) and include a completed checklist as supporting information. Authors must complete the appropriate reporting checklist not only with page references, but also with sufficient text excerpted from the manuscript to explain how they addressed all applicable items.

## Observational studies

For observational studies, including case control, cohort, and cross-sectional studies, authors must adhere to the [STROBE Statement](#) or alternative guidelines appropriate to the study design (see the [EQUATOR web site](#)) and include a completed checklist as supporting information. Authors must complete the appropriate reporting checklist not only with page references, but also with sufficient text excerpted from the manuscript to explain how they addressed all applicable items.

For observational studies, authors are required to clearly specify (a) What specific hypotheses the researchers intended to test, and the analytical methods by which they planned to test them; (b) What analyses they actually performed; and (c) When reported analyses differ from those that were planned, authors must provide transparent explanations for differences that affect the reliability of the study's results.

If a prospective analysis plan (from the study's funding proposal, IRB or other ethics committee submission, study protocol, or other planning document written before analyzing the data) was used in designing an observational study, authors must include the relevant prospectively written document with the manuscript submission for access by editors and reviewers and eventual publication alongside the accepted paper. If no prospectively written document exists, authors should explain how and when they determined the analyses being reported.

## Microarray experiments

Reports of microarray experiments must conform to the [MIAME guidelines](#), and the data from the experiments must be deposited in a publicly accessible database.

## Other Article Types

If you are submitting content other than a research article, [read the guidelines for other article types](#).

## You may be eligible for APC support

Many institutional partners globally have publishing agreements with PLOS to allow their corresponding authors to publish with reduced or no APCs. To determine if your corresponding author is eligible, please [visit our institutional partners page](#) to determine what kind of agreement your institution has with PLOS.

If your corresponding author is affiliated with a participating institution, they must follow the instructions below to demonstrate eligibility.

Read the full instructions for [submitting to a journal with the Flat Fee Agreement](#).

If your corresponding author is not from a participating institution and requires assistance paying publishing fees, please consider [applying for a fee waiver](#) at submission.