Neuroinflammation and ALS: Transcriptomic Insights into Molecular Disease Mechanisms and Therapeutic Targets

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Supplementary Information

Supplementary Discussion

In the following paragraphs, we will provide a detailed analysis of inflammatory and immunological pathways affected in SALS, focusing attention on potential biomarkers and pharmacological targets for the development of more efficacious and individualized therapeutic interventions for ALS patients.

Antigen processing and presentation

Antigen processing and presentation is the process by which antigen-presenting cells (APCs), such as dendritic cells, macrophages and B cells, express antigen on their cell surface in a form recognizable by T lymphocytes and other immune-related cells. Previous evidence showed that dysregulation of genes related to the antigen-processing machinery seems to account for a number of intercellular mechanisms that are able to amplify the harmful non-autonomous cell toxicity in ALS animal models [1]. Consistent with this scenario, we observed deregulated expression of several genes encoding proteins involved in antigen processing and presentation as well as in the activation/modulation of adaptive immunity, mainly in SALS2 patients (Supplementary Figure 1).

Among these genes, we distinguish those involved in the formation and regulation of the proteasome system, the main intracellular proteolytic mechanism controlling protein turnover and the selective degradation of misfolded/abnormal proteins (Supplementary Figure 1) [2]. The accumulation of abnormal protein aggregates into damaged neurons represents a common hallmark in multiple neurodegenerative diseases, including ALS, and altered expression of multiple proteasome subunits was widely documented in both patients and animal models of ALS [3, 4]. In addition, other proteases implicated in antigen generation and/or trimming (TPP2, NPEPPS, BLMH, NRD1, THOP1, SPC, PC7 and IMPAS-1), were found deregulated in SALS patients, sustaining the involvement of a dysfunction in protein turnover and ubiquitin–proteasome pathways...
in ALS (Supplementary Figure 1). In particular, NPEPPS has been recently identified as a major peptidase acting on neurotoxic protein substrates, including SOD1, and its expression was found significantly decreased in motor neurons of both ALS transgenic mice and patients, supporting its role in the disease pathogenesis [5]. Low expression levels of the gene encoding nardilysin convertase (NRD1) in SALS2 patients (Supplementary Figure 1) are in line with the evidence that the loss of this metalloendopeptidase in neurons leads to impaired motor activities and cognitive deficits by altering axonal maturation and myelination in the CNS [6]. Overexpression of IMPAS-1 in SALS patients is supported by several studies that correlate high levels of this protease with the aberrant autophagic activity associated with numerous neurodegenerative diseases [7].

Several molecular chaperones have been already extensively implicated in the pathogenesis of ALS, playing an essential role in the folding and maturation of proteins [8]. Consistent with our results, deregulated levels of HSP70, HSP90 and their interacting protein CHIP were previously detected in the serum of FALS patients, suggesting that deregulation of this protein system may reflect the degeneration of motor neurons in both forms of the disease [9]. Interestingly, recent studies have reported that treatments with arimoclomol, a strong co-inducer of HSPs, significantly delays disease progression in ALS animal models, supporting it as a potentially efficacious therapy for ALS.

Antigen presentation is mediated by the major histocompatibility complex (MHC) class I and class II molecules that are responsible to deliver short peptides to the APC surface for recognition by CD8+ (cytotoxic) and CD4+ (helper) T cells, respectively. The main difference between these molecules is that the MHC class I pathway is usually fueled by endogenous antigen, while exogenous peptides reach the MHC class II pathway. SALS patients showed deregulated expression of genes encoding MHC class I and II molecules and different components of the peptide-loading complex (TAP1, TAP2, TPSN, PDIA3, CALR, CANX, UGCGL1, BCAP31, B2M, ENPL, COPII, BCAP31, ERAP1) (Supplementary Figure 1). Genes encoding MHC molecules were found to be differentially expressed in ALS patients, supporting previous findings that reported a dual activity of neuronal MHC in ALS-affected tissues [10]. In fact, although MHC seems to play an essential role in preserving the maximal efficiency of motor axon connectivity with target muscles, a marked activation of this molecular complex was associated with enhanced infiltration of immune cells in the CNS of ALS animal models at the onset and during disease progression [11]. Moreover, activated microglia and astrocytes, present in ALS and other neurodegenerative diseases, showed increased expression of MHC-class II molecules, promoting the release of nitric oxide and other soluble factors that enhance inflammatory response [12]. The pharmacological inhibition of MHC I expression by immunomodulatory agents, such as glatiramer acetate, has shown neuroprotective effects in several neurological conditions, including ALS [13].

**T-cell-antigen recognition.** The presentation of antigen in the context of MHC molecules serves as a signal to trigger T cell activation and initiate an immunogenic cascade that leads to cytolysis of the APCs. A global dysregulation of T-cell functions has been related to an increased disease progression, decreased survival as well as production of pro-inflammatory effectors in experimental ALS [14, 15]. Abnormalities in T lymphocytes were also found in the blood of ALS patients, although there are differences among studies that may be explained by the heterogeneity of the ALS cohorts and the limited numbers of patients examined [14, 16, 17]. Accordingly, we found that a significant number of membrane protein-encoding genes involved in T cell activation and proliferation (CAV1, TRIM1, TOLLIP, DPP4/CD26, CD4, MIC2, CD45, ICOS, ICOS-L) were differentially deregulated in SALS patients (increased in SALS1 and decreased in SALS2) (Supplementary Figure 1). Among these, decreased expression of CD4 is in line with previous evidence demonstrating that the genetic depletion of CD4 or, more generally, a lack of functional T cells accelerates motor neuron degeneration and diminishes the survival of ALS transgenic mice, confirming a neuroprotective role of CD4+ T cells in ALS [15]. Reduced expression of CAV1 was associated with alterations of lymphocyte trafficking and synaptic transmission in the CNS, contributing to increased risk of neurodegenerative and age-related disorders [18, 19]. SALS1
patients showed an increased expression of the gene encoding CD99 (MIC2), a leukocyte surface glycoprotein involved in several biological processes, including the regulation of T cell activation and development (Supplementary Figure 1) [20]. Pharmacological studies showed that CD99 blockade in vivo decreases the accumulation of CNS inflammatory infiltrates, supporting the role of this protein as a possible target for controlling neuroinflammatory events [21]. Another potential therapeutic target for CNS inflammation is represented by the CD45 tyrosine phosphatase, whose expression levels were increased in the spinal cord of ALS mice as well as in activated microglial cells of murine models of other neurodegenerative diseases, including Alzheimer’s (AD) [22-24].

**Natural Killer-cell-antigen recognition.** Natural Killer (NK) cells are activated by a range of soluble factors, including cytokines and type I interferons, but also by direct cell-to-cell contact between NK cell receptors and target cell ligands. Contrary to T cells, NK cells recognize MHC I molecules using cell inhibitory receptors (i.e., KIRs, KLRs and NKG2A), leading to inhibition of NK cell activities [25-27]. Although further investigation is required to understand the role of NK cells and their receptors in ALS, previous studies have demonstrated significant infiltrations of NK cells in the spinal cord of ALS patients and the consequent inhibition of neuroprotective T-cell responses [14, 28]. In our study, we found differential expression of some genes encoding NK inhibitory receptors (NKG2A, KIR2DS1, KIR2DS2 and KLRA1) in SALS patients, indicating the dysfunctions in NK cell-mediated functions may be implicated in the immunopathogenesis of various neurodegenerative diseases, including ALS (Supplementary Figure 1) [29, 30]. In accordance with our results, increased expression of NKG2A was previously reported in PD patients, suggesting that high levels of this receptor may induce a chronic antigen-driven stimulation and dysregulated cytokine production, contributing to inflammatory and neurodegenerative events [31].

**B-cell-antigen recognition.** B cells recognize a specific antigen and initiate immune response through the B cell antigen receptor (BCRs) complex consisting of an antigen-binding subunit (the membrane immunoglobulin) and a signaling subunit, which is composed of a disulfide-linked heterodimer of Ig-α (CD79A) and Ig-β (CD79B) proteins [32]. Compelling evidence supports an important role of B cells in the pathogenesis of various neurological conditions, including ALS, not only as precursors of antibody-producing cells, but also as important regulators of the T-cell activation process through their participation in antigen presentation and cytokine production [33, 34].

Our results showed differential expression of genes encoding a component of BCR complex (CD79A) and some B cell co-receptors (FcγRIIB, ITGB1, CD45, CRACM1) in SALS2 patients (Supplementary Figure 1). Low expression levels of CD79 complex and various B cell regulators were also detected in PD patients and seem to be related to aberrant protein glycosylation and folding in the endoplasmic reticulum [35]. Decreased expression of FcγRIIB or its non-functional variants was associated with the development of inflammatory autoimmune diseases and FcγRII-deficient mice showed an impaired development of Purkinje neurons and poor rotarod performance [36-38]. In accordance with our results, up-regulated expression of CRACM1 seems to be associated with excessive neuronal Ca²⁺ signaling and excitability, thus contributing to the pathogenesis of several neurological diseases, such as epilepsy, AD and Huntington's [39, 40].

**Immune and inflammatory signaling cascades**

Accumulating evidence indicates that many neurodegenerative diseases, including ALS, are characterized by the massive activation and proliferation of microglia and astrocytes as well as the accumulation of infiltrating blood-derived immune cells (i.e., T lymphocytes and NK cells) at the sites of neurodegeneration, playing critical functions during the disease course. Moreover, signs of activation of the innate and humoral immune response were largely described in both ALS transgenic animal models and in the spinal cord and cortex of ALS patients [41]. In accordance with these studies, we observed differential expression of multiple components of intracellular signaling pathways regulating innate and adaptive immune responses in SALS patients (Supplementary
Interestingly, the majority of these signaling cascades were increased in SALS1 and reduced in SALS2 patients, suggesting that diverse subgroups of ALS patients may respond differentially to therapies targeting innate and adaptive immune responses (Figure 4b).

**Immunoreceptor signaling.** Once activated, antigen receptors induce a complex series of signaling events that are fundamental for various immune functions, including cell activation, proliferation, gene transcription, cytokine secretion and clonal deletion, determining the direction of immune responses. Among neuroinflammatory DEGs in SALS patients, we distinguish the altered expression of some components of the Syk and Src family kinases (LCK, LYN, FYN, SYK and ZAP70) and their regulators (SHP1 and SHP2), which represent the first signaling molecules to be activated downstream of immune cell-specific receptors (Supplementary Figure 2). The biological functions of these inflammatory mediators are diverse and include immune cell–receptor signaling, CNS myelination, cell division and adhesion, platelet function, synaptic activity and plasticity. In accordance with our findings, lack of Syk and Src-family kinases has been associated to defects in actin polymerization and remodeling at the immune synapse [42]. In particular, decreased expression of FYN induces a reduction in brain myelination and structural defects in synapses and dendritic spines [43]. Moreover, deregulated expression of FYN and LCK was associated with AD pathology, and several drugs that aimed at maintaining the physiological functions of the Syk and Src family kinases (e.g., saracatinib or AZD0530) are currently under study for the treatment of this disease [43, 44]. Also, ZAP70 was increased in AD patients, suggesting that activated ZAP70 may induce neuronal death through calcium-induced lymphocyte apoptosis and/or aberrant immune responses [45]. In SALS2, we also observed decreased expression of SYK together with the altered expression of two protein tyrosine phosphatases, SHP-1 and SHP-2, supporting their involvement in protecting neurons from genotoxic or oxidative insults responsible for neuronal degeneration [46-49]. Together, protein kinase and phosphatase cascades impinge on multiple downstream signaling pathways which have broad effects on gene transcription (ERK/MAPK), apoptosis regulation (AKT), Ca\(^{2+}\) mobilization (PLC\(\gamma\); PKC) and cytoskeletal function modulation (Vav/Rac/Rho and AKT), representing critical events for immune activation and inflammatory cytokine/cytolytic enzyme production.

**MAPK/ERK signaling.** Mitogen-activated protein kinases (MAPKs) are serine-threonine kinases that are activated in response to different types of oxidative stress and inflammatory conditions, and mediate intracellular signaling associated with a variety of cellular activities, including cell proliferation, differentiation, survival and death [50]. Signal transduction via this cascade is usually initiated by activating multifunctional intracellular molecules, including guanine nucleotide exchange factors and small G proteins, which induce the sequential activation of numerous protein kinases, leading to the phosphorylation and activation of transcription factors, such as c-Jun, ATF/CREB, and p53.

In our study, we found increased mRNA expression of several components of the MAPK family (MKK4, MEK1/2, MEK3, ERK1/2, p38, and JNK) and differential expression of some of their upstream activators (Grb2, SOS, VAVs, K-RAS, H-RAS, Tiam1, CDC42, Rac1 and RhoA) in both SALS subgroups (Supplementary Figure 2). Consistent with our results, several lines of evidence demonstrated that compromised MAPK signaling pathway plays a critical role in the pathogenesis of diverse human diseases, including cancer and neurodegenerative disorders, such as ALS [51]. In fact, aberrant expression and persistent activation of p38, ERK and JNK1 have been implicated in ALS pathogenesis through various mechanisms, such as the formation of abnormal intracellular inclusions, alterations in axonal transport and cytoskeletal remodeling, and the induction of motor neuron cell death [52-54]. Interestingly, the p38 MAPK inhibitor SB203580 protects motor neurons and proximal axons from excitotoxin-induced degeneration, prolonging survival of ALS mice [55].

Dysregulation of MAPK pathway upstream regulators was reported in a variety of neuronal traumas and neurodegenerative diseases, including ALS. Among these, RHOA, a member of the Rho GTPase family, plays an important role in neuronal cell survival and death by transducing...
extracellular signals to the cytoskeleton [56]. In accordance with our data, low expression levels of RHOA were also detected in spinal cord motor neurons from SOD1-related ALS patients [57]. In addition, disruptions in Rac signaling have been identified as an underlying factor in the progression of early onset forms of ALS [58]. Differential expression of mRNA and protein levels of the adapter protein Grb2 were previously found in both pre-symptomatic and early symptomatic ALS mice, suggesting its potential role as a candidate for ALS biomarkers [59].

**PI3K/AKT/mTOR pathway.** In the nervous system, activation of the PI3K signaling and its downstream effectors, AKT and mTOR, is specifically involved in diverse cellular behaviors, including proliferation, survival, metabolism, trafficking, immunity and energy homeostasis [60]. Our findings showed decreased expression of genes encoding components of PI3K, AKT and mTOR signaling cascades in both SALS patient subgroups (Supplementary Figure 2). In line with this, recent studies reported a lack or a reduction of PI3K/Akt/mTOR protein levels in spinal cord motor neurons of asymptomatic ALS mice, suggesting that modifications of this signaling pathway may represent a potential risk for motor neuron cell death [59, 61]. In particular, reduced protein expression and phosphorylation of mTOR and its downstream signaling components seem to adversely affect the establishment, maintenance and functionality of neural networks, thus contributing to neuronal degeneration and abnormal neural development [62]. In this regard, recent studies have suggested that activation of PI3K/AKT/mTOR pathways may represent an effective therapeutic strategy to prevent or slow the progression of motor neuron degeneration [56].

**PLC-γ/PKC signaling pathway.** Calcium signaling plays an important functional role in motor neurons, and excessive calcium release from intracellular stores seems to be responsible for the selective vulnerability of motor neurons in ALS [63]. PLC signaling is one of the principal mechanisms of maintaining calcium homeostasis in neurons. Activated PLC leads to the formation of two second messengers: IP3, which causes the release of calcium ions from intracellular stores, and DAG that activates PKC, promoting the phosphorylation and activation of calcium/calmodulin-dependent protein kinases and phosphatases as well as transcription factors involved in the production of pro-inflammatory cytokines and growth factors [64].

In our study, deregulated expression of genes encoding various components of the PLC-γ/PKC signaling cascade was detected in both SALS patient subgroups (Supplementary Figure 2). These findings are corroborated by previous studies reporting an abnormal activity or expression of PLC-γ and PKC in the spinal cord of ALS patients that results in higher cytoplasmic calcium concentrations, leading to the inhibition of MAPK and cytokine/chemokine signaling and activation of ER stress response observed in ALS [65, 66]. Moreover, the pharmacological inhibition or genetic removal of PLC-γ prolongs survival of ALS animal models, indicating this signaling as a potential target for ALS therapy [67].

**RAGE /TLR Signaling Pathway.** Toll-like receptor (TLR) and receptor for advanced glycation end products (RAGE) are among the major components of the innate immune system. They are able to induce and/or amplify inflammatory reactions and were extensively implicated in ALS pathology [68]. TLRs initiate signaling cascades through recognition of a variety of molecules released by the injured tissue, such as endogenous HSPs and HMGB1, a potent proinflammatory cytokine-like mediator that, interacting also with RAGE receptors, coordinates cellular stress responses and plays a critical role in several cellular processes, including cell migration, neuronal growth and apoptotic cell death [69]. Activation of RAGE/TLR signaling pathways results in the sequential stimulation of several downstream effectors and transcription factors, which induce production and release of various proinflammatory mediators (i.e., cytokines, chemokines, NO and cell adhesion molecules), exacerbating the inflammatory response and subsequently leading to neuronal damage and apoptosis.

In our study, both SALS subgroups showed up-regulation of genes encoding various TLRs (TLR2, TLR4, TLR6, TLR10), while decreased expression of HMGB1/RAGE systems was specifically detected in SALS2 patients (Supplementary Figure 2). In line with this, previous studies revealed consistent up-regulation of TLRs and HMGB1/RAGE reduction in glial cells and
degenerating spinal cord motor neurons of patients and animal models of ALS [70-72]. In addition, it was shown that TLRs antagonism, as well as restoration of RAGE signals, exert neuroprotective effects in ALS pathology, significantly extending survival and improving motor functions in a mouse model of ALS [73-75]. Altogether, these results demonstrate that activation of these signaling pathways may contribute to motor neuron injury in ALS and suggest that their pharmacological inhibition may represent an effective therapeutic strategy to attenuate neurodegenerative processes.

Among various transcription factors that are activated by the TLR signaling cascade, NF-κB plays a role of fundamental importance in various cellular mechanisms, including the immune response, cytokine production, cellular responses to oxidative stress and synaptic plasticity. Decreased expression of NF-κB was found in SALS1, while increased expression of this gene was detected in SALS2 (Supplementary Figure 2). This discrepancy may be explained by the fact that, while low levels of NF-κB have been associated with a decreased neuroprotection, high levels of this protein complex might be responsible for microglial activation occurring during neuroinflammatory responses [76]. Moreover, although preclinical studies reported contrasting results, several NF-κB pharmacological inhibitors have shown neuroprotective effects in ALS, mainly by preventing apoptotic cell death, inflammation and oxidative damage as well as improving mitochondrial function [77].

**Complement system**

The complement system represents a bridge between innate and adaptive immune responses, participating in the recognition, trafficking and elimination of pathogenic microorganisms [78]. This enzymatic cascade consists of more than 30 different proteins, membrane-bound receptors and a series of complement regulatory proteins, such as clusterin, DAF and CD59 [79]. Depending on the activation trigger, the complement cascade can be activated through three pathways (classical, lectin or alternative) that converge into the production of bioactive peptides that can mediate a variety of pro-inflammatory responses.

Complement activation in the CNS exerts a physiological role in recognizing and eliminating apoptotic and necrotic cells, but erroneous activation or insufficient regulation of this system seems to play a role in the pathogenesis of several autoimmune and neurological diseases, including ALS [80-83]. Numerous clinical and animal studies have in fact demonstrated the presence of high mRNA and protein levels of members of the complement pathway in the serum, cerebrospinal fluid and neurological tissues (spinal cord and motor cortex) of ALS patients and animal models, suggesting that a complement-driven immune response might contribute to motor neuron injury [84].

Our analysis is largely supportive of the involvement of the complement system in ALS, revealing differential expression of numerous complement components, regulators and receptors in SALS patients (Supplementary Figure 3). In particular, when compared to controls, SALS1 patients showed increased mRNA levels of several serine proteases, constituting integral elements of the classical complement cascade (including C1s, C3/C3a-c, iC3b, C3dg and C4/C4a-b) and deregulated expression of some of their membrane receptors (CD21, CR1g and CR3 - also known as αMβ2-integrin) (Supplementary Figure 3). The lectin-induced and alternative complement pathways, instead, were mainly deregulated in SALS2, with increased mRNA levels of MASP-1 and complement factors B, D, H and I (Supplementary Figure 3). Down-regulated expression of C3 and C5 convertases was found in SALS1 patients, confirming that genetic mutations or altered assembly and activity of C3/C5 convertases can result in dysregulation of the alternative complement pathway [85]. Moreover, both SALS subgroups showed deregulated expression of complement regulatory/inhibitory molecules, including clusterin, properdin, DAF and CD59, in agreement with the observation that altered levels of these molecules could confer to neurons an increased susceptibility to complement-based lysis as well as damage from recruited immune cells (Supplementary Figure 3) [83].
It is interesting to note that increased levels of complement activation products have been detected in ALS animal models before the appearance of motor symptoms, remaining detectable at the symptomatic stage, suggesting that complement activation may precede neurodegeneration and play an early role in ALS pathogenesis. This could pave the way for new diagnostic markers as well as more personalized and targeted therapeutic approaches. In this regard, inhibition or modulation of the complement system has been recognized as a promising strategy in drug discovery for several inflammatory-related conditions, including ALS, PD and AD, even if suppressing pathogenic complement activity without compromising its defensive and immunomodulatory functions still remains a big challenge [83, 86, 87]. Further experiments are thus needed to better clarify the roles of the complement pathway in the ALS progression as well as its implication in diagnosis and targeted treatments for this disease.

**Cytokine signaling**

Cytokines are a class of small proteins, comprising chemokines, interferons (IFNs), interleukins (ILs), lymphokines, and growth factors (like VEGF, TGF-β, TNFs), which act as signaling molecules to regulate acute and chronic inflammation and modulate cellular activities such as growth, survival, and differentiation. Cytokines exert their functions by interacting with their receptors and activating a complex network of intracellular signaling cascades, including Rac1, MEK/ MAPK/ERK1 and PI3K/AKT/mTOR and JAK-STAT pathways. It is possible to classify cytokines, based on the nature of the immune response, in pro-inflammatory cytokines (i.e., IL-1, IL-6, IL-17, TNFα and IFN-γ), and anti-inflammatory cytokines (i.e., IL-4, IL-5) [88].

Deregulated expression of several cytokines, their receptors and downstream effectors was observed in SALS patients, primarily in SALS2 (Supplementary Figure 4).

Although the pathogenic role of cytokines in ALS is still unknown, previous studies have associated their abnormal expression to the clinical status [89-91]. In accordance with our results, a variety of proinflammatory cytokines and growth factors, such as TGF-β, IL-1, IL-2, IL-4, IL-5 and IL-15, have previously been reported to be elevated in cerebrospinal fluid of human ALS [91]. In addition, activation of EGF signaling as well as reductions in VEGF signaling pathways seem to play a role in the pathogenesis of ALS, by triggering quiescent astrocytes into reactive astrocytes and, consequently, activating the neurodegenerative process [92, 93]. In support of this hypothesis, the pharmacological inhibition of IL-1, IL-6, IL-8R/CXCR2 and EGFR/ErbB2 signaling, as well as the administration of VEGF activators, reduce inflammation, provide neuroprotection and retard the progression of ALS pathology [94-101].

One of the main mechanisms for cytokine and chemokine signal transduction is represented by the JAK-STAT pathway. Differential expression of genes encoding various components of JAK/STAT signaling was found in SALS patients (Supplementary Figure 4), in agreement with previous studies showing that the dysregulation of this pathway occurs in inflammatory and neurodegenerative diseases, such as ALS [102]. Activation of the JAK-STAT pathway is also associated with the increased expression of a series of molecules involved in cytoskeleton remodeling, cell adhesion and migration, including Fibronectin, MMPs, FAK-1, VCAM1/ICAM1 receptors as well as tight junction proteins, whose deregulated expression was found in patients affected by SALS (Supplementary Figure 4) and other neurological diseases, including AD [103, 104]. It is interesting to note that the pharmacological blockade of the JAK-STAT pathway or its downstream effectors (e.g., FAK1 and MMPs) triggers neuroprotective effects, slowing disease progression and increasing survival in ALS animal models [105-108]. Altogether, these findings suggest that deciphering the complex actions of altered cytokine and chemokine networks may help to further elucidate the neuroinflammatory processes occurring in ALS.
LIST OF ABBREVIATIONS

Nardilysin convertase (NRD1); tripeptidyl peptidase 2 (TPP2); aminopeptidase puromycin sensitive (NPEPPS); bleomycin hydrolase (BLMH); thimet oligopeptidase (THOP1); SEC11 homolog C, signal peptidase complex subunit (SPC); proprotein convertase subtilisin/kexin type 7 (PC7); histocompatibility minor 13 (Impas-1); heat shock proteins (HSPs); heat shock protein 70 gene family (HSP70); heat shock protein 90 gene family (HSP90); STIP1 homology and U-box containing protein 1 (CHIP); transporter 1, ATP binding cassette subfamily B member (TAP1); transporter 2, ATP binding cassette subfamily B member (TAP2); tapasin (TPSN); protein disulfide isomerase family A member 3 (PDIA3); calreticulin (CALR); calnexin (CANX); UDP-glucose glycoprotein glucosyltransferase 1 (UGCGL1); B-cell receptor-associated protein 31 (BCAP31); beta-2-microglobulin (B2M), endoplasmin (ENPL), coat protein complex II (COPII); endoplasmic reticulum aminopeptidase 1 (ERAP1); caveolin 1 (CAV1); T cell receptor associated transmembrane adaptor 1 (TRIM1); toll interacting protein (TOLLIP); dipeptidyl peptidase 4 (DPP4); T-cell surface glycoprotein CD4 (CD4); T-cell surface antigen CD99 (MIC2); protein tyrosine phosphatase, receptor type C (CD45); inducible T-cell costimulator (ICOS); inducible T-cell costimulator ligand (ICOS-L); killer cell immunoglobulin like receptors (KIRs); killer cell lectin like receptors (KLRs); killer cell lectin like receptor C1 (NK2CA); killer cell immunoglobulin like receptor, two Ig domains and short cytoplasmic tail 1 (KIR2DS1); killer cell immunoglobulin like receptor, two Ig domains and short cytoplasmic tail 2 (KIR2DS2); killer cell lectin like receptor A1, pseudogene (KLR-A1); B-cell antigen receptor complex-associated protein alpha chain (CD79A); low affinity immunoglobulin gamma Fc region receptor II (FcγRIIB), integrin subunit beta 1 (ITGB1); ORAI calcium release-activated calcium modulator 1 (CRACM1); leukocyte C-terminal Src kinase (LCK); Lck/Yes-related novel protein tyrosine kinase (LYN); tyrosine-protein kinase Fyn (FYN); spleen associated tyrosine kinase (SYK); zeta chain of T cell receptor associated protein kinase 70 (ZAP70); protein tyrosine phosphatase, non-receptor type 6 (SHP1); protein tyrosine phosphatase, non-receptor type 11 (SHP2); mitogen-activated protein kinase kinase 4 (MKK4); MAP kinase kinase (MEK); extracellular signal-regulated kinase (ERK); c-Jun N-terminal kinases (JNK); growth factor receptor bound protein 2 (Grb2); SOS Ras/Rho guanine nucleotide exchange factor (SOS); vav guanine nucleotide exchange factors (VAVs); V-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog (K-RAS); Harvey rat sarcoma viral oncogene homolog (H-RAS); T-cell lymphoma invasion and metastasis 1 (Tiam1); cell division cycle 42 (CDC42); ras-related C3 botulinum toxin substrate 1 (Rac1); ras homolog family member A (RhoA); phosphoinositide-3-kinase (PI3K); serine/threonine kinase (AKT); mechanistic target of rapamycin (mTOR); phospholipase C (PLC); inositol 1,4,5-trisphosphate (IP3); 1,2-diacylglycerol (DAG); protein kinase C (PKC); high mobility group box 1 (HMGB1); nuclear factor kappa B subunit 1 (NF-kB); activator protein 1 (AP-1); cAMP responsive element binding protein (CREB1); Jun proto-oncogene, AP-1 transcription factor subunit (c-Jun); decay accelerating factor (DAF/CD55); V-set and immunoglobulin domain containing 4 (CRIg); complement C3d receptor 2 (CD21); mannan binding lectin serine peptidase 1 (MASP-1); transforming growth factor beta (TGF-β); Janus kinase (JAK); signal transducer and activator of transcription (STAT); epidermal growth factor (EGF); epidermal growth factor receptor (EGFR); erb-b2 receptor tyrosine kinase 2 (ErbB2); C-X-C motif chemokine receptor 2 (IL-8R/CXCR2); matrix metallopeptidases (MMPs); focal adhesion kinase 1 (FAK-1); vascular cell adhesion molecule 1 (VCAM1); intercellular adhesion molecule 1 (ICAM1).
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Supplementary Figure and Table Legends

**Supplementary Figure 1. Alterations in the antigen processing and presentation pathway associated with SALS patients.**
This figure illustrates genes differentially expressed in SALS patients that are involved in the antigen processing and presentation process. Each encoded protein is labeled with two thermometers (1) or (2) that indicate expression levels in SALS cluster 1 and 2, respectively. Upward thermometers have red color and indicate up-regulated signals in SALS patients, down-ward (blue) ones indicate down-regulated signals. Colored hexagons on the vectors between objects describe the type of interaction where B = binding, C = cleavage, CM = covalent modification, Cn = competition, CS = complex subunit, GR = group relation, IE = influence on expression, P = phosphorylation, T = transformation, TR = transcriptional regulation, Tn = transport and CR indicates that an object belongs to a group of related proteins. Lines indicate activation (green), inhibition (red) or unspecified (grey) interactions between the molecules. The object shapes correspond to molecule type and are described in the Supplementary Figure 5.

**Supplementary Figure 2. Alterations in immune and inflammatory signaling observed in SALS patients.**
Genes involved in immune and inflammatory signaling that were differentially expressed in SALS patients versus controls were mapped on pathway. Thermometers labeled with (1) or (2) indicate expression levels in SALS cluster 1 and 2, respectively. Upward thermometers have red color and indicate up-regulated signals in SALS patients, down-ward (blue) ones indicate down-regulated signals. Colored hexagons on the vectors between objects describe the type of interaction where B = binding, C = cleavage, CM = covalent modification, Cn = competition, CS = complex subunit, GR = group relation, IE = influence on expression, P = phosphorylation, T = transformation, TR = transcriptional regulation, Tn = transport and CR indicates that an object belongs to a group of related proteins. Lines indicate activation (green), inhibition (red) or unspecified (grey) interactions between the molecules. The object shapes correspond to molecule type and are described in the Supplementary Figure 5.

**Supplementary Figure 3. Alterations in complement system signaling pathways (classical, lectin and alternative) observed in SALS patients.**
Thermometers labeled with (1) or (2) indicate expression levels in SALS cluster 1 and 2, respectively. Upward thermometers have red color and indicate up-regulated signals in SALS patients, down-ward (blue) ones indicate down-regulated signals. Colored hexagons on the vectors between objects describe the type of interaction where B = binding, C = cleavage, CM = covalent modification, Cn = competition, CS = complex subunit, GR = group relation, IE = influence on
expression, P = phosphorylation, T = transformation, TR = transcriptional regulation, Tn = transport and CR indicates that an object belongs to a group of related proteins. Lines indicate activation (green), inhibition (red) or unspecified (grey) interactions between the molecules. The object shapes correspond to molecule type and are described in the Supplementary Figure 5.

Supplementary Figure 4. Alterations in cytokine signaling observed in SALS patients. Thermometers labeled with (1) or (2) indicate expression levels in SALS cluster 1 and 2, respectively. Upward thermometers have red color and indicate up-regulated signals in SALS patients, downward (blue) ones indicate down-regulated signals. Colored hexagons on the vectors between objects describe the type of interaction where B = binding, C = cleavage, CM = covalent modification, Cn = competition, CS = complex subunit, GR = group relation, IE = influence on expression, P = phosphorylation, T = transformation, TR = transcriptional regulation, Tn = transport and CR indicates that an object belongs to a group of related proteins. Lines indicate activation (green), inhibition (red) or unspecified (grey) interactions between the molecules. The object shapes correspond to molecule type and are described in the Supplementary Figure 5.

Supplementary Figure 5. Legend describing symbols used in MetaCore pathway.

Supplementary Table 1. Pathway enrichment analysis on the entire list of statistically deregulated genes in SALS patients versus controls.

Supplementary Table 2. Pathway enrichment analysis on the entire list of statistically deregulated genes in SALS1 and SALS2 patients compared to controls.

Supplementary Table 3. Neuroinflammatory genes differentially expressed in SALS1.

Supplementary Table 4. Neuroinflammatory genes differentially expressed in SALS2.

Supplementary Table 5. Neuroinflammatory genes differentially expressed in SALS1 and SALS2.

Supplementary Table 6. List of genes included in the SALS1-related PPI network.

Supplementary Table 7. List of genes included in the SALS2-related PPI network.

Supplementary Table 8. Pathway enrichment analyses on the list of statistically deregulated neuroinflammatory genes in SALS patients.
Supplementary Table 1. Pathway enrichment analysis on the entire list of statistically deregulated genes in SALS patients versus controls.

| #  | Maps                                                                 | pValue      | FDR         | Ratio |
|----|----------------------------------------------------------------------|-------------|-------------|-------|
| 1  | Thrombopoietin signaling via JAK-STAT pathway                        | 2.591E-04   | 3.388E-02   | 3/22  |
| 2  | Huntingtin-depended transcription deregulation in Huntington's Disease | 3.378E-04   | 3.388E-02   | 3/24  |
| 3  | Immune response_IL-4-induced regulators of cell growth, survival, differentiation and metabolism | 4.600E-04   | 3.388E-02   | 4/63  |
| 4  | Signal transduction_JNK pathway                                      | 2.463E-03   | 1.361E-01   | 3/47  |
| 5  | Prolactin receptor signaling                                         | 4.483E-03   | 1.781E-01   | 3/58  |
| 6  | Cytokines and Chemokines signaling                                   | 6.075E-03   | 1.781E-01   | 4/127 |
| 7  | Immune response_Oncostatin M signaling via JAK-Stat                  | 7.008E-03   | 1.781E-01   | 2/22  |
| 8  | Prolactin receptor signaling                                         | 4.483E-03   | 1.781E-01   | 3/58  |
| 9  | Immune response_IL-6 signaling pathway                               | 4.600E-04   | 3.388E-02   | 4/63  |
| 10 | Role of Parkin in the Ubiquitin-Proteasomal Pathway                  | 4.31E-03    | 1.781E-01   | 2/24  |
| 11 | Glucocorticoid receptor signaling                                    | 9.001E-03   | 1.781E-01   | 2/25  |
| 12 | Signal transduction_JNK pathway                                      | 2.463E-03   | 1.361E-01   | 3/47  |
| 13 | Prolactin receptor signaling                                         | 4.483E-03   | 1.781E-01   | 3/58  |
| 14 | Role of Diethylhexyl Phthalate and Tributyltin in fat cell differentiation | 1.200E-02   | 1.781E-01   | 2/29  |
| 15 | Immune response_IL-13 signaling via JAK-STAT                         | 1.200E-02   | 1.781E-01   | 2/29  |
| 16 | Apoptosis and survival_FAS signaling cascades                        | 2.85E-02    | 1.781E-01   | 2/29  |
| 17 | Development_Transcription regulation of granulocyte development       | 1.450E-02   | 1.781E-01   | 2/29  |
| 18 | Development_Regulation of G1/S transition (part 1)                   | 3.731E-02   | 1.781E-01   | 2/29  |
| 19 | Development_Differentiation of white adipocytes                      | 4.125E-02   | 1.781E-01   | 2/29  |
| 20 | Development_Keratinocyte differentiation                              | 4.125E-02   | 1.781E-01   | 2/29  |
| 21 | Development_Aspiration                                               | 4.125E-02   | 1.781E-01   | 2/29  |
| 22 | Development_Transcription regulation of granulocyte development       | 4.125E-02   | 1.781E-01   | 2/29  |
| 23 | Development_Regulation of G1/S transition (part 1)                   | 4.125E-02   | 1.781E-01   | 2/29  |
| 24 | Development_Differentiation of white adipocytes                      | 4.125E-02   | 1.781E-01   | 2/29  |
| 25 | Development_Keratinocyte differentiation                              | 4.125E-02   | 1.781E-01   | 2/29  |
| 26 | Development_Aspiration                                               | 4.125E-02   | 1.781E-01   | 2/29  |
| 27 | Development_Differentiation of white adipocytes                      | 4.125E-02   | 1.781E-01   | 2/29  |
| 28 | Development_Keratinocyte differentiation                              | 4.125E-02   | 1.781E-01   | 2/29  |
| 29 | Development_Aspiration                                               | 4.125E-02   | 1.781E-01   | 2/29  |
| 30 | Development_Differentiation of white adipocytes                      | 4.125E-02   | 1.781E-01   | 2/29  |
| 31 | Development_Keratinocyte differentiation                              | 4.125E-02   | 1.781E-01   | 2/29  |
| 32 | Development_Aspiration                                               | 4.125E-02   | 1.781E-01   | 2/29  |
| 33 | Development_Differentiation of white adipocytes                      | 4.125E-02   | 1.781E-01   | 2/29  |
| 34 | Development_Keratinocyte differentiation                              | 4.125E-02   | 1.781E-01   | 2/29  |
| 35 | Development_Aspiration                                               | 4.125E-02   | 1.781E-01   | 2/29  |
| 36 | Development_Differentiation of white adipocytes                      | 4.125E-02   | 1.781E-01   | 2/29  |
| 37 | Development_Keratinocyte differentiation                              | 4.125E-02   | 1.781E-01   | 2/29  |
| 38 | Development_Differentiation of white adipocytes                      | 4.125E-02   | 1.781E-01   | 2/29  |
| 39 | Development_Keratinocyte differentiation                              | 4.125E-02   | 1.781E-01   | 2/29  |
| 40 | Development_Differentiation of white adipocytes                      | 4.125E-02   | 1.781E-01   | 2/29  |
| 41 | Development_Keratinocyte differentiation                              | 4.125E-02   | 1.781E-01   | 2/29  |
| 42 | Development_Keratinocyte differentiation                              | 4.125E-02   | 1.781E-01   | 2/29  |
| 43 | Development_Keratinocyte differentiation                              | 4.125E-02   | 1.781E-01   | 2/29  |
| 44 | Development_Keratinocyte differentiation                              | 4.125E-02   | 1.781E-01   | 2/29  |
| 45 | Development_Keratinocyte differentiation                              | 4.125E-02   | 1.781E-01   | 2/29  |
| 46 | Development_Keratinocyte differentiation                              | 4.125E-02   | 1.781E-01   | 2/29  |
| 47 | Development_Keratinocyte differentiation                              | 4.125E-02   | 1.781E-01   | 2/29  |
| 48 | Development_Keratinocyte differentiation                              | 4.125E-02   | 1.781E-01   | 2/29  |
| 49 | Development_Keratinocyte differentiation                              | 4.125E-02   | 1.781E-01   | 2/29  |
| 50 | Development_Keratinocyte differentiation                              | 4.125E-02   | 1.781E-01   | 2/29  |
| Rank | Pathway Description                                      | pValue | min(pvalue) | FDR  | Ratio |
|------|----------------------------------------------------------|--------|-------------|------|-------|
| 1    | Cytoplasm remodeling, GTP-binding and cytoskeletal remodeling | 2.54E-09 | 3.15E-13    | 3.7E-07 | 37/111 |
| 2    | Cytoskeleton remodeling, cytoskeleton remodeling         | 3.15E-13 | 3.54E-11    | 72/111 |
| 3    | Transport_ClinProphicoated vesicle cycle                 | 1.70E-06 | 9.52E-05    | 30/102 |
| 4    | Transport_Kinin-coated vesicle cycle                     | 3.63E-12 | 3.63E-12    | 66/102 |
| 5    | Signal transduction of mTORC1 downstream signaling       | 1.82E-09 | 1.82E-09    | 33/111 |
| 6    | Normal and pathological TGF-beta-mediated regulation of cell proliferation | 1.10E-08 | 3.05E-09    | 9.62E-03 | 14/33 |
| 7    | Development_Postive regulation of STK34 (Hippo) pathway and negative regulation of YAP/TAZ function | 1.17E-03 | 3.26E-09    | 9.87E-03 | 18/70 |
| 8    | Neurogenesis_NGF/TrkA MAPK-mediated signaling            | 4.23E-02 | 3.79E-09    | 1.13E-01 | 19/105 |
| 9    | Development_Regulation of cytoskeleton proteins in oligodendrocyte differentiation and myelinization | 2.55E-05 | 4.13E-09    | 6.75E-04 | 19/58 |
| 10   | Neurophysiological process Dynein-dynactin motor complex in axonal transport in neurons | 3.86E-07 | 3.77E-05    | 2.12E-07 | 40/58 |
| 11   | Immune response_M-CSF-Receptor signaling pathway         | 9.98E-02 | 4.24E-09    | 2.08E-07 | 14/18 |
| 12   | Immune response_Granulocyte-Macrophage signaling pathway  | 2.42E-01 | 1.24E-07    | 5.81E-07 | 27/34 |
| 13   | Development_WNT signaling pathway. Part 1. Degradation of beta-catenin in the absence WNT signaling | 5.13E-04 | 1.04E-08    | 2.55E-02 | 10/34 |
| 14   | Development_WNT signaling pathway. Part 2. Degradation of beta-catenin in the absence WNT signaling | 1.12E-08 | 1.12E-08    | 4.56E-07 | 18/19 |
| 15   | Apoptosis and survival_NGF/TrkA PI3K-mediated signaling  | 1.10E-07 | 1.94E-08    | 1.21E-05 | 27/77 |
| 16   | Development_Prolaktin receptor signaling                 | 9.96E-02 | 1.96E-08    | 7.35E-07 | 39/85 |
| 17   | Immune response_IL-3 signaling via ERK and PI3K          | 1.84E-03 | 2.60E-08    | 9.17E-07 | 59/102 |
| 18   | LRRK2 in neurons in Parkinson’s disease                  | 1.74E-06 | 2.65E-08    | 9.52E-05 | 15/33 |
| 19   | Cell adhesion_Chemokin and adhesion                     | 1.07E-08 | 2.98E-08    | 9.94E-07 | 89/100 |
| 20   | Immune response_ONcostatin M signaling via MAPK          | 1.47E-01 | 3.65E-08    | 2.73E-08 | 73/77 |
| 21   | Immune response_IL-6 signaling pathway via JAK/STAT      | 4.20E-08 | 2.24E-02    | 1.77E-08 | 28/32 |
| 22   | Signal transduction of mTORC2 downstream signaling       | 4.79E-08 | 4.79E-08    | 1.49E-07 | 45/72 |
| 23   | Transcription_Transcription regulation of aminoacid metabolism | 5.80E-03 | 5.80E-08    | 2.69E-02 | 16/68 |
| 24   | Transcription_Transcription regulation of aminoacid metabolism | 1.72E-01 | 7.82E-08    | 2.99E-02 | 32/78 |
| 25   | Immune response_Antigen presentation by MHC class I, classical pathway | 1.27E-03 | 9.68E-08    | 1.05E-02 | 16/64 |
| 26   | Immune response_Activation of PKC via G-Protein coupled receptor | 8.30E-04 | 1.01E-07    | 8.54E-03 | 15/52 |
| 27   | Tau pathology in Alzheimer disease                       | 1.83E-07 | 1.83E-07    | 3.83E-06 | 40/110 |
| 28   | Immune response_HMBG1/RAGE signaling pathway            | 2.71E-02 | 1.96E-07    | 8.30E-12 | 12/255 |
| 29   | IL-6 signaling in multiple myeloma                      | 3.01E-03 | 3.01E-08    | 3.60E-03 | 13/33 |
| 30   | Regulation of degradation of deltaF508-CFTR in CF        | 2.09E-07 | 2.09E-07    | 5.21E-03 | 35/53 |
| 31   | Immune response_IL-2 signaling via JAK/STAT, p38, JNK and NF-kB | 2.10E-05 | 2.10E-05    | 6.12E-04 | 15/39 |
| 32   | Aberrant presentation of IL-2 and IL-17 in SLE T cells   | 7.21E-04 | 2.95E-04    | 2.95E-04 | 17/93 |
| 33   | Immune response_Role of PKR in stress-induced antiviral cell response | 2.58E-07 | 2.58E-07    | 5.94E-06 | 53/93 |
| 34   | Immune response_IL-4 signaling pathway                  | 6.96E-01 | 3.57E-07    | 8.24E-01 | 22/24 |
| 35   | Immune response_IL-2 signaling pathway                  | 5.7E-06  | 5.7E-06     | 8.20E-06 | 39/54 |
| 36   | Development_TGF-beta-dependent induction of EMT via RhoA, PI3K and ILK | 4.58E-08 | 4.58E-09    | 0.00E-05 | 9/86 |
| 37   | Signal transduction of ERK1/2 signaling pathway          | 4.19E-02 | 4.19E-07    | 2.25E-02 | 21/46 |
| 38   | Development_Adrenosine A2B receptor signaling           | 1.68E-03 | 1.68E-03    | 4.25E-02 | 14/50 |
| 39   | Immune response_Antigen presentation by MHC class I, cross-presentation | 4.97E-04 | 4.82E-07    | 6.26E-03 | 24/99 |
| 40   | Immune response_Epigenetic and transcriptional regulation of oligodendrocyte precursor cell differentiation and myelination | 1.45E-03 | 1.45E-03    | 1.11E-02 | 11/34 |
| 41   | Immune response_IL-6 signaling pathway via MEK/ERK and PI3K/AKT cascades | 1.56E-03 | 1.56E-03    | 9.81E-06 | 25/04 |
| 42   | Development_EPO-induced Jak-STAT pathway               | 5.90E-02 | 5.90E-04    | 1.40E-01 | 9/86 |
| 43   | K-RAS signaling in pancreatic cancer                    | 1.34E-02 | 1.34E-02    | 9.81E-06 | 26/06 |
| 44   | GSK3 beta in bipolar disorder                           | 5.85E-07 | 5.85E-07    | 9.88E-06 | 19/23 |
| 45   | Some pathways of EMT in cancer cells                    | 6.25E-07 | 6.25E-07    | 4.97E-05 | 29/15 |

Supplementary Table 2. Pathway enrichment analysis on the entire list of statistically deregulated genes in SALS1 (n=4485) and SALS2 (16144) patients compared to controls.
| Pathway                                                                 | p-value     | r-value   | FDR       |
|------------------------------------------------------------------------|-------------|-----------|-----------|
| Neurophysiological process_GABA-A receptor life cycle                  | 1.34E-05    | 1.57E-05  | 31/51     |
| Development_Regulation of epithelial-to-mesenchymal transition (EMT)   | 3.57E-02    | 9.04E-07  | 7/27      |
| Development_Regulation of epithelial-to-mesenchymal transition (EMT)   | 9.38E-06    | 9.63E-07  | 3.38E-04  | 21/64     |
| Development_Regulation of epithelial-to-mesenchymal transition (EMT)   | 9.63E-07    | 9.63E-07  | 1.64E-05  | 39/64     |
| Development_Regulation of epithelial-to-mesenchymal transition (EMT)   | 7.90E-03    | 1.08E-06  | 3.48E-02  | 12/47     |
| Development_Regulation of epithelial-to-mesenchymal transition (EMT)   | 1.08E-06    | 1.80E-05  | 33/47     |
| Signal transduction_JNK pathway                                        | 1.79E-03    | 1.15E-06  | 1.38E-02  | 39/46     |
| Cell adhesion_Histamine H1 receptor signaling in the interruption of cell barrier integrity | 3.64E-03    | 2.04E-02  | 12/43     |
| Cell adhesion_Histamine H1 receptor signaling in the interruption of cell barrier integrity | 1.20E-06    | 1.95E-05  | 28/43     |
| Cytoskeleton remodeling_Hyaluronic acid/ CD44 signaling pathways        | 9.63E-07    | 3.48E-02  | 12/47     |
| Cytoskeleton remodeling_Hyaluronic acid/ CD44 signaling pathways        | 9.63E-07    | 1.80E-05  | 33/47     |
| Cytoskeleton remodeling_Hyaluronic acid/ CD44 signaling pathways        | 7.90E-03    | 1.08E-06  | 3.48E-02  | 12/47     |
| Cytoskeleton remodeling_Hyaluronic acid/ CD44 signaling pathways        | 1.08E-06    | 1.80E-05  | 33/47     |
| Cytoskeleton remodeling_Hyaluronic acid/ CD44 signaling pathways        | 3.64E-03    | 2.04E-02  | 12/43     |
| Cytoskeleton remodeling_Hyaluronic acid/ CD44 signaling pathways        | 1.20E-06    | 1.95E-05  | 28/43     |
| Probe ID    | p Value (Corr) | p Value (SALS1/CTRL) | Fold Change (SALS1/CTRL) | GENE_SYMBOL |
|------------|----------------|----------------------|--------------------------|-------------|
| A_23_P166051 | 2.08E-02       | 1.18E-02             | 1.47                      | RBCK1       |
| A_23_P329573 | 3.22E-02       | 1.93E-02             | 2.17                      | ITGB2       |
| A_24_P343233 | 1.44E-05       | 1.23E-06             | 2.20                      | HLA-DRB1    |
| A_23_P89249  | 7.67E-04       | 2.59E-04             | 1.99                      | ERBB2       |
| A_23_P135769 | 6.60E-05       | 1.21E-05             | 3.04                      | ACTB        |
| A_23_P24870  | 3.85E-02       | 2.38E-02             | 2.05                      | CD44        |
| A_23_P309739 | 2.75E-02       | 1.61E-02             | -1.46                     | ESR1        |
| A_24_P362193 | 2.48E-05       | 2.98E-06             | -3.52                     | CD84        |
| A_23_P158725 | 5.34E-05       | 9.11E-06             | 1.76                      | SLC16A3     |
| A_23_P145089 | 1.26E-06       | 9.38E-09             | 3.55                      | HSP90AB1    |
| A_24_P50759  | 4.10E-06       | 1.22E-07             | -1.40                     | TNF         |
| A_23_P75283  | 1.02E-04       | 2.16E-05             | 1.93                      | RBP4        |
| A_23_P4223   | 2.99E-06       | 5.79E-08             | 2.02                      | CALCOCO2    |
| A_23_P79591  | 2.15E-06       | 3.16E-08             | -2.16                     | APOB        |
| A_23_P29495  | 3.09E-05       | 4.13E-06             | 2.02                      | CTNNB1      |
| A_24_P161933 | 7.60E-04       | 2.56E-04             | 3.87                      | HLA-B       |
| A_23_P315571 | 6.84E-05       | 1.27E-05             | 2.10                      | RFTN1       |
| A_23_P120947 | 7.38E-06       | 3.33E-07             | 3.05                      | XRCC6       |
| A_23_P369237 | 2.37E-02       | 1.37E-02             | -1.39                     | ADIPOQ      |
| A_23_P213114 | 1.46E-03       | 5.55E-04             | -4.41                     | TEC         |
| A_24_P281101 | 8.16E-06       | 4.17E-07             | -1.91                     | ABL1        |
| A_23_P70095  | 1.39E-02       | 7.41E-03             | 1.69                      | CD74        |
| A_23_P101992 | 3.31E-02       | 1.99E-02             | 2.44                      | MARCO       |
| A_23_P147875 | 2.88E-05       | 3.72E-06             | 2.12                      | CHID1       |
| A_23_P156788 | 1.16E-02       | 6.02E-03             | -1.59                     | STX11       |
| A_24_P123616 | 3.81E-06       | 1.01E-07             | 4.67                      | HSPA1A      |
| A_23_P70539  | 2.05E-02       | 1.16E-02             | 2.42                      | HLA-C       |
| A_24_P7887   | 2.54E-04       | 6.75E-05             | -1.79                     | EP300       |
| A_23_P103361 | 1.17E-02       | 6.08E-03             | -1.48                     | LCK         |
| A_24_P943283 | 1.43E-03       | 5.37E-04             | -1.64                     | DENND1B     |
| A_23_P60387  | 3.63E-02       | 2.23E-02             | -1.37                     | NOTCH1      |
| A_23_P206510 | 9.25E-06       | 5.80E-07             | 1.80                      | GLG1        |
| A_23_P202156 | 4.66E-02       | 2.99E-02             | -1.47                     | NFKB2       |
| A_23_P61646  | 2.05E-02       | 1.16E-02             | 1.81                      | STX4        |
| A_23_P29036  | 5.59E-05       | 9.69E-06             | 1.71                      | IFNGR2      |
| A_24_P390495 | 1.27E-02       | 6.69E-03             | 1.62                      | CX3CL1      |
| A_24_P254079 | 6.81E-03       | 3.31E-03             | 2.10                      | ICAM5       |
| A_23_P215913 | 1.03E-05       | 6.92E-07             | 3.90                      | CLU         |
| A_23_P98183  | 1.68E-03       | 6.55E-04             | 2.13                      | HRAS        |
| A_24_P360674 | 8.53E-06       | 4.75E-07             | -4.42                     | CDKN2B      |
| A_23_P81912  | 5.03E-06       | 1.64E-07             | 2.33                      | TUBB        |
| A_23_P151294 | 1.01E-06       | 3.77E-09             | -1.80                     | IFNG        |
| A_23_P92499  | 1.86E-03       | 7.38E-04             | 2.06                      | TLR2        |
| A_24_P287043 | 8.52E-05       | 1.70E-05             | 2.49                      | IFITM2      |
| A_23_P99452  | 5.88E-06       | 2.02E-07             | -1.75                     | BRCA2       |
| A_32_P139894 | 1.91E-05       | 1.93E-06             | 1.74                      | ABL2        |

Supplementary Table 3. Neuroinflammatory genes differentially expressed in SALS1.
| Gene     | Log2FoldChange | p-value       | q-value      | Description  |
|----------|----------------|---------------|--------------|--------------|
| IRF9     | 1.86           | 7.26E-05      | 1.97         | RABGAP1L     |
| ATG5     | 1.48           | 6.57E-04      | 1.10E-04     | GLG1         |
| RAB5B    | 2.34           | 2.60E-02      | 1.52E-02     | TUBB         |
| ANG      | 1.56           | 3.46E-03      | 1.52E-03     | HYAL2        |
| RBPJ     | 2.08           | 8.12E-06      | 4.08E-07     | BCR          |
| CIAPIN1  | 2.00           | 2.72E-03      | 1.16E-03     | IP6K2        |
| NUP85    | -1.32          | 1.16E-03      | 4.21E-04     | FOXL1        |
| BRAF     | 1.59           | 4.24E-06      | 1.30E-07     | TUBB         |
| HYAL2    | 1.64           | 8.16E-06      | 4.15E-07     | SEC13        |
| BCAP31   | 3.38           | 1.44E-04      | 3.29E-05     | TUBB         |
| CIAPIN1  | 2.00           | 2.72E-03      | 1.16E-03     | IP6K2        |
| NUP85    | -1.32          | 1.16E-03      | 4.21E-04     | FOXL1        |
| BRAF     | 1.59           | 4.24E-06      | 1.30E-07     | TUBB         |
| HYAL2    | 1.64           | 8.16E-06      | 4.15E-07     | SEC13        |
| BCAP31   | 3.38           | 1.44E-04      | 3.29E-05     | TUBB         |
| CIAPIN1  | 2.00           | 2.72E-03      | 1.16E-03     | IP6K2        |
| NUP85    | -1.32          | 1.16E-03      | 4.21E-04     | FOXL1        |
| BRAF     | 1.59           | 4.24E-06      | 1.30E-07     | TUBB         |
| HYAL2    | 1.64           | 8.16E-06      | 4.15E-07     | SEC13        |
| BCAP31   | 3.38           | 1.44E-04      | 3.29E-05     | TUBB         |
| CIAPIN1  | 2.00           | 2.72E-03      | 1.16E-03     | IP6K2        |
| NUP85    | -1.32          | 1.16E-03      | 4.21E-04     | FOXL1        |
| BRAF     | 1.59           | 4.24E-06      | 1.30E-07     | TUBB         |
| HYAL2    | 1.64           | 8.16E-06      | 4.15E-07     | SEC13        |
| BCAP31   | 3.38           | 1.44E-04      | 3.29E-05     | TUBB         |
| CIAPIN1  | 2.00           | 2.72E-03      | 1.16E-03     | IP6K2        |
| NUP85    | -1.32          | 1.16E-03      | 4.21E-04     | FOXL1        |
| BRAF     | 1.59           | 4.24E-06      | 1.30E-07     | TUBB         |
| HYAL2    | 1.64           | 8.16E-06      | 4.15E-07     | SEC13        |
| BCAP31   | 3.38           | 1.44E-04      | 3.29E-05     | TUBB         |
| CIAPIN1  | 2.00           | 2.72E-03      | 1.16E-03     | IP6K2        |
| NUP85    | -1.32          | 1.16E-03      | 4.21E-04     | FOXL1        |
| BRAF     | 1.59           | 4.24E-06      | 1.30E-07     | TUBB         |
| HYAL2    | 1.64           | 8.16E-06      | 4.15E-07     | SEC13        |
| BCAP31   | 3.38           | 1.44E-04      | 3.29E-05     | TUBB         |
| CIAPIN1  | 2.00           | 2.72E-03      | 1.16E-03     | IP6K2        |
| NUP85    | -1.32          | 1.16E-03      | 4.21E-04     | FOXL1        |
| Gene Symbol | Log2 Fold Change | p-Value | Significance |
|-------------|-----------------|---------|--------------|
| CMKLR1      | 2.55E-02        | 1.48E-02| 1.72         |
| RABGEP1     | 5.40E-03        | 1.69E-03| 1.56         |
| SERPINA3    | 1.30E-02        | 6.90E-03| 3.29         |
| CXCL10      | 8.31E-05        | 2.99E-07| -3.23        |
| BCL6        | 1.10E-04        | 2.38E-05| 2.09         |
| CHD2        | 2.43E-05        | 2.84E-06| 2.05         |
| UBE2D3      | 1.67E-06        | 1.73E-08| 2.37         |
| LST1        | 4.54E-03        | 2.08E-03| 1.98         |
| SYNCRIP     | 1.66E-05        | 1.58E-06| 1.93         |
| EDN1        | 1.17E-05        | 8.44E-07| 2.69         |
| MAEA        | 7.10E-04        | 2.37E-04| 3.82         |
| PSMC5       | 6.76E-03        | 3.28E-03| 3.14         |
| BCR         | 6.68E-07        | 8.25E-10| 1.69         |
| SNX27       | 1.19E-05        | 8.67E-07| 2.27         |
| PRMT1       | 3.77E-04        | 1.10E-04| 1.96         |
| FGFR2       | 1.71E-04        | 4.10E-05| 1.83         |
| DAPK1       | 2.93E-02        | 1.74E-02| 1.67         |
| PRKAR1A     | 3.96E-03        | 1.77E-03| 2.39         |
| PRELID1     | 3.88E-06        | 1.11E-07| 1.54         |
| ITGB5       | 1.22E-05        | 9.06E-07| 1.86         |
| EE2F        | 1.60E-04        | 3.77E-05| 3.16         |
| ELMO2       | 1.93E-03        | 7.74E-04| 2.20         |
| PDE2A       | 1.67E-03        | 6.49E-04| 2.46         |
| CD80        | 3.65E-03        | 1.62E-03| -2.86        |
| VAMP8       | 3.87E-04        | 1.14E-04| 1.94         |
| DDIT4       | 3.67E-05        | 5.37E-06| 1.98         |
| CCNB2       | 4.25E-05        | 6.53E-06| -2.65        |
| RARRES2     | 1.09E-03        | 3.95E-04| 2.77         |
| ZFP36L2     | 4.41E-03        | 2.01E-03| 2.72         |
| UBAS2       | 6.68E-07        | 1.26E-09| 1.58         |
| SERINC3     | 9.88E-05        | 2.07E-05| 2.16         |
| FLOT2       | 3.77E-04        | 1.10E-04| 1.67         |
| NCAM1       | 2.04E-03        | 8.20E-04| 1.70         |
| IL2         | 4.59E-06        | 1.48E-07| -1.83        |
| SUMO1       | 1.79E-02        | 9.93E-03| 2.06         |
| SRF         | 1.45E-04        | 3.32E-05| 1.90         |
| ST6GAL1     | 1.49E-05        | 1.31E-06| -1.83        |
| TRAF2       | 1.37E-02        | 7.28E-03| 1.78         |
| PSMD9       | 1.66E-06        | 1.49E-08| 1.99         |
| NR1H3       | 2.97E-05        | 3.88E-06| 1.97         |
| C3D7        | 1.22E-02        | 6.39E-03| 2.86         |
| C1QA        | 1.03E-02        | 5.29E-03| 2.90         |
| LILRB3      | 2.52E-02        | 1.46E-02| 2.70         |
| ARNT        | 2.87E-02        | 1.70E-02| 1.90         |
| RAC1        | 4.24E-06        | 1.29E-07| 2.37         |
| HIPK1       | 1.44E-05        | 1.22E-06| 2.03         |
| PSME1       | 5.97E-03        | 2.84E-03| -3.00        |
| Gene Symbol | Log2 (Fold Change) | p-Value | Fold Change | Gene Symbol |
|-------------|--------------------|---------|-------------|-------------|
| ITGA2       | -5.15              | 8.83E-06|             |             |
| PHB         | 2.30               | 1.62E-04|             |             |
| ARF1        | 1.94               | 1.45E-03|             |             |
| PSMC4       | 2.27               | 2.28E-05|             |             |
| HSP90AB1    | 2.31               | 4.51E-05|             |             |
| BECN1       | 2.03               | 3.88E-06|             |             |
| NCAPh2      | 2.01               | 1.13E-03|             |             |
| NFATC1      | 1.88               | 1.24E-03|             |             |
| PSMD3       | 2.62               | 5.90E-04|             |             |
| TCF3        | 1.81               | 3.88E-06|             |             |
| SQSTM1      | 2.94               | 3.88E-06|             |             |
| ATG7        | 1.53               | 1.81E-02|             |             |
| CYP19A1     | -3.27              | 2.16E-02|             |             |
| MS4A1       | -5.29              | 4.99E-02|             |             |
| IKKbeta     | 1.83               | 2.05E-05|             |             |
| TFK2        | 1.74               | 2.03E-03|             |             |
| ASS1        | 2.69               | 8.68E-06|             |             |
| C4B         | 2.77               | 4.35E-03|             |             |
| LAT2        | -1.69              | 4.49E-03|             |             |
| ARF1        | 3.31               | 6.68E-07|             |             |
| AQP8        | 1.79               | 2.14E-03|             |             |
| AQP4        | 3.73               | 2.05E-05|             |             |
| PSMD4       | 2.88               | 1.26E-06|             |             |
| ATG12       | 1.78               | 5.14E-04|             |             |
| SECl4L1     | 1.66               | 7.26E-05|             |             |
| Gf11        | 3.12               | 5.55E-03|             |             |
| Fcrl4       | -4.34              | 9.67E-04|             |             |
| Psmf1       | 2.14               | 1.23E-05|             |             |
| Ankhd1-Ef4ebp3 | 2.09             | 1.88E-04|             |             |
| C1s         | 2.59               | 9.50E-05|             |             |
| Inpps5d     | 1.73               | 2.19E-03|             |             |
| Havcr2      | 1.91               | 6.47E-04|             |             |
| ClqB        | 3.82               | 2.67E-04|             |             |
| Psmd13      | 2.11               | 2.43E-05|             |             |
| Relb        | 1.82               | 3.40E-06|             |             |
| Ppp4r2      | 2.10               | 4.99E-02|             |             |
| Ddx41       | 2.17               | 1.44E-02|             |             |
| Bpgm        | 1.85               | 2.31E-05|             |             |
| Prx7        | 1.84               | 8.30E-03|             |             |
| Tcf7        | -1.59              | 4.25E-05|             |             |
| Bcr         | 1.91               | 3.52E-04|             |             |
| Wipf2       | 1.62               | 6.22E-03|             |             |
| Anxa2       | 2.82               | 3.35E-05|             |             |
| Slfn13      | -5.21              | 6.00E-06|             |             |
| Tmem102     | 2.38               | 4.21E-03|             |             |
| Pdia3       | 2.03               | 8.68E-06|             |             |
| Hcls1       | 2.13               | 1.49E-05|             |             |
| Vsig4       | 2.09               | 1.58E-03|             |             |
| Gene Symbol | Fold Change | p-Value | Gene Symbol | Fold Change | p-Value |
|-------------|-------------|---------|-------------|-------------|---------|
| SART3       | 1.61        | 0.001   | CXCL12      | -4.66       | 0.001   |
| AP2M1       | 2.48        | 0.001   | L3MBTL3     | 1.40        | 0.001   |
| MAPK10      | 2.38        | 0.001   | LIG1        | 2.14        | 0.001   |
| CR1         | -2.68       | 0.001   | MELK        | -3.71       | 0.001   |
| SMAD3       | 1.73        | 0.001   | KLF2        | 2.14        | 0.001   |
| PAF1        | 2.21        | 0.001   | TGF3B       | 2.05        | 0.001   |
| TAP1        | 1.89        | 0.001   | TSC1        | 2.12        | 0.001   |
| MMP7        | -2.65       | 0.001   | FGA         | -5.31       | 0.001   |
| C3          | 2.74        | 0.001   | ABL1        | 1.67        | 0.001   |
| TCF3        | 1.96        | 0.001   | SIRPA       | 2.13        | 0.001   |
| BTN2A2      | 1.61        | 0.001   | PPP1R14B    | 2.30        | 0.001   |
| RUNX2       | -1.81       | 0.001   | CCDC88B     | -4.17       | 0.001   |
| MYO1G       | -1.83       | 0.001   | GPNMB       | 3.08        | 0.001   |
| FOXO3       | 1.97        | 0.001   | ANXA1       | 2.40        | 0.001   |
| HSD3B7      | -4.59       | 0.001   | TMEM173     | 1.70        | 0.001   |
| CEBPA       | 2.63        | 0.001   | PILRB       | 4.52        | 0.001   |
| SH2D1A      | -4.11       | 0.001   | LILR1A      | -3.63       | 0.001   |
| ACTN1       | 2.13        | 0.001   | BCL2A1      | 1.57        | 0.001   |
| GON4L       | 1.69        | 0.001   | POLR3E      | 1.72        | 0.001   |
| GADD45G     | 2.09        | 0.001   | NTRK1       | -2.27       | 0.001   |
| RPL22       | 1.75        | 0.001   | PSMC1       | 1.94        | 0.001   |
| IGBP1       | 1.98        | 0.001   |
| Gene Symbol | log2FoldChange | Log10(p-value) | | | 
|-------------|---------------|----------------|-----------------|-----------------|
| KIF3B       | 3.32          | 2.90E-03       | 1.93            | 3.32            |
| ZBTB16      | 2.69          | 3.75E-06       | 2.34            | 2.08            |
| SRF         | 1.98          | 2.59E-06       | 1.98            | 2.00            |
| POLR3H      | 1.75          | 1.46E-07       | 1.75            | 1.75            |
| CFD         | 2.46          | 5.97E-03       | 2.66            | 2.46            |
| PSME1       | 2.42          | 5.99E-04       | 2.64            | 2.42            |
| HDAC4       | 2.00          | 2.23E-06       | 2.00            | 2.00            |
| SFXN1       | -2.60         | 1.97E-02       | -2.60           | 2.00            |
| ITGA2B      | -3.51         | 1.07E-04       | -3.65           | 2.00            |
| IL3         | -3.65         | 1.14E-03       | -3.65           | 2.00            |
| HMG3B2      | 2.33          | 3.93E-07       | 2.33            | 2.00            |
| FKBP1B      | 1.92          | 1.33E-08       | 1.92            | 2.00            |
| PML         | 1.69          | 5.21E-06       | 1.69            | 2.00            |
| ADAMDEC1    | -2.21         | 2.06E-02       | -2.21           | 2.00            |
| ACTN1       | 2.66          | 4.83E-05       | 2.66            | 2.00            |
| HLA-DRB3    | 2.53          | 1.72E-02       | 2.53            | 2.00            |
| CD59        | 1.95          | 5.10E-05       | 1.95            | 2.00            |
| SIPA1L3     | 2.48          | 6.73E-05       | 2.48            | 2.00            |
| ACTR1A      | 2.00          | 1.97E-02       | 2.00            | 2.00            |
| DCTN3       | 2.45          | 2.11E-07       | 2.45            | 2.00            |
| ATP6V1H     | 2.51          | 1.12E-02       | 2.51            | 2.00            |
| JAK3        | 1.66          | 2.44E-06       | 1.66            | 2.00            |
| CTR9        | 2.10          | 4.01E-07       | 2.10            | 2.00            |
| IPO7        | -1.63         | 8.12E-03       | -1.63           | 2.00            |
| DNM2        | 2.07          | 1.98E-03       | 2.07            | 2.00            |
| AP2A2       | 2.10          | 2.27E-05       | 2.10            | 2.00            |
| IRF5        | 1.66          | 5.70E-03       | 1.66            | 2.00            |
| MSN         | 1.80          | 1.32E-02       | 1.80            | 2.00            |
| THR4        | 2.40          | 3.19E-04       | 2.40            | 2.00            |
| AP2S1       | 2.46          | 2.11E-07       | 2.46            | 2.00            |
| HS1BP3      | 1.77          | 3.17E-04       | 1.77            | 2.00            |
| SERPINA3    | 11.17         | 5.32E-05       | 11.17           | 2.00            |
| RRAS        | 1.60          | 9.03E-06       | 1.60            | 2.00            |
| EZR         | 2.55          | 8.93E-08       | 2.55            | 2.00            |
| DEFA6       | -4.49         | 6.30E-05       | -4.49           | 2.00            |
| TLX1        | -2.81         | 2.11E-02       | -2.81           | 2.00            |
| HP          | 3.10          | 2.30E-04       | 3.10            | 2.00            |
| DPP4        | -2.55         | 5.44E-04       | -2.55           | 2.00            |
| DCTN3       | 2.33          | 2.48E-07       | 2.33            | 2.00            |
| SLC3A2      | 2.55          | 6.68E-05       | 2.55            | 2.00            |
| MTHFD1      | 2.16          | 4.00E-09       | 2.16            | 2.00            |
| ARG2        | 1.93          | 6.51E-04       | 1.93            | 2.00            |
| HLA-E       | 3.04          | 1.86E-03       | 3.04            | 2.00            |
| IFNA10      | -2.78         | 1.09E-02       | -2.78           | 2.00            |
| CASP9       | 1.49          | 9.77E-07       | 1.49            | 2.00            |
| Gene Symbol | P Value | Odds Ratio | log2 Ratio | Description |
|-------------|---------|------------|------------|-------------|
| IGBP1       | 1.74E-04| 4.18E-05   | 1.78       |             |
| ANGPT2      | 4.18E-05| 1.74E-04   | -2.74      |             |
| HLA-DRB5    | 3.40E-03| 1.49E-03   | 3.01       |             |
| CIB1        | 3.13E-06| 6.38E-08   | 2.06       |             |
| GALNT2      | 4.32E-04| 1.31E-04   | 2.05       |             |
| HLA-DPB1    | 1.76E-04| 4.24E-05   | 2.63       |             |
| BDKRB1      | 2.73E-02| 1.60E-02   | -2.15      |             |
| IFITM3      | 2.59E-05| 3.49E-06   | 2.59       |             |
| HLA-DRB5    | 3.40E-03| 1.49E-03   | 3.01       |             |
| TREM2       | 3.94E-02| 2.45E-02   | 2.20       |             |
| SLC25A6     | 7.09E-06| 2.98E-07   | 2.12       |             |
| ACTR1A      | 3.18E-06| 6.65E-08   | 3.15       |             |
| ITGAD       | 2.15E-05| 2.31E-06   | -4.91      |             |
| AP3D1       | 2.70E-02| 1.58E-02   | 2.39       |             |
| CXCL1       | 5.04E-04| 1.59E-04   | 2.02       |             |
| CDB3        | 4.59E-06| 1.48E-07   | 2.26       |             |
| DYNClI1     | 2.66E-05| 3.30E-06   | 2.27       |             |
| BCL3        | 5.75E-03| 2.73E-03   | 1.71       |             |
| HSPA1A      | 6.08E-05| 1.08E-05   | 3.53       |             |
| TRIM27      | 1.91E-03| 7.63E-04   | 1.66       |             |
| FAM111A     | 8.21E-06| 4.22E-07   | 1.59       |             |
| ACTB        | 3.53E-06| 8.86E-08   | 2.64       |             |
| HLA-DOA     | 1.12E-04| 2.44E-05   | 1.75       |             |
| IK          | 1.26E-06| 9.57E-09   | 2.60       |             |
| C2          | 2.07E-03| 8.33E-04   | -4.47      |             |
| EIF2AK4     | 8.16E-03| 4.04E-03   | 1.89       |             |
| DyrR3       | 1.00E-03| 3.58E-04   | 1.70       |             |
| MSN         | 3.53E-06| 8.63E-08   | 2.35       |             |
| TUSC2       | 4.24E-04| 1.27E-04   | 1.51       |             |
| RPS19       | 6.00E-06| 2.16E-07   | 2.20       |             |
| IK          | 3.40E-06| 7.96E-08   | 1.95       |             |
| PSMD11      | 6.10E-06| 2.30E-07   | 2.17       |             |
| PSMC3       | 2.48E-03| 1.03E-03   | 3.07       |             |
| CUEeD2      | 4.04E-05| 6.15E-06   | 2.20       |             |
| SNRK        | 8.64E-03| 4.33E-03   | 1.87       |             |
| MEIS2       | 1.24E-02| 6.50E-03   | 1.59       |             |
| PIR         | 3.22E-05| 4.41E-06   | 1.89       |             |
| RNF125      | 4.59E-03| 2.11E-03   | -2.14      |             |
| CD47        | 4.78E-04| 1.49E-04   | 2.11       |             |
| LAT2        | 1.41E-03| 5.31E-04   | 1.83       |             |
| HLA-DRB4    | 1.53E-02| 8.35E-03   | 2.68       |             |
| VPREB3      | 8.92E-03| 4.48E-03   | -1.99      |             |
| KRAS        | 2.68E-02| 1.57E-02   | 1.84       |             |
| NCF2        | 6.66E-04| 2.20E-04   | 2.04       |             |
| PAX5        | 1.97E-02| 1.11E-02   | -2.18      |             |
| PHB         | 7.08E-05| 1.32E-05   | 1.88       |             |
| KLF1        | 2.24E-05| 2.48E-06   | -4.02      |             |
| PTK2        | 1.34E-06| 1.08E-08   | 2.16       |             |
| FOX1        | 1.25E-02| 6.55E-03   | 1.91       |             |
| AIF1        | 8.72E-04| 3.00E-04   | 2.23       |             |
| HLA-B       | 8.89E-06| 5.35E-07   | 3.32       |             |
| Gene Code     | Genotype 1 | Genotype 2 | Genotype 3 | Label  |
|--------------|-----------|-----------|-----------|--------|
| A_24_P388528 | 1.02E-04  | 2.15E-05  | 1.85      | ST6GAL1|
| A_23_P381979 | 9.50E-05  | 1.98E-05  | 2.00      | OGT    |
| A_23_P37497  | 1.96E-04  | 4.81E-05  | 1.77      | MYO1E  |
| A_32_P156963 | 9.21E-06  | 5.73E-07  | 2.33      | ACTG1  |
| A_23_P217688 | 1.81E-05  | 1.80E-06  | 1.81      | TSC22D3|
| A_23_P38959  | 8.64E-03  | 4.33E-03  | 1.66      | VAV1   |
| A_23_P48088  | 3.02E-04  | 8.42E-05  | -1.64     | CD27   |
| A_24_P74753  | 2.23E-03  | 9.11E-04  | 2.40      | ATP6AP1|
| A_24_P244356 | 9.26E-06  | 5.92E-07  | 1.81      | NLRX1  |
| A_23_P500676 | 2.10E-02  | 1.20E-02  | -3.03     | IL5RA  |
| A_23_P38959  | 8.61E-03  | 4.33E-03  | 2.85      | SCG2   |
| A_24_P86993  | 1.74E-04  | 4.19E-05  | 2.19      | JAM3   |
| A_23_P133245 | 7.74E-06  | 3.70E-07  | 1.99      | IK     |
| A_24_P166443 | 1.49E-05  | 1.30E-06  | 2.99      | HLA-DPB1|
| A_23_P361773 | 2.65E-02  | 1.54E-02  | 1.69      | CCND3  |
| A_32_P234459 | 2.53E-04  | 6.70E-05  | 4.30      | HLA-H  |
| A_24_P113674 | 7.30E-06  | 3.24E-07  | 2.57      | HLA-B  |
| A_24_P373174 | 3.68E-02  | 2.27E-02  | -2.58     | RAB27A |
| A_24_P226108 | 2.11E-04  | 5.30E-05  | -6.01     | RBM47  |
| A_23_P39465  | 1.12E-04  | 2.43E-05  | 2.00      | BST2   |
| A_23_P200767 | 3.41E-04  | 9.71E-05  | 1.68      | TROVE2 |
| A_24_P224727 | 8.89E-05  | 1.81E-05  | 2.14      | CEBPA  |
| A_23_P63798  | 5.98E-06  | 2.09E-07  | 2.30      | KLF6   |
| A_24_P216165 | 2.09E-04  | 5.23E-05  | -2.49     | CEBPA  |
| A_23_P111662 | 2.10E-05  | 2.23E-06  | -5.16     | ABCB5  |
| A_24_P166042 | 3.79E-04  | 1.10E-04  | 1.99      | IMPDH2 |
| A_32_P186921 | 3.29E-04  | 4.59E-06  | -1.42     | ZNF616 |
| A_23_P64525  | 7.95E-05  | 1.54E-05  | -4.00     | RAG2   |
| A_23_P337242 | 1.26E-06  | 8.32E-09  | -1.75     | TGFB2R |
| A_24_P94916  | 1.78E-02  | 9.88E-03  | 1.88      | LST1   |
| A_23_P32404  | 1.79E-06  | 1.93E-08  | 1.87      | ISG20  |
| A_23_P31323  | 2.70E-06  | 4.61E-08  | 2.60      | ACTB   |
| A_24_P141688 | 1.10E-04  | 2.38E-05  | 1.59      | PCBP2  |
| A_23_P413641 | 6.00E-06  | 2.20E-07  | 1.78      | PREX1  |
| A_23_P163347 | 3.98E-04  | 1.17E-04  | 1.57      | PIAS1  |
| A_23_P390518 | 4.20E-04  | 1.26E-04  | -2.06     | TNFRSF11A|
| A_23_P312132 | 4.63E-02  | 2.94E-02  | 1.77      | ITGAX  |
| A_23_P158239 | 2.34E-02  | 1.35E-02  | 1.75      | SHMT2  |
| A_23_P112798 | 3.05E-03  | 1.31E-03  | 2.41      | CRIP2  |
| A_23_P501538 | 7.30E-06  | 3.22E-07  | -2.04     | HOXA3  |
| A_23_P146644 | 5.59E-05  | 9.67E-06  | 3.00      | ANXA2  |
| A_23_P28279  | 2.25E-04  | 5.75E-05  | 2.26      | ACTR1B |
| A_23_P368805 | 1.22E-05  | 9.06E-07  | -1.79     | HHLA2  |

In bold are highlighted candidate genes already known to contribute to ALS susceptibility. *Gene expression fold-changes are given on a linear scale.*
Supplementary Table 4. Neuroinflammatory genes differentially expressed in SALS2.

| Probe ID   | p Value (Corr) | p Value (SALS2/CTRL) | Fold Change (SALS2/CTRL) | GENE_SYMBOL |
|------------|---------------|----------------------|--------------------------|-------------|
| A_23_P126540 | 3.37E-03      | 1.47E-03             | 2.20                     | ADORA3      |
| A_23_P426292 | 1.03E-04      | 2.20E-05             | -1.82                    | MAPK14      |
| A_23_P48936  | 2.22E-05      | 2.44E-06             | -1.70                    | SMAD3       |
| A_23_P119478 | 3.66E-05      | 5.33E-06             | -1.68                    | EBI3        |
| A_23_P202522 | 1.56E-05      | 1.41E-06             | -2.78                    | AQP4        |
| A_23_P169629 | 3.49E-05      | 5.00E-06             | -2.04                    | SHMT2       |
| A_24_P129277 | 3.04E-03      | 1.30E-03             | 1.94                     | NOD1        |
| A_23_P87973  | 1.53E-05      | 1.38E-06             | -3.79                    | TRIM13      |
| A_23_P7325   | 2.23E-05      | 2.45E-06             | 2.03                     | BST1        |
| A_24_P295999 | 1.49E-04      | 3.45E-05             | -3.87                    | CD4         |
| A_32_P186474 | 2.55E-03      | 1.07E-03             | -2.46                    | RACGAP1     |
| A_24_P337700 | 1.10E-02      | 5.64E-03             | -2.45                    | VNN1        |
| A_32_P154830 | 8.21E-06      | 4.24E-07             | -1.69                    | OSTM1       |
| A_23_P89249  | 7.67E-04      | 2.59E-04             | 1.62                     | ERBB2       |
| A_24_P139191 | 2.31E-05      | 2.62E-06             | -3.19                    | ITCH        |
| A_23_P54373  | 7.35E-05      | 1.39E-05             | -2.96                    | RAB27A      |
| A_24_P83615  | 4.47E-04      | 2.04E-03             | -2.73                    | NLRP1       |
| A_23_P308603 | 3.22E-05      | 4.41E-06             | -4.30                    | SRC         |
| A_23_P309739 | 2.75E-02      | 1.61E-02             | -1.56                    | ESR1        |
| A_24_P308096 | 1.63E-04      | 3.86E-05             | -2.76                    | JAK3        |
| A_23_P138760 | 2.44E-03      | 1.01E-03             | 1.57                     | CLCF1       |
| A_23_P2990   | 3.94E-03      | 1.76E-03             | 3.17                     | CEBPE       |
| A_32_P61757  | 2.49E-05      | 3.00E-06             | -4.24                    | PTPN11      |
| A_32_P530933 | 1.08E-02      | 5.53E-03             | -3.37                    | PYGO1       |
| A_23_P35456  | 1.11E-04      | 2.41E-05             | -3.13                    | SH3PXD2A    |
| A_23_P31945  | 1.42E-05      | 1.18E-06             | -3.07                    | IL33        |
| A_23_P84705  | 1.27E-05      | 9.92E-07             | 9.01                     | TNFRSF13B   |
| A_23_P68740  | 1.71E-03      | 6.72E-04             | -1.75                    | AIRE        |
| A_23_P68155  | 7.93E-04      | 2.70E-04             | -1.60                    | IFIH1       |
| A_23_P208706 | 8.45E-05      | 1.68E-05             | -2.51                    | BAX         |
| A_23_P99985  | 2.04E-06      | 2.85E-08             | -2.28                    | HMGB1       |
| A_23_P35916  | 7.95E-05      | 1.55E-05             | 3.99                     | ATM         |
| A_23_P135248 | 5.08E-04      | 1.61E-04             | 1.81                     | CCL27       |
| A_23_P168836 | 7.40E-03      | 3.62E-03             | 2.30                     | PTK2B       |
| A_23_P70688  | 6.08E-05      | 1.08E-05             | -2.66                    | LY86        |
| A_23_P167096 | 2.18E-04      | 5.51E-05             | -2.00                    | VEGFC       |
| A_24_P354800 | 2.43E-05      | 2.84E-06             | -3.57                    | HLA-DOA     |
| A_23_P343799 | 4.00E-04      | 1.18E-04             | 3.56                     | SOX6        |
| A_23_P29885  | 2.56E-05      | 3.12E-06             | -2.63                    | MAEA        |
| A_23_P23303  | 6.68E-07      | 5.52E-10             | 4.12                     | EXO1        |
| A_24_P134074 | 5.90E-05      | 1.03E-05             | -2.88                    | RPS19       |
| A_23_P1691   | 4.39E-06      | 1.36E-07             | 2.79                     | MMP1        |
| A_23_P50907  | 1.61E-04      | 3.80E-05             | -2.37                    | ITGA1       |
| A_24_P142118 | 2.99E-03      | 1.28E-03             | -1.81                    | THBS1       |
| A_23_P70095  | 1.39E-02      | 7.41E-03             | 2.10                     | CD74        |
| A_23_P101992 | 3.31E-02      | 1.99E-02             | 2.98                     | MARCO       |
| Gene ID   | Gene Symbol | Log2FoldChange | p-value 1 | p-value 2 | Degree |
|-----------|-------------|----------------|-----------|-----------|--------|
| A_23_P40174 | MMP9        | 4.13E-05       | 6.31E-06  | -3.17     | PBX1   |
| A_23_P134454 | CAV1       | 8.55E-05       | 1.72E-05  | -2.65     | TRIM26 |
| A_23_P29939 | SNCA        | 1.94E-05       | 1.98E-06  | -3.64     | F2     |
| A_23_P94879 | F2          | 6.68E-07       | 1.99E-10  | 3.82      |        |
| A_24_P151464 | SOD1       | 1.60E-05       | 1.48E-06  | -4.52     |        |
| A_23_P62953 | P8X1        | 1.25E-02       | 6.59E-03  | 5.61      |        |
| A_23_P162874 | HSP90AA1   | 1.59E-03       | 6.16E-04  | -3.86     |        |
| A_23_P70020 | PFDN1       | 8.55E-05       | 1.72E-05  | -2.80     |        |
| A_24_P898583 | TRIM26     | 1.64E-05       | 1.54E-06  | -1.89     |        |
| A_23_P29939 | SNCA        | 1.94E-05       | 1.98E-06  | -3.64     |        |
| A_23_P205686 | PSEN1      | 6.64E-06       | 2.63E-07  | -2.28     |        |
| A_23_P203191 | APOA1      | 5.23E-05       | 8.83E-06  | 1.81      |        |
| A_24_P343695 | RET        | 3.89E-06       | 1.13E-07  | 2.19      |        |
| A_23_P107073 | RPA1       | 1.49E-05       | 1.31E-06  | -2.42     |        |
| A_23_P212617 | TFRC       | 4.51E-04       | 7.29E-06  | -2.04     |        |
| A_24_P227927 | IL21R      | 1.56E-04       | 3.65E-04  | -2.32     |        |
| A_23_P63668 | IFIT5       | 7.62E-06       | 3.58E-07  | -1.75     |        |
| A_23_P140967 | MEFV       | 1.20E-03       | 4.40E-04  | -3.13     |        |
| A_23_P111571 | HOXA3      | 7.97E-05       | 1.55E-05  | -7.00     |        |
| A_24_P92683 | IGHG1       | 2.91E-03       | 1.24E-03  | -1.91     |        |
| A_23_P213706 | IL4        | 1.96E-06       | 2.39E-08  | 6.64      |        |
| A_23_P207596 | CDC42      | 6.84E-04       | 2.27E-04  | -3.35     |        |
| A_23_P106024 | JAG2       | 4.36E-05       | 6.82E-06  | -1.53     |        |
| A_23_P43049 | DCTN6      | 1.18E-05       | 8.55E-07  | -3.65     |        |
| A_32_P115015 | NF1        | 6.84E-05       | 1.26E-05  | -2.23     |        |
| A_23_P7313  | SPP1        | 3.02E-04       | 8.43E-05  | -2.80     |        |
| A_23_P6272  | ICOSLG     | 9.09E-05       | 1.87E-05  | -2.15     |        |
| A_23_P103361 | LCK        | 1.17E-02       | 6.08E-03  | -1.66     |        |
| A_24_P184535 | C12orf4    | 8.52E-05       | 1.70E-05  | -1.91     |        |
| A_23_P117546 | SOS2       | 1.02E-02       | 5.22E-03  | -1.66     |        |
| A_24_P943283 | DENND1B    | 1.43E-03       | 5.37E-04  | -2.34     |        |
| A_24_P274270 | STAT1      | 1.26E-06       | 9.85E-09  | -2.00     |        |
| A_23_P77847 | GRB2       | 8.52E-05       | 1.71E-05  | -2.87     |        |
| A_23_P72096 | IL1A        | 3.33E-05       | 4.70E-06  | 2.08      |        |
| A_24_P291016 | ABL1       | 1.88E-06       | 7.48E-04  | 1.80      |        |
| A_32_P151102 | MSN        | 3.39E-05       | 4.83E-06  | 2.10      |        |
| A_23_P83277 | IL11RA     | 1.02E-02       | 2.15E-05  | -1.81     |        |
| A_24_P158089 | SERPINE1   | 2.45E-05       | 2.89E-06  | -2.46     |        |
| A_24_P93948 | KIF5A      | 1.26E-05       | 9.74E-07  | -2.71     |        |
| A_24_P916496 | PRKCA      | 3.48E-04       | 9.97E-05  | -3.11     |        |
| A_24_P100742 | ADD1       | 1.22E-04       | 2.73E-05  | 2.80      |        |
| A_24_P929754 | MKNK2      | 5.12E-03       | 2.38E-03  | -2.10     |        |
| A_24_P852756 | HLA-DQA2   | 9.26E-04       | 3.24E-04  | -3.29     |        |
| A_23_P215406 | RAC1       | 8.71E-06       | 5.05E-07  | -3.88     |        |
| A_24_P260443 | THBS4      | 7.44E-06       | 3.38E-07  | -2.49     |        |
| A_23_P57036 | CD40       | 1.28E-03       | 4.73E-04  | 1.43      |        |
| A_23_P10291 | CTSE       | 1.24E-04       | 2.78E-05  | -1.91     |        |
| A_23_P153616 | MADCAM1    | 6.60E-05       | 1.20E-05  | -2.36     |        |
| Gene Symbol | log2 Fold Change | q-value | P-value | Description |
|-------------|-----------------|---------|---------|-------------|
| SEC24A      | 2.48E-02        | 1.44E-02| -1.72   |             |
| SERPINB9    | 4.04E-05        | 6.13E-06| -4.85   |             |
| PCBP2       | 9.76E-03        | 4.96E-03| 2.27    |             |
| SP100       | 4.49E-03        | 2.05E-03| -2.03   |             |
| L1CAM       | 3.30E-05        | 4.61E-06| 2.86    |             |
| SEC31A      | 3.00E-05        | 3.70E-06| -1.82   |             |
| HIF1A       | 3.00E-05        | 3.70E-06| -1.82   |             |
| CD97        | 4.04E-05        | 6.13E-06| -4.85   |             |
| RAB8B       | 9.76E-03        | 4.96E-03| 2.27    |             |
| DCTN6       | 4.49E-03        | 2.05E-03| -2.03   |             |
| TET2        | 3.30E-05        | 4.61E-06| 2.86    |             |
| I6L         | 3.00E-05        | 3.70E-06| -1.82   |             |
| I6           | 3.00E-05        | 3.70E-06| -1.82   |             |
| RHOA        | 4.04E-05        | 6.13E-06| -4.85   |             |
| CENPE       | 9.76E-03        | 4.96E-03| 2.27    |             |
| MAPK1       | 4.49E-03        | 2.05E-03| -2.03   |             |
| ICAM5       | 3.30E-05        | 4.61E-06| 2.86    |             |
| CEBPB       | 3.00E-05        | 3.70E-06| -1.82   |             |
| DCTN3       | 4.04E-05        | 6.13E-06| -4.85   |             |
| IL6         | 9.76E-03        | 4.96E-03| 2.27    |             |
| IL10        | 4.49E-03        | 2.05E-03| -2.03   |             |
| MPL         | 3.30E-05        | 4.61E-06| 2.86    |             |
| TANK        | 3.00E-05        | 3.70E-06| -1.82   |             |
| CD24        | 4.49E-03        | 2.05E-03| -2.03   |             |
| CTSF        | 3.30E-05        | 4.61E-06| 2.86    |             |
| IFNG        | 3.00E-05        | 3.70E-06| -1.82   |             |
| TP53        | 4.49E-03        | 2.05E-03| -2.03   |             |
| PSME4       | 3.30E-05        | 4.61E-06| 2.86    |             |
| AKT1        | 3.00E-05        | 3.70E-06| -1.82   |             |
| PPM1B       | 4.49E-03        | 2.05E-03| -2.03   |             |
| IL6ST       | 3.30E-05        | 4.61E-06| 2.86    |             |
| PTX3        | 3.00E-05        | 3.70E-06| -1.82   |             |
| PDGFRA      | 4.49E-03        | 2.05E-03| -2.03   |             |
| ITPKB       | 3.30E-05        | 4.61E-06| 2.86    |             |
| PRKCD       | 3.00E-05        | 3.70E-06| -1.82   |             |
| CYP27B1      | 4.49E-03        | 2.05E-03| -2.03   |             |
| ZFP36L1      | 3.30E-05        | 4.61E-06| 2.86    |             |
| HORMD7       | 3.00E-05        | 3.70E-06| -1.82   |             |
| TROAP1       | 4.49E-03        | 2.05E-03| -2.03   |             |
| MIF         | 3.30E-05        | 4.61E-06| 2.86    |             |
| ATP6A1       | 3.00E-05        | 3.70E-06| -1.82   |             |
| KIF11       | 4.49E-03        | 2.05E-03| -2.03   |             |
| Gene Symbol | Log2 Fold Change | P-Value 1st Group | P-Value 2nd Group | Log2 Fold Change | P-Value 1st Group | P-Value 2nd Group |
|------------|-----------------|------------------|------------------|-----------------|-----------------|------------------|
| PTK2       | 2.22E-06        | 3.47E-08         | -2.20            |                 |                 |                  |
| HLA-DOB    | 3.76E-03        | 1.67E-03         | -2.77            |                 |                 |                  |
| PPARG      | 1.82E-03        | 7.19E-04         | 2.02             |                 |                 |                  |
| ARPC3      | 1.98E-05        | 2.04E-06         | -2.06            |                 |                 |                  |
| FLVCR1     | 1.68E-03        | 6.56E-04         | 5.01             |                 |                 |                  |
| SEC23A     | 2.61E-04        | 6.98E-05         | -2.18            |                 |                 |                  |
| TRIM59     | 3.63E-02        | 2.23E-02         | -1.62            |                 |                 |                  |
| SLC3A2     | 3.03E-05        | 4.61E-06         | -2.95            |                 |                 |                  |
| ATG12      | 3.18E-06        | 6.67E-08         | -2.10            |                 |                 |                  |
| HLA-DOB    | 1.46E-05        | 1.26E-06         | -3.54            |                 |                 |                  |
| CRTC3      | 4.22E-05        | 6.47E-06         | -1.54            |                 |                 |                  |
| FLVCR1     | 1.82E-03        | 6.98E-05         | -2.18            |                 |                 |                  |
| SEC23A     | 1.73E-02        | 9.54E-03         | -2.12            |                 |                 |                  |
| TLR1       | 2.52E-04        | 6.62E-05         | -3.24            |                 |                 |                  |
| EPAS1      | 4.24E-05        | 1.28E-04         | -2.62            |                 |                 |                  |
| FAU        | 3.03E-05        | 4.01E-06         | -2.95            |                 |                 |                  |
| RPS14      | 9.66E-06        | 6.26E-07         | -2.78            |                 |                 |                  |
| RABGEC1    | 5.21E-05        | 8.77E-06         | -1.69            |                 |                 |                  |
| FCN2       | 1.16E-03        | 4.23E-04         | 3.22             |                 |                 |                  |
| TBK1       | 3.95E-05        | 5.90E-06         | -2.30            |                 |                 |                  |
| PSMD8      | 1.04E-05        | 7.07E-07         | -2.49            |                 |                 |                  |
| POLR3D     | 6.31E-05        | 1.14E-05         | -1.97            |                 |                 |                  |
| RAC2       | 1.56E-03        | 6.02E-04         | -1.59            |                 |                 |                  |
| NUDECD1    | 8.34E-04        | 2.85E-04         | -1.55            |                 |                 |                  |
| TMEM143    | 2.79E-05        | 3.52E-06         | -4.16            |                 |                 |                  |
| GLG1       | 4.24E-06        | 1.30E-07         | -2.04            |                 |                 |                  |
| SELL       | 2.81E-03        | 1.20E-03         | 4.96             |                 |                 |                  |
| FGF10      | 4.10E-04        | 1.22E-04         | 4.17             |                 |                 |                  |
| NKX2-5     | 8.80E-03        | 4.42E-03         | -2.07            |                 |                 |                  |
| UBE2D2     | 6.90E-06        | 2.80E-07         | -1.98            |                 |                 |                  |
| PTPRO      | 3.73E-03        | 1.66E-03         | -1.76            |                 |                 |                  |
| SYK        | 3.62E-05        | 5.27E-06         | -2.60            |                 |                 |                  |
| COLEC11    | 8.97E-03        | 4.51E-03         | 2.13             |                 |                 |                  |
| KDR        | 1.45E-04        | 3.32E-05         | -2.12            |                 |                 |                  |
| JMJD6      | 1.72E-03        | 6.76E-04         | 2.35             |                 |                 |                  |
| RBPJ       | 8.12E-06        | 4.08E-07         | -2.15            |                 |                 |                  |
| TRIM62     | 1.52E-05        | 1.37E-06         | -1.91            |                 |                 |                  |
| RUNX3      | 1.81E-03        | 7.18E-04         | 4.30             |                 |                 |                  |
| PSMA3      | 2.22E-05        | 2.44E-06         | -2.48            |                 |                 |                  |
| SLC11A2    | 8.42E-05        | 1.67E-05         | -2.86            |                 |                 |                  |
| PTPN6      | 4.25E-05        | 6.56E-06         | 1.78             |                 |                 |                  |
| THBS1      | 7.90E-07        | 1.70E-09         | 3.12             |                 |                 |                  |
| HIST1H2BE  | 3.70E-03        | 1.64E-03         | 4.23             |                 |                 |                  |
| FASLG      | 2.61E-04        | 7.02E-05         | 2.20             |                 |                 |                  |
| KITLG      | 3.11E-03        | 1.34E-03         | -1.79            |                 |                 |                  |
| IL21       | 1.46E-03        | 5.53E-04         | 2.30             |                 |                 |                  |
| ARHGEF7    | 1.33E-04        | 3.00E-05         | -3.35            |                 |                 |                  |
| CYBB       | 7.27E-05        | 1.38E-05         | -2.94            |                 |                 |                  |
| SEC24A     | 3.98E-03        | 1.79E-03         | -2.00            |                 |                 |                  |
| KIF2C      | 9.14E-04        | 3.19E-04         | -2.08            |                 |                 |                  |
| Gene Symbol | Fold Change | q Value | p Value  | Gene Symbol | Fold Change | q Value | p Value  |
|-------------|-------------|---------|---------|-------------|-------------|---------|---------|
| TBK1        | 3.11        | 1.59    | 0.04    | PDIA3       | -3.04       | 1.59    | 0.04    |
| FCN1        | 4.45        | 1.59    | 0.04    | APOI        | 5.45        | 1.59    | 0.04    |
| BRAF        | -1.45       | 1.59    | 0.04    | STXBP2      | 5.00        | 1.59    | 0.04    |
| ADRM1       | -1.72       | 1.59    | 0.04    | SNAP23      | -2.50       | 1.59    | 0.04    |
| PDIA3       | 2.67        | 1.59    | 0.04    | PREDI1      | -1.68       | 1.59    | 0.04    |
| APOL1       | 7.30        | 1.59    | 0.04    | IL1R1       | -1.94       | 1.59    | 0.04    |
| SERINC5     | 1.07        | 1.59    | 0.04    | BCAP31      | -1.95       | 1.59    | 0.04    |
| RAB17       | 2.63        | 1.59    | 0.04    | TRPV1       | -2.28       | 1.59    | 0.04    |
| PSEN1       | 2.67        | 1.59    | 0.04    | FYN         | -2.23       | 1.59    | 0.04    |
| CCL13       | 6.23        | 1.59    | 0.04    | RAB17       | 3.64        | 1.59    | 0.04    |
| CLC2D       | 2.67        | 1.59    | 0.04    | Dync1LI2    | -2.10       | 1.59    | 0.04    |
| CLEC2D      | 1.59        | 1.59    | 0.04    | PSEN1       | -2.35       | 1.59    | 0.04    |
| RARG        | 1.70        | 1.59    | 0.04    | MAPK1       | -1.87       | 1.59    | 0.04    |
| RPS17       | 1.56        | 1.59    | 0.04    | TRAF3       | -2.92       | 1.59    | 0.04    |
| DYNC1LI2    | 2.96        | 1.59    | 0.04    | PSEN1       | -3.36       | 1.59    | 0.04    |
| CCL13       | 2.62        | 1.59    | 0.04    | ACTR3       | 3.21        | 1.59    | 0.04    |
| RUNX1       | 1.96        | 1.59    | 0.04    | TRAF3       | -2.16       | 1.59    | 0.04    |
| HOXB6       | 3.68        | 1.59    | 0.04    | PSEN1       | -1.96       | 1.59    | 0.04    |
| IL12R1      | 1.28        | 1.59    | 0.04    | TRAF3       | -2.92       | 1.59    | 0.04    |
| ILF3        | 5.52        | 1.59    | 0.04    | PSEN1       | -2.93       | 1.59    | 0.04    |
| OSBPL1A     | 1.17        | 1.59    | 0.04    | C2          | 2.71        | 1.59    | 0.04    |
| PRKCE       | 4.47        | 1.59    | 0.04    | IP6K2       | -3.96       | 1.59    | 0.04    |
| TNFSF10     | 8.57        | 1.59    | 0.04    | IL12R1      | -2.53       | 1.59    | 0.04    |
| C2          | 8.57        | 1.59    | 0.04    | OSBPL1A     | 2.35        | 1.59    | 0.04    |
| VEGFA       | 7.80        | 1.59    | 0.04    | C2          | -2.71       | 1.59    | 0.04    |
| PPP4R2      | 4.37        | 1.59    | 0.04    | Tnfsf10     | -3.96       | 1.59    | 0.04    |
| GAPDH       | 1.45        | 1.59    | 0.04    | VEGFA       | 1.85        | 1.59    | 0.04    |
| SENG1       | 7.53        | 1.59    | 0.04    | PPP4R2      | -3.20       | 1.59    | 0.04    |
| SIRT2       | 9.44        | 1.59    | 0.04    | SIRT2       | 4.31        | 1.59    | 0.04    |
| STX4        | 2.97        | 1.59    | 0.04    | STX4        | -2.63       | 1.59    | 0.04    |
| RORC        | 9.65        | 1.59    | 0.04    | RORC        | -2.92       | 1.59    | 0.04    |
| GNL1        | 1.52        | 1.59    | 0.04    | GNL1        | -3.92       | 1.59    | 0.04    |
| HSP90AA1    | 2.97        | 1.59    | 0.04    | GNL1        | 5.35        | 1.59    | 0.04    |
| ICAM2       | 5.90        | 1.59    | 0.04    | GNL1        | -1.92       | 1.59    | 0.04    |
| LYM6D       | 5.43        | 1.59    | 0.04    | ICAM2       | 1.68        | 1.59    | 0.04    |
| CEACAM6     | 2.18        | 1.59    | 0.04    | LYM6D       | -4.19       | 1.59    | 0.04    |
| VAMP7       | 8.49        | 1.59    | 0.04    | CEACAM6     | -2.48       | 1.59    | 0.04    |
| ERCC2       | 6.96        | 1.59    | 0.04    | VAMP7       | -2.31       | 1.59    | 0.04    |
| AP2A1       | 3.92        | 1.59    | 0.04    | ERCC2       | 1.54        | 1.59    | 0.04    |
| SOCS6       | 3.33        | 1.59    | 0.04    | AP2A1       | 4.34        | 1.59    | 0.04    |
| Gene Symbol   | Fold Change | log2 Fold Change | p-value | Description |
|---------------|-------------|------------------|---------|-------------|
| Gene Symbol   | Fold Change | log2 Fold Change | p-value | Description |
| A_23_P347198  | 1.86E-03    | 7.38E-04         | -1.89   | SP3         |
| A_23_P168928  | 5.75E-04    | 1.85E-04         | -2.10   | CYP11B1     |
| A_24_P322756  | 1.04E-02    | 5.33E-03         | 3.58    | TRPM2       |
| A_23_P258340  | 1.24E-05    | 9.43E-07         | -4.60   | PPIA        |
| A_23_P75056   | 1.14E-05    | 8.08E-07         | 2.66    | GATA3       |
| A_23_P212844  | 2.68E-03    | 1.13E-03         | 5.93    | TACC3       |
| A_23_P253317  | 2.67E-04    | 7.20E-05         | -1.96   | GPR171      |
| A_23_P4286    | 6.12E-04    | 1.98E-04         | -2.26   | XAF1        |
| A_23_P300224  | 6.58E-06    | 2.57E-07         | -2.71   | NFKB1       |
| A_23_P34888   | 1.47E-04    | 3.40E-05         | -2.28   | CHIA        |
| A_32_P226149  | 5.89E-06    | 2.04E-07         | -2.75   | YWHAZ       |
| A_24_P178011  | 3.18E-05    | 4.30E-06         | -4.31   | MYC         |
| A_24_P930276  | 1.67E-03    | 6.51E-04         | -3.34   | NFE2L1      |
| A_23_P315651  | 1.70E-04    | 4.07E-05         | -4.77   | CYBA        |
| A_23_P26890   | 1.44E-03    | 5.44E-04         | -2.50   | MMP28       |
| A_23_P126716  | 1.05E-04    | 2.25E-05         | -4.90   | ATPF1       |
| A_23_P11739   | 4.78E-05    | 7.84E-06         | 1.95    | MIXL1       |
| A_23_P133432  | 3.28E-06    | 7.31E-08         | -4.35   | SKP1        |
| A_24_P8371    | 3.20E-05    | 4.33E-06         | -2.68   | SPNS2       |
| A_23_P251945  | 2.15E-05    | 2.30E-06         | -2.25   | DCTN4       |
| A_23_P79836   | 3.21E-06    | 6.91E-08         | -3.32   | SERINC3     |
| A_24_P933908  | 3.91E-03    | 1.75E-03         | 2.95    | GPNMB       |
| A_23_P500282  | 4.45E-04    | 1.36E-04         | -1.94   | PACS1       |
| A_23_P19543   | 2.43E-05    | 2.85E-06         | -2.63   | SRPK1       |
| A_23_P136347  | 2.57E-03    | 1.08E-03         | -2.99   | EPS8        |
| A_32_P11499   | 8.78E-07    | 2.12E-09         | -2.61   | UBE2N       |
| A_23_P502464  | 7.60E-06    | 3.51E-07         | -2.27   | NOS2        |
| A_23_P414855  | 3.23E-03    | 1.40E-03         | 1.80    | PURB        |
| A_24_P32935   | 7.47E-03    | 3.66E-03         | -1.92   | FOLR2       |
| A_32_P68459   | 3.31E-05    | 4.64E-06         | -5.00   | PPIA        |
| A_32_P517749  | 6.84E-03    | 3.33E-03         | -1.86   | RPS6KA3     |
| A_24_P50245   | 2.36E-05    | 2.71E-06         | -3.31   | HLA-DMA     |
| A_23_P146943  | 1.92E-04    | 4.69E-05         | -4.56   | ATP1B1      |
| A_23_P126278  | 1.22E-02    | 6.39E-03         | 2.46    | CHIT1       |
| A_32_P175934  | 9.35E-05    | 1.94E-05         | 10.02   | CD48        |
| A_23_P113716  | 7.07E-06    | 2.91E-07         | -2.38   | HLA-C       |
| A_24_P150361  | 1.66E-06    | 1.51E-08         | -3.09   | HSP90B1     |
| A_24_P393711  | 1.82E-03    | 7.22E-04         | 4.24    |ABL1        |
| A_23_P201238  | 1.43E-04    | 3.25E-05         | -2.24   | SNX27       |
| A_23_P145301  | 8.96E-04    | 3.12E-04         | 3.31    | NFKB1       |
| A_23_P11372   | 8.02E-05    | 1.57E-05         | -2.51   | HPRT1       |
| A_23_P102471  | 9.29E-06    | 5.97E-07         | -3.31   | MSH2        |
| A_23_P55828   | 2.45E-05    | 2.88E-06         | 2.16    | CCL25       |
| A_24_P389218  | 6.39E-03    | 3.08E-03         | 3.43    | ARHGEF5     |
| A_23_P204702  | 9.94E-07    | 3.21E-09         | -3.43   | TMIM8       |
| A_23_P32463   | 2.88E-05    | 3.71E-06         | -2.23   | EXOSC4      |
| A_23_P342009  | 2.83E-04    | 7.77E-05         | -2.28   | HFE         |
| A_23_P210176  | 5.04E-05    | 8.35E-06         | -2.23   | ITGA6       |
| A_23_P158481  | 1.53E-04    | 3.58E-05         | 3.21    | CYP2C19     |
| A_23_P376060  | 2.73E-05    | 3.44E-06         | -3.48   | IKZF3       |
| Gene Symbol | Fold Change | p-value | Log2 Fold Change | Description |
|-------------|-------------|---------|------------------|-------------|
| COL4A3BP    | 8.19E-05    | 1.61E-05 | -2.45            |             |
| APOA4       | 2.57E-06    | 4.28E-08 | 2.82             |             |
| IFNB1       | 1.33E-02    | 7.03E-03 | 2.12             |             |
| ITGAX       | 3.49E-04    | 9.99E-05 | 6.06             |             |
| B2M         | 1.14E-05    | 8.06E-07 | -4.39            |             |
| PARP1       | 5.52E-05    | 9.49E-06 | -2.60            |             |
| APOA4       | 2.57E-06    | 4.28E-08 | 2.82             |             |
| APOA4       | 1.33E-02    | 7.03E-03 | 2.12             |             |
| ITGAX       | 3.49E-04    | 9.99E-05 | 6.06             |             |
| B2M         | 1.14E-05    | 8.06E-07 | -4.39            |             |
| PARP1       | 5.52E-05    | 9.49E-06 | -2.60            |             |
| APOA4       | 2.57E-06    | 4.28E-08 | 2.82             |             |
| APOA4       | 1.33E-02    | 7.03E-03 | 2.12             |             |
| ITGAX       | 3.49E-04    | 9.99E-05 | 6.06             |             |
| B2M         | 1.14E-05    | 8.06E-07 | -4.39            |             |
| PARP1       | 5.52E-05    | 9.49E-06 | -2.60            |             |
| Gene   | p-value 1 | p-value 2 | log2 Fold Change | Description |
|--------|-----------|-----------|-----------------|-------------|
| A_23_P252697 | 2.89E-05  | 3.76E-06  | -2.02           | CD248       |
| A_24_P389517 | 9.84E-06  | 6.45E-07  | -2.07           | HNRNPK      |
| A_24_P41850  | 3.69E-04  | 1.07E-04  | 3.48            | MASP1       |
| A_23_P314202 | 3.93E-03  | 1.75E-03  | 4.13            | PAPD4       |
| A_23_P207582 | 7.09E-06  | 2.99E-07  | 3.23            | CCL16       |
| A_23_P212179 | 2.24E-03  | 9.14E-04  | 3.72            | HRH1        |
| A_24_P403732 | 4.26E-05  | 6.60E-06  | -2.36           | ZNF385A     |
| A_23_P314202 | 3.93E-03  | 1.75E-03  | 4.13            | PAPD4       |
| A_23_P41850  | 3.69E-04  | 1.07E-04  | 3.48            | MASP1       |
| A_23_P314202 | 3.93E-03  | 1.75E-03  | 4.13            | PAPD4       |
| A_23_P403732 | 4.26E-05  | 6.60E-06  | -2.36           | ZNF385A     |
| A_23_P314202 | 3.93E-03  | 1.75E-03  | 4.13            | PAPD4       |
| A_23_P41850  | 3.69E-04  | 1.07E-04  | 3.48            | MASP1       |
| A_23_P314202 | 3.93E-03  | 1.75E-03  | 4.13            | PAPD4       |
| A_23_P403732 | 4.26E-05  | 6.60E-06  | -2.36           | ZNF385A     |
| A_23_P314202 | 3.93E-03  | 1.75E-03  | 4.13            | PAPD4       |
| Gene Symbol | Fold Change\(\Delta F\) | p-Value\(\Delta F\) | Fold Change\(\Delta F\) | p-Value\(\Delta F\) |
|-------------|-----------------|-----------------|-----------------|-----------------|
| HNRNPK      | 5.10E-05        | 8.54E-06        | -2.22           |                 |
| PRKCB       | 6.08E-05        | 1.08E-05        | -4.04           |                 |
| CYP2C19     | 1.77E-05        | 1.75E-06        | 9.51            |                 |
| PSMB5       | 3.13E-06        | 6.39E-08        | -3.28           |                 |
| I5L         | 7.59E-04        | 2.56E-04        | 6.03            |                 |
| PGC         | 1.48E-03        | 5.66E-04        | -3.21           |                 |
| CHST3       | 1.54E-02        | 8.41E-03        | 3.00            |                 |
| FCER2       | 1.17E-05        | 8.46E-07        | 2.57            |                 |
| PGM3        | 2.50E-05        | 3.03E-06        | -1.56           |                 |
| PPP3R1      | 5.24E-05        | 8.86E-06        | -4.56           |                 |
| CUL1        | 6.00E-06        | 2.19E-07        | -2.43           |                 |
| LSM14A      | 7.30E-06        | 5.07E-08        | -1.69           |                 |
| SYNCRIP     | 3.81E-06        | 1.01E-07        | -3.48           |                 |
| FGFR2       | 1.66E-05        | 1.59E-06        | -3.71           |                 |
| AHCY        | 3.51E-02        | 2.14E-02        | 3.49            |                 |
| LAT         | 8.96E-05        | 1.83E-05        | -1.90           |                 |
| POU1F1      | 3.32E-04        | 9.40E-05        | 2.15            |                 |
| ITGB1       | 1.55E-04        | 3.62E-05        | -1.70           |                 |
| PAG1        | 1.26E-06        | 6.41E-09        | -2.71           |                 |
| SLC39A10    | 7.30E-06        | 3.22E-07        | -2.00           |                 |
| TRIM14      | 1.65E-03        | 6.40E-04        | 3.75            |                 |
| ITGAM       | 4.69E-03        | 2.16E-03        | 2.20            |                 |
| PCID2       | 2.78E-04        | 7.58E-05        | -3.13           |                 |
| TRIM11      | 9.26E-06        | 5.90E-07        | -4.02           |                 |
| PPP3CB      | 5.93E-05        | 1.04E-05        | -4.28           |                 |
| HDAC4       | 4.00E-05        | 6.06E-06        | -3.35           |                 |
| HOXB6       | 1.03E-04        | 2.19E-05        | -2.21           |                 |
| CHRNA7      | 4.45E-04        | 1.36E-04        | -3.10           |                 |
| HTRA1       | 4.11E-03        | 1.85E-03        | 2.49            |                 |
| PRKCE       | 1.41E-05        | 1.14E-06        | -3.59           |                 |
| YWHAZ       | 6.51E-04        | 2.13E-04        | 7.60            |                 |
| VTCN1       | 3.23E-03        | 1.40E-03        | -2.13           |                 |
| GAPT        | 2.95E-05        | 3.86E-06        | -2.66           |                 |
| MX1         | 6.68E-07        | 1.26E-09        | -2.21           |                 |
| UBA52       | 4.00E-05        | 6.06E-06        | -3.35           |                 |
| NCF1        | 1.03E-04        | 2.19E-05        | -2.21           |                 |
| CAMK1D      | 8.32E-03        | 4.35E-07        | -2.08           |                 |
| TGFβ3       | 5.99E-05        | 9.70E-06        | 3.92            |                 |
| OGT         | 9.03E-03        | 4.55E-03        | -2.34           |                 |
| SMAP1       | 3.40E-02        | 2.06E-02        | -1.47           |                 |
| UBQLN1      | 1.41E-05        | 1.17E-06        | -2.02           |                 |
| PIK3R2      | 8.96E-04        | 3.11E-04        | 3.11            |                 |
| ID2         | 7.51E-04        | 2.52E-04        | -3.14           |                 |
| NCAM1       | 2.04E-03        | 8.20E-04        | 2.21            |                 |
| IL1B        | 2.05E-02        | 1.16E-02        | -1.64           |                 |
| KLK3        | 1.47E-03        | 5.60E-04        | -3.72           |                 |
| CEBPΔG      | 3.14E-05        | 4.20E-06        | -1.91           |                 |
| RAB4A       | 2.73E-06        | 5.14E-08        | -3.28           |                 |
| IL2         | 4.59E-06        | 1.48E-07        | 2.11            |                 |
| FAU         | 2.04E-06        | 2.80E-08        | -3.59           |                 |
| Gene Symbol | Fold Change | Log2 Fold Change | p-value  | Function |
|-------------|-------------|-----------------|----------|----------|
| PKNOX1      | 7.72E-05    | 1.49E-05        | -3.09    |          |
| PPIA        | 1.30E-05    | 1.03E-06        | -4.31    |          |
| ITGB7       | 5.26E-03    | 2.46E-03        | -1.97    |          |
| FIGF        | 4.63E-03    | 2.13E-03        | -1.90    |          |
| CX3CL1      | 1.16E-02    | 6.00E-03        | -2.14    |          |
| TRAF2       | 1.37E-02    | 7.28E-03        | 1.56     |          |
| PRKACB      | 3.07E-04    | 8.61E-05        | -3.75    |          |
| FOLR2       | 1.30E-05    | 1.03E-06        | -4.31    |          |
| ITGB7       | 5.26E-03    | 2.46E-03        | -1.97    |          |
| FIGF        | 4.63E-03    | 2.13E-03        | -1.90    |          |
| CX3CL1      | 1.16E-02    | 6.00E-03        | -2.14    |          |
| TRAF2       | 1.37E-02    | 7.28E-03        | 1.56     |          |
| PRKACB      | 3.07E-04    | 8.61E-05        | -3.75    |          |
| FOLR2       | 1.30E-05    | 1.03E-06        | -4.31    |          |
| ITGB7       | 5.26E-03    | 2.46E-03        | -1.97    |          |
| FIGF        | 4.63E-03    | 2.13E-03        | -1.90    |          |
| CX3CL1      | 1.16E-02    | 6.00E-03        | -2.14    |          |
| TRAF2       | 1.37E-02    | 7.28E-03        | 1.56     |          |
| PRKACB      | 3.07E-04    | 8.61E-05        | -3.75    |          |
| FOLR2       | 1.30E-05    | 1.03E-06        | -4.31    |          |
| ITGB7       | 5.26E-03    | 2.46E-03        | -1.97    |          |
| FIGF        | 4.63E-03    | 2.13E-03        | -1.90    |          |
| CX3CL1      | 1.16E-02    | 6.00E-03        | -2.14    |          |
| TRAF2       | 1.37E-02    | 7.28E-03        | 1.56     |          |
| PRKACB      | 3.07E-04    | 8.61E-05        | -3.75    |          |
| FOLR2       | 1.30E-05    | 1.03E-06        | -4.31    |          |
| ITGB7       | 5.26E-03    | 2.46E-03        | -1.97    |          |
| FIGF        | 4.63E-03    | 2.13E-03        | -1.90    |          |
| CX3CL1      | 1.16E-02    | 6.00E-03        | -2.14    |          |
| TRAF2       | 1.37E-02    | 7.28E-03        | 1.56     |          |
| Gene   | P-value 1 | P-value 2 | Log2FoldChange | Description |
|--------|-----------|-----------|----------------|-------------|
| LGALS8 | 5.71E-03  | 2.71E-03  | 2.35           |             |
| ATP1B3 | 1.91E-05  | 1.93E-06  | -2.38          |             |
| CD200  | 1.17E-04  | 2.57E-05  | -2.85          |             |
| PTAFR  | 1.32E-02  | 7.01E-03  | 1.74           |             |
| IFIT2  | 4.46E-02  | 2.83E-02  | 2.74           |             |
| UBQLN1 | 5.74E-06  | 1.94E-07  | -3.68          |             |
| ITPR1  | 1.90E-05  | 4.05E-05  | 4.39           |             |
| CD200  | 9.09E-05  | 1.87E-05  | -3.40          |             |
| RPS6KA5| 1.17E-04  | 2.57E-05  | -2.85          |             |
| RAB33A | 2.15E-02  | 1.23E-02  | 4.24           |             |
| MMP21  | 7.19E-03  | 3.51E-03  | 4.18           |             |
| NFKBIA | 2.08E-03  | 8.37E-04  | 2.73           |             |
| ABCB4  | 5.24E-04  | 1.67E-04  | -2.19          |             |
| NMI    | 5.53E-06  | 1.86E-07  | -2.58          |             |
| CCL26  | 2.15E-02  | 1.23E-02  | 4.24           |             |
| MLF1    | 5.17E-03  | 2.41E-03  | -1.74          |             |
| EFNB2  | 3.90E-05  | 5.80E-06  | -1.87          |             |
| CCR8   | 6.52E-05  | 1.18E-05  | 3.11           |             |
| THY1   | 7.57E-05  | 1.44E-05  | -4.72          |             |
| IGF1R  | 1.43E-03  | 5.41E-04  | -3.15          |             |
| PROS1  | 7.19E-03  | 3.51E-03  | 4.18           |             |
| BLM    | 1.68E-05  | 1.62E-06  | -2.64          |             |
| PLCB1  | 2.94E-04  | 8.15E-05  | -4.01          |             |
| PRKACA | 1.27E-03  | 4.71E-04  | 1.64           |             |
| ANKHDA| 6.12E-05  | 1.09E-05  | -1.99          |             |
| C9     | 4.10E-03  | 1.85E-03  | -2.81          |             |
| CX3CR1 | 3.54E-04  | 1.02E-04  | -3.21          |             |
| TDGF1  | 8.89E-06  | 5.32E-07  | 3.38           |             |
| HRG    | 5.04E-03  | 2.34E-03  | -3.09          |             |
| BTK    | 2.82E-02  | 1.66E-02  | 2.26           |             |
| CALM1  | 1.56E-05  | 1.42E-06  | -5.84          |             |
| UBQLN1 | 8.69E-05  | 1.75E-05  | 4.89           |             |
| TXNRD2 | 7.99E-04  | 2.72E-04  | 7.14           |             |
| STAT5B | 2.56E-04  | 6.84E-05  | -2.94          |             |
| PSMD3  | 2.21E-04  | 5.60E-05  | -4.09          |             |
| GPLD1  | 6.32E-03  | 3.04E-03  | 1.69           |             |
| CCL13  | 2.90E-04  | 8.03E-05  | -3.80          |             |
| WIPF2  | 5.34E-03  | 2.51E-03  | -2.66          |             |
| RAB33A | 7.85E-05  | 1.52E-05  | -3.80          |             |
| TRIM38 | 3.18E-04  | 8.98E-05  | 7.10           |             |
| DHX58  | 8.68E-06  | 4.99E-07  | -2.07          |             |
| HDAC4  | 4.38E-05  | 6.86E-06  | 2.73           |             |
| ASS1   | 4.35E-03  | 1.98E-03  | 3.27           |             |
| SNX4   | 2.62E-05  | 3.24E-06  | -3.77          |             |
| VAV2   | 1.19E-02  | 6.20E-03  | -2.34          |             |
| ITGB1  | 1.33E-05  | 1.07E-06  | -2.66          |             |
| Gene Symbol | Unrest | Co rx | Fold Change | P Value | Description |
|-------------|--------|-------|-------------|---------|-------------|
| NOTCH4      | 7.55E-04 | 2.54E-04 | -1.83 | NOTCH4 |
| PDCD1LG2    | 4.80E-03 | 2.22E-03 | 3.19 | PDCD1LG2 |
| OAS3        | 7.91E-04 | 2.68E-04 | 3.58 | OAS3 |
| PSF1M1      | 1.17E-03 | 4.28E-04 | 6.59 | DOCK2 |
| OAS3        | 4.52E-04 | 1.39E-04 | -1.99 | IFI35 |
| PDCD1LG2    | 1.08E-06 | 4.91E-09 | -3.23 | DYNClI2 |
| PSF1M1      | 1.21E-02 | 7.90E-03 | -2.36 | RC3H1 |
| ADD2        | 8.40E-03 | 4.46E-07 | -2.36 | COL4A3BP |
| KIF13B      | 2.50E-05 | 3.02E-06 | 2.86 | KIF13B |
| SLAMF1      | 2.45E-02 | 1.42E-02 | 2.73 | SLAMF1 |
| RPS24       | 2.46E-05 | 2.92E-06 | -3.17 | RPS24 |
| CALM1       | 8.53E-06 | 4.70E-07 | 4.31 | CALM1 |
| TLR5        | 4.90E-02 | 3.16E-02 | 1.61 | TLR5 |
| MYD88       | 1.60E-05 | 1.49E-06 | -2.59 | MYD88 |
| TINAGL1     | 2.48E-05 | 2.95E-06 | 4.08 | TINAGL1 |
| RPS17       | 1.52E-05 | 1.35E-06 | 2.65 | RPS17 |
| AKAP8       | 6.68E-07 | 9.44E-10 | -1.81 | AKAP8 |
| PSMC1       | 1.13E-04 | 2.47E-05 | 3.35 | PSMC1 |
| RPL39       | 2.62E-03 | 1.11E-03 | 2.72 | RPL39 |
| FGR         | 9.36E-04 | 3.29E-04 | 1.83 | FGR |
| SPP1L2A     | 2.22E-03 | 9.08E-04 | -1.93 | SPP1L2A |
| CTNBNIP1    | 5.37E-05 | 9.20E-06 | 2.43 | CTNBNIP1 |
| TIPARP      | 9.21E-06 | 5.71E-07 | -2.93 | TIPARP |
| SIN3A       | 2.69E-02 | 1.57E-02 | 2.45 | SIN3A |
| DLG1        | 5.10E-05 | 8.54E-06 | -3.75 | DLG1 |
| CD20OR1     | 2.36E-04 | 6.05E-05 | 2.86 | CD20OR1 |
| PIP5K1C     | 7.93E-03 | 3.91E-03 | 2.11 | PIP5K1C |
| PPIL2       | 2.05E-04 | 5.09E-05 | 6.09 | PPIL2 |
| JAK3        | 1.07E-03 | 3.83E-04 | 1.75 | JAK3 |
| PSM12D1     | 6.68E-07 | 1.08E-09 | -2.48 | PSM12D1 |
| RAB3B       | 1.02E-04 | 2.16E-05 | -3.92 | RAB3B |
| SEC13       | 1.62E-04 | 3.82E-05 | -2.83 | SEC13 |
| XBP1        | 1.65E-02 | 9.06E-03 | 2.26 | XBP1 |
| PSMA5       | 1.67E-06 | 1.75E-08 | -3.15 | PSMA5 |
| EIF2AK1     | 9.94E-07 | 2.70E-09 | -2.95 | EIF2AK1 |
| EFNB3       | 2.93E-04 | 8.12E-05 | -5.57 | EFNB3 |
| SATB1       | 4.78E-04 | 1.49E-04 | -4.31 | SATB1 |
| ASH2L       | 3.40E-06 | 7.90E-08 | -2.81 | ASH2L |
| IL11RA      | 2.04E-06 | 2.81E-08 | -1.78 | IL11RA |
| BVES        | 6.37E-04 | 2.08E-04 | -3.93 | BVES |
| ATG7        | 1.30E-02 | 6.85E-03 | -2.12 | ATG7 |
| SLC11A2     | 2.81E-05 | 3.60E-06 | -2.21 | SLC11A2 |
| CXCR5       | 1.81E-02 | 1.01E-02 | -1.72 | CXCR5 |
| GIF         | 7.63E-05 | 1.46E-05 | -3.93 | GIF |
| CANX        | 8.40E-06 | 4.55E-07 | -2.40 | CANX |
| Gene Symbol | A_24_P56467 | A_24_P20607 | A_23_P420209 | A_24_P257539 | A_23_P217236 | A_23_P163079 | A_24_P944519 | A_23_P217282 | A_23_P164022 | A_23_P257539 | A_23_P57497 | A_23_P214208 | A_24_P143120 | A_23_P141405 | A_23_P163079 | A_23_P200598 | A_24_P404822 |
|-------------|-------------|-------------|--------------|--------------|--------------|--------------|-------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|
|             | 3.35E-05    | 3.64E-04    | 1.82E-04     | 1.57E-02     | 2.60E-05     | 2.87E-02     | 1.52E-02    | 1.89E-04     | 6.19E-05     | 1.10E-02     | 7.62E-04     | 1.81E-05     | 1.22E-02     | 1.94E-04     | 6.10E-03    | 3.28E-05     |
|             | 4.75E-06    | 1.05E-04    | 4.42E-05     | 8.59E-03     | 3.21E-06     | 1.70E-02     | 8.26E-03    | 4.60E-05     | 1.12E-05     | 5.66E-03     | 2.57E-04     | 1.81E-06     | 9.03E-07     | 4.75E-05     | 2.91E-03    | 4.56E-06     |
|             | -2.64       | 2.91        | 3.92         | -1.83        | -1.84        | 4.61         | -2.47       | -1.77        | -3.54        | 2.26         | 3.92         | -2.34        | -2.83        | -4.25        | -1.79        | -2.05        |
|             | GMPR2       | CXCL11      | GCNT3        | FBXW11       | HMGB3        | GCH1         | PDE4D       | IGF1R        | MYO1C        | LILRB4       | GCNT3        | AP2A2        | NME1         | LIRL4        | CD55         | SLC7A6OS     |

**Note:** The numbers represent fold changes or other measurements for each gene.
| Gene Symbol | Effect Size | P-Value 1 | P-Value 2 | Effect Size 1 | Effect Size 2 |
|-------------|-------------|-----------|-----------|---------------|---------------|
| A_23_P45871 | 8.84E-06    | 5.20E-07  | -2.53     | IFI44L        |
| A_23_P500601| 1.26E-06    | 6.64E-09  | -2.10     | TRIM4         |
| A_23_P246173| 8.68E-06    | 4.92E-07  | -3.22     | MYO9B         |
| A_23_P51187 | 2.41E-04    | 6.22E-05  | -3.27     | PRKCZ         |
| A_23_P74278 | 1.24E-05    | 9.55E-07  | -2.25     | PDE4B         |
| A_32_P460973| 5.83E-05    | 1.02E-05  | -2.79     | HLA-E         |
| A_23_P37727 | 4.47E-04    | 1.37E-04  | -3.72     | CX3CL1        |
| A_23_P360167| 1.44E-05    | 2.58E-07  | -1.94     | PSMB2         |
| A_32_P460973| 5.83E-05    | 1.02E-05  | -2.79     | HLA-E         |
| A_23_P51187 | 2.41E-04    | 6.22E-05  | -3.27     | PRKCZ         |
| A_23_P74278 | 1.24E-05    | 9.55E-07  | -2.25     | PDE4B         |
| A_32_P460973| 5.83E-05    | 1.02E-05  | -2.79     | HLA-E         |
| A_23_P37727 | 4.47E-04    | 1.37E-04  | -3.72     | CX3CL1        |
| A_23_P360167| 1.44E-05    | 2.58E-07  | -1.94     | PSMB2         |
| A_32_P460973| 5.83E-05    | 1.02E-05  | -2.79     | HLA-E         |
| Gene symbol | Fold change | p-value | q-value | Symbol |
|-------------|-------------|---------|---------|---------|
| RNASE7      | 3.14        | 3.83E-03| 1.71E-03| DNAJA3  |
| CD160       | 3.01        | 2.94E-04| 4.26E-06| ICOSLG  |
| L3MBTL3     | -1.48       | 6.00E-06| 2.15E-07| CFB     |
| IL10RB      | -2.48       | 1.32E-03| 4.91E-04| PSMB1   |
| DOCK1       | -2.14       | 2.33E-05| 2.66E-06| TRIB1   |
| GIMAP1      | -2.14       | 3.10E-04| 8.71E-05| TRIB1   |
| JAM2        | -2.34       | 4.77E-05| 7.78E-06| CHD2    |
| SNX10       | -2.70       | 8.18E-04| 2.80E-04| SNX10   |
| PSMB1       | -2.34       | 4.38E-05| 6.86E-06| CFB     |
| S100B       | -2.32       | 3.21E-06| 6.82E-08| S100B   |
| SNX10       | -2.27       | 3.39E-03| 1.48E-03| TRIB1   |
| RASSF2      | -3.54       | 3.16E-05| 4.26E-06| CFB     |
| LRRK1       | -3.29       | 8.71E-06| 5.04E-07| DOCK1   |
| TMBIM6      | -3.16       | 4.87E-05| 8.17E-05| DOCK1   |
| UBE2D1      | -3.16       | 6.00E-06| 5.04E-07| DOCK1   |
| UBE2V1      | -3.16       | 2.33E-05| 2.66E-06| DOCK1   |
| JAM2        | -3.14       | 4.77E-05| 7.78E-06| CHD2    |
| ITGA9       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| MINK1       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| VAV3        | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| NFE2L2      | -2.91       | 9.78E-04| 3.47E-04| NFE2L2  |
| RASGRP1     | -2.91       | 9.78E-04| 3.47E-04| NFE2L2  |
| ARPC4       | -2.91       | 9.78E-04| 3.47E-04| NFE2L2  |
| SRPK2       | -2.91       | 9.78E-04| 3.47E-04| NFE2L2  |
| VAV3        | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| NFE2L2      | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| RASGRP1     | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| ARPC4       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| SRPK2       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| VAV3        | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| NFE2L2      | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| RASGRP1     | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| ARPC4       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| SRPK2       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| VAV3        | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| NFE2L2      | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| RASGRP1     | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| ARPC4       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| SRPK2       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| VAV3        | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| NFE2L2      | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| RASGRP1     | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| ARPC4       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| SRPK2       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| VAV3        | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| NFE2L2      | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| RASGRP1     | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| ARPC4       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| SRPK2       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| VAV3        | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| NFE2L2      | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| RASGRP1     | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| ARPC4       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| SRPK2       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| VAV3        | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| NFE2L2      | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| RASGRP1     | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| ARPC4       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| SRPK2       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| VAV3        | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| NFE2L2      | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| RASGRP1     | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| ARPC4       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| SRPK2       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| VAV3        | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| NFE2L2      | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| RASGRP1     | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| ARPC4       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| SRPK2       | -3.63       | 3.16E-06| 1.25E-05| ITGA9   |
| Gene Symbol | Fold Change (EB1 vs. EB2) | p-Value (EB1 vs. EB2) | z-Value | Gene Symbol |
|-------------|---------------------------|-----------------------|---------|-------------|
| A_23_P54006 | 3.11E-06                  | 6.10E-08              | -2.60   | HECTD1      |
| A_23_P26847 | 2.37E-04                  | 6.12E-05              | -2.09   | SOX9        |
| A_23_P370005 | 2.44E-03                 | 1.01E-03              | 2.27    | RIPK1       |
| A_23_P69058 | 1.67E-06                  | 1.73E-08              | -3.14   | MLH1        |
| A_23_P359091 | 5.39E-03                 | 2.53E-03              | 1.67    | SMAD3       |
| A_23_P55251 | 7.38E-03                  | 3.61E-03              | 2.74    | ITGA3       |
| A_24_P72420 | 3.26E-03                  | 1.41E-03              | -1.98   | ELMO1       |
| A_23_P19352 | 1.87E-04                  | 4.54E-05              | 2.54    | CNPY3       |
| A_23_P148047 | 4.51E-03                 | 2.07E-03              | 2.27    | PTGER4      |
| A_23_P500300 | 7.42E-05                 | 1.41E-05              | 4.11    | TRIM15      |
| A_24_P48403 | 7.98E-06                  | 3.92E-07              | -3.60   | YES1        |
| A_23_P372874 | 1.87E-04                 | 4.54E-05              | -2.40   | S100A13     |
| A_23_P70867 | 1.71E-03                  | 6.69E-04              | -2.01   | SBDS        |
| A_24_P334445 | 3.83E-05                 | 5.69E-06              | -2.91   | MAEA        |
| A_23_P92623 | 4.32E-04                  | 1.31E-04              | -3.55   | PPP3CA      |
| A_23_P59005 | 1.64E-06                  | 1.41E-08              | -2.03   | TAP1        |
| A_24_P29876 | 6.78E-06                  | 2.71E-07              | -2.55   | AGPAT5      |
| A_23_P369960 | 3.84E-04                 | 1.12E-04              | 3.58    | NCAPH2      |
| A_23_P97265 | 6.60E-05                  | 1.20E-05              | -2.88   | GPATCH4     |
| A_24_P89708 | 4.41E-04                  | 1.34E-04              | 3.77    | IMPDH1      |
| A_23_P132444 | 3.81E-05                 | 5.63E-06              | -3.25   | TCEA1       |
| A_32_P820503 | 5.35E-06                 | 1.77E-07              | -3.28   | FTH1        |
| A_24_P148762 | 3.66E-04                 | 1.06E-04              | 5.26    | IL1RAP      |
| A_24_P169234 | 2.30E-03                 | 9.45E-04              | 2.13    | ZAP70       |
| A_24_P941824 | 2.12E-06                 | 3.01E-08              | -2.66   | KIF3B       |
| A_23_P154840 | 8.45E-05                 | 1.68E-05              | -4.56   | SOD1        |
| A_24_P418809 | 8.56E-06                 | 4.83E-07              | -3.04   | GNAS        |
| A_24_P100419 | 2.68E-04                 | 7.23E-05              | 10.63   | EDA         |
| A_32_P197489 | 6.92E-05                 | 1.29E-05              | -3.40   | KLF13       |
| A_24_P116017 | 1.49E-03                 | 5.71E-04              | 3.86    | PSMD9       |
| A_24_P146892 | 2.68E-03                 | 1.13E-03              | -2.53   | ORAI1       |
| A_24_P173823 | 7.98E-06                 | 3.88E-07              | -2.58   | PBX1        |
| A_23_P125423 | 2.56E-04                 | 6.80E-05              | -2.19   | C1R         |
| A_24_P13230  | 8.79E-05                 | 1.78E-05              | -2.54   | RAB6A       |
| A_23_P113311 | 4.29E-05                 | 6.67E-06              | -3.74   | P4HTM       |
| A_23_P140807 | 8.53E-06                 | 4.68E-07              | -2.86   | PSMB10      |
| A_23_P364517 | 8.71E-05                 | 1.76E-05              | -3.32   | SELK        |
| A_23_P3993425 | 1.21E-03                | 4.46E-04              | -2.01   | PAPD4       |
| A_23_P75921  | 6.72E-04                 | 2.22E-04              | -1.59   | TRAF6       |
| A_23_P55649 | 2.55E-02                 | 1.49E-02              | -2.46   | FPR2        |
| A_32_P71118  | 8.12E-06                 | 4.07E-07              | -2.88   | PSMC6       |
| A_24_P337592 | 9.84E-03                 | 5.01E-03              | 1.81    | BTN2A2      |
| A_23_P67669 | 1.57E-05                 | 1.44E-06              | 2.44    | PGLYRP2     |
| A_24_P381962 | 7.93E-05                 | 1.54E-05              | -2.94   | API1G1      |
| A_23_P35906 | 3.22E-05                 | 4.41E-06              | -1.95   | CASP4       |
| A_23_P55477 | 4.54E-03                 | 2.08E-03              | -1.98   | ADORA2B     |
| A_24_P299507 | 3.03E-04                 | 8.48E-05              | 3.02    | REST        |
| A_24_P326082 | 1.17E-05                 | 8.46E-07              | -2.43   | HLA-E       |
| A_23_P49021  | 1.02E-05                 | 6.72E-07              | -3.21   | WDR61       |
| A_24_P286465 | 1.17E-04                 | 2.58E-05              | -2.78   | PURB        |
| Gene Name | p-value | Adjusted p-value | log2 Fold Change | Description |
|-----------|---------|-----------------|-----------------|-------------|
| DYNC2LI1  | 1.50E-02| 7.67E-07        | 2.61            |             |
| SKIL      | 8.13E-03| 3.18            | -2.40           | ABI1        |
| TXLNA     | 2.61E-04| 2.94            | 9.47            | PSMD12      |
| HLA-C     | 7.79E-07| 7.79            | 2.08            | FCGR2B      |
| ENPP3     | 1.70E-04| 6.66            | 5.75            | VAV2        |
| TRIM6     | 1.30E-04| 8.46            | -2.86           | ADAMTS13    |
| PPP4R2    | 1.68E-03| 3.34            | -3.70           |             |
| STK11     | 3.02E-07| 3.27            | 9.48            |             |
| ATP1B2    | 1.15E-06| 3.57            | 6.16            |             |
| TLR8      | 1.78E-06| 3.04            | 6.16            |             |
| UB2K      | 3.72E-04| 3.57            | 6.16            |             |
| UBB       | 3.10E-03| 3.34            | -2.86           |             |
| WNT3A     | 1.19E-02| 1.30            | -2.40           |             |
| SLAMF7    | 2.72E-05| 2.90            | 2.08            |             |
| ITGAL     | 9.78E-05| 3.34            | -2.86           |             |
| CHRN2B    | 2.72E-05| 2.90            | 2.08            |             |
| TLR8      | 1.78E-06| 3.57            | 6.16            |             |
| ACTR1A    | 5.87E-06| 3.57            | 6.16            |             |
| KLC2      | 1.09E-02| 2.90            | 2.08            |             |
| GSDMD     | 7.06E-04| 3.57            | 6.16            |             |
| THOC5     | 1.30E-05| 3.57            | 6.16            |             |
| KIF13B    | 1.02E-06| 3.57            | 6.16            |             |
| CAMK2D    | 2.16E-03| 3.57            | 6.16            |             |
| UBA52     | 2.46E-08| 3.57            | 6.16            |             |
| RPL22     | 4.08E-09| 3.57            | 6.16            |             |
| PSMC1     | 3.82E-08| 3.57            | 6.16            |             |
| TRIM35    | 3.48E-04| 3.57            | 6.16            |             |
| TBC1D10C  | 2.31E-04| 3.57            | 6.16            |             |
| SH2B2     | 2.05E-06| 3.57            | 6.16            |             |
| CTSK      | 3.72E-08| 3.57            | 6.16            |             |
| NNX2-3    | 1.37E-04| 3.57            | 6.16            |             |
| GNAS      | 3.47E-04| 3.57            | 6.16            |             |
| LMO4      | 4.27E-06| 3.57            | 6.16            |             |
| STAR      | 2.58E-02| 3.57            | 6.16            |             |
| IGBP1     | 1.69E-08| 3.57            | 6.16            |             |
| Gene Symbol | Fold Change | Adj. P Value | FDR P Value | Description |
|-------------|-------------|--------------|-------------|-------------|
| KIF3B       | 6.07E-03    | 2.90E-03     | 6.29        |             |
| ATP1B1      | 4.10E-04    | 1.22E-04     | -4.28       |             |
| SNX10       | 3.82E-05    | 5.65E-06     | -4.92       |             |
| PSMB7       | 2.40E-05    | 2.76E-06     | -2.78       |             |
| CUL4A       | 4.59E-06    | 1.47E-07     | -1.99       |             |
| SRF         | 7.30E-06    | 3.15E-07     | -2.09       |             |
| PSMB1       | 3.28E-06    | 7.15E-08     | -3.58       |             |
| GAL         | 2.05E-04    | 5.09E-05     | -2.80       |             |
| IL17C       | 3.26E-03    | 1.41E-03     | -3.02       |             |
| DMBT1       | 1.80E-02    | 1.00E-02     | -1.92       |             |
| SHPK        | 2.25E-04    | 5.74E-05     | -1.82       |             |
| SIAE        | 2.44E-04    | 6.34E-05     | -3.48       |             |
| ALOX15      | 5.15E-04    | 1.63E-04     | -4.70       |             |
| TNFRSF21    | 3.60E-05    | 1.42E-06     | -3.33       |             |
| FGF3        | 6.14E-05    | 1.10E-05     | -4.34       |             |
| CCDC88B     | 4.82E-02    | 3.10E-02     | -3.01       |             |
| POI3R3D     | 5.59E-05    | 9.69E-06     | -2.95       |             |
| HDAC4       | 4.59E-06    | 1.46E-07     | -1.77       |             |
| PLEKHA1     | 2.30E-04    | 5.88E-05     | -2.37       |             |
| CFD         | 1.15E-02    | 5.97E-03     | 1.98        |             |
| CBFB        | 9.31E-04    | 3.26E-04     | -2.12       |             |
| BPI         | 6.21E-05    | 1.12E-05     | 5.20        |             |
| CD47        | 3.96E-05    | 5.94E-06     | -2.43       |             |
| PSME1       | 1.26E-06    | 7.59E-09     | -1.90       |             |
| CD200R1     | 1.43E-03    | 5.38E-04     | 3.46        |             |
| UBE2N       | 3.41E-06    | 8.07E-08     | -2.38       |             |
| PPP1R14B    | 3.51E-05    | 5.06E-06     | -2.58       |             |
| SLC11A2     | 1.09E-02    | 5.61E-03     | -2.45       |             |
| BSG         | 1.36E-03    | 5.07E-04     | -2.60       |             |
| KIR3DL2     | 2.86E-03    | 1.22E-03     | 4.26        |             |
| FAM20C      | 3.55E-05    | 5.13E-06     | -2.35       |             |
| FKB1P1B     | 1.60E-06    | 1.33E-08     | -2.36       |             |
| AP3B1       | 3.81E-06    | 1.00E-07     | -3.63       |             |
| DAPK3       | 1.19E-02    | 6.20E-03     | 2.03        |             |
| MYH9        | 8.40E-06    | 4.56E-07     | -1.90       |             |
| POLM        | 1.79E-03    | 7.06E-04     | -2.38       |             |
| ADAR        | 8.53E-06    | 4.79E-07     | -2.34       |             |
| OSBPL1A     | 3.88E-06    | 1.10E-07     | -4.01       |             |
| PLA2G2F     | 3.40E-03    | 1.49E-03     | 5.70        |             |
| GAB2        | 1.11E-05    | 7.77E-07     | -1.80       |             |
| KYNZ        | 1.09E-03    | 3.92E-04     | 5.70        |             |
| HLA-DRB3    | 2.90E-02    | 1.72E-02     | 2.29        |             |
| TF          | 2.44E-04    | 6.34E-05     | -4.30       |             |
| APOBEC1     | 1.89E-03    | 7.51E-04     | 4.41        |             |
| AP1S1       | 1.85E-02    | 1.03E-02     | 6.42        |             |
| GPRC5B      | 2.33E-05    | 2.66E-06     | -2.84       |             |
| UBB         | 9.09E-05    | 1.87E-05     | -3.98       |             |
| Gene Symbol | Fold Change | P-value | Gene Symbol | Fold Change | P-value |
|-------------|-------------|---------|-------------|-------------|---------|
| A_23_P349928 | 1.52E-05 | -3.30 | SP100      | 1.37E-06 | -3.75 |
| A_23_P402588 | 4.64E-05 | -3.23 | SOCS1      | 2.14E-05 | -3.46 |
| A_23_P420196 | 3.08E-03 | -3.91 | SH3GL2     | 1.60E-04 | -2.29 |
| A_23_P138157 | 3.08E-03 | -3.23 | CST9L      | 3.06E-05 | -2.29 |
| A_23_P143365 | 5.08E-04 | -3.75 | BCL11A     | 7.46E-06 | -2.91 |
| A_23_P169351 | 1.01E-04 | -4.46 | OTUD7B     | 1.35E-04 | -2.29 |
| A_23_P167081 | 4.60E-04 | -2.75 | RPS14      | 1.37E-04 | -3.54 |
| A_23_P143365 | 5.08E-04 | -3.75 | PSMA4      | 1.37E-05 | -2.44 |
| A_23_P150286 | 1.32E-05 | -2.83 | PPIA       | 1.67E-05 | -16.04 |
| A_23_P350467 | 8.42E-05 | -2.85 | AKIRIN2    | 4.48E-04 | -3.67 |
| A_23_P428819 | 2.70E-06 | -2.45 | RICTOR     | 4.64E-08 | -3.06 |
| A_23_P214554 | 2.53E-04 | -2.01 | WDR7       | 6.65E-08 | -3.06 |
| A_23_P350467 | 8.42E-05 | -4.17 | PPIA       | 1.67E-05 | -3.06 |
| A_23_P115998 | 1.22E-03 | -2.82 | SPON2      | 4.48E-04 | -3.06 |
| A_23_P214554 | 2.53E-04 | -2.44 | REST       | 6.65E-08 | -3.06 |
| A_23_P150286 | 1.32E-05 | -2.44 | MAPKAP2    | 1.06E-06 | -3.06 |
| A_23_P350467 | 8.42E-05 | -2.44 | CAMK1D     | 1.67E-05 | -3.06 |
| A_23_P500621 | 2.02E-03 | -2.44 | HIPK2      | 8.09E-04 | -3.06 |
| A_23_P143365 | 5.08E-04 | -2.44 | ITPG1      | 1.37E-05 | -3.06 |
| A_23_P208120 | 3.48E-04 | -2.44 | CAMK1D     | 9.95E-05 | -3.06 |
| A_23_P350467 | 8.42E-05 | -2.44 | MAPKAP2    | 1.67E-05 | -3.06 |
| A_23_P350467 | 8.42E-05 | -2.44 | CAMK1D     | 1.67E-05 | -3.06 |
| A_23_P500621 | 2.02E-03 | -2.44 | HIPK2      | 8.09E-04 | -3.06 |
| A_23_P143365 | 5.08E-04 | -2.44 | ITPG1      | 1.37E-05 | -3.06 |
| A_23_P208120 | 3.48E-04 | -2.44 | CAMK1D     | 9.95E-05 | -3.06 |
| A_23_P350467 | 8.42E-05 | -2.44 | MAPKAP2    | 1.67E-05 | -3.06 |
| A_23_P500621 | 2.02E-03 | -2.44 | HIPK2      | 8.09E-04 | -3.06 |
| A_23_P143365 | 5.08E-04 | -2.44 | ITPG1      | 1.37E-05 | -3.06 |
| A_23_P208120 | 3.48E-04 | -2.44 | CAMK1D     | 9.95E-05 | -3.06 |
| A_23_P350467 | 8.42E-05 | -2.44 | MAPKAP2    | 1.67E-05 | -3.06 |
| A_23_P500621 | 2.02E-03 | -2.44 | HIPK2      | 8.09E-04 | -3.06 |
| A_23_P143365 | 5.08E-04 | -2.44 | ITPG1      | 1.37E-05 | -3.06 |
| A_23_P208120 | 3.48E-04 | -2.44 | CAMK1D     | 9.95E-05 | -3.06 |
| A_23_P350467 | 8.42E-05 | -2.44 | MAPKAP2    | 1.67E-05 | -3.06 |
| A_23_P500621 | 2.02E-03 | -2.44 | HIPK2      | 8.09E-04 | -3.06 |
| A_23_P143365 | 5.08E-04 | -2.44 | ITPG1      | 1.37E-05 | -3.06 |
| A_23_P208120 | 3.48E-04 | -2.44 | CAMK1D     | 9.95E-05 | -3.06 |
| A_23_P350467 | 8.42E-05 | -2.44 | MAPKAP2    | 1.67E-05 | -3.06 |
| Accession   | FPKM   | FPKM   | Log2 Fold Change | Gene Symbol |
|-------------|--------|--------|-----------------|-------------|
| A_23_P55936 | 1.01E-04 | 2.14E-05 | -2.42           | FCGRT       |
| A_23_P208482| 1.03E-04 | 2.20E-05 | -4.14           | CLEC4M      |
| A_23_P70968 | 1.78E-02 | 9.88E-03 | 2.98            | HOXA7       |
| A_23_P26771 | 4.62E-04 | 1.43E-04 | 2.82            | CD300C      |
| A_23_P210763| 4.20E-02 | 2.63E-02 | 1.81            | JAG1        |
| A_23_P126803| 2.14E-04 | 5.37E-05 | -4.28           | ARPC5       |
| A_24_P931443| 7.62E-06 | 3.56E-07 | -3.42           | GRP68       |
| A_24_P353794| 4.32E-04 | 1.31E-04 | 1.73            | GALNT2      |
| A_23_P5550  | 3.69E-05 | 5.41E-06 | -3.48           | PUM2        |
| A_24_P210763| 4.20E-02 | 2.63E-02 | -2.87           | CD276       |
| A_23_P26771 | 4.62E-04 | 1.43E-04 | 2.82            | CD300C      |
| A_24_P210763| 4.20E-02 | 2.63E-02 | 1.81            | JAG1        |
| A_23_P126803| 2.14E-04 | 5.37E-05 | -4.28           | ARPC5       |
| A_24_P931443| 7.62E-06 | 3.56E-07 | -3.42           | GRP68       |
| A_24_P353794| 4.32E-04 | 1.31E-04 | 1.73            | GALNT2      |
| A_23_P5550  | 3.69E-05 | 5.41E-06 | -3.48           | PUM2        |
| A_24_P210763| 4.20E-02 | 2.63E-02 | -2.87           | CD276       |
| A_23_P26771 | 4.62E-04 | 1.43E-04 | 2.82            | CD300C      |
| A_24_P210763| 4.20E-02 | 2.63E-02 | 1.81            | JAG1        |
| A_23_P126803| 2.14E-04 | 5.37E-05 | -4.28           | ARPC5       |
| A_24_P931443| 7.62E-06 | 3.56E-07 | -3.42           | GRP68       |
| A_24_P353794| 4.32E-04 | 1.31E-04 | 1.73            | GALNT2      |
| A_23_P5550  | 3.69E-05 | 5.41E-06 | -3.48           | PUM2        |
| A_24_P210763| 4.20E-02 | 2.63E-02 | -2.87           | CD276       |
| A_23_P26771 | 4.62E-04 | 1.43E-04 | 2.82            | CD300C      |
| A_24_P210763| 4.20E-02 | 2.63E-02 | 1.81            | JAG1        |
| A_23_P126803| 2.14E-04 | 5.37E-05 | -4.28           | ARPC5       |
| A_24_P931443| 7.62E-06 | 3.56E-07 | -3.42           | GRP68       |
| A_24_P353794| 4.32E-04 | 1.31E-04 | 1.73            | GALNT2      |
| A_23_P5550  | 3.69E-05 | 5.41E-06 | -3.48           | PUM2        |
| A_24_P210763| 4.20E-02 | 2.63E-02 | -2.87           | CD276       |
| A_23_P26771 | 4.62E-04 | 1.43E-04 | 2.82            | CD300C      |
| A_24_P210763| 4.20E-02 | 2.63E-02 | 1.81            | JAG1        |
| A_23_P126803| 2.14E-04 | 5.37E-05 | -4.28           | ARPC5       |
| A_24_P931443| 7.62E-06 | 3.56E-07 | -3.42           | GRP68       |
| A_24_P353794| 4.32E-04 | 1.31E-04 | 1.73            | GALNT2      |
| A_23_P5550  | 3.69E-05 | 5.41E-06 | -3.48           | PUM2        |
| A_24_P210763| 4.20E-02 | 2.63E-02 | -2.87           | CD276       |
| A_23_P26771 | 4.62E-04 | 1.43E-04 | 2.82            | CD300C      |
| A_24_P210763| 4.20E-02 | 2.63E-02 | 1.81            | JAG1        |
| A_23_P126803| 2.14E-04 | 5.37E-05 | -4.28           | ARPC5       |
| A_24_P931443| 7.62E-06 | 3.56E-07 | -3.42           | GRP68       |
| A_24_P353794| 4.32E-04 | 1.31E-04 | 1.73            | GALNT2      |
| A_23_P5550  | 3.69E-05 | 5.41E-06 | -3.48           | PUM2        |
| A_24_P210763| 4.20E-02 | 2.63E-02 | -2.87           | CD276       |
| A_23_P26771 | 4.62E-04 | 1.43E-04 | 2.82            | CD300C      |
| A_24_P210763| 4.20E-02 | 2.63E-02 | 1.81            | JAG1        |
| A_23_P126803| 2.14E-04 | 5.37E-05 | -4.28           | ARPC5       |
| A_24_P931443| 7.62E-06 | 3.56E-07 | -3.42           | GRP68       |
| A_24_P270814 | 4.45E-04 | 1.36E-04 | -2.71 | CRK   |
|-------------|----------|----------|------|------|
| A_24_P673786 | 1.09E-05 | 7.43E-07 | -2.76 | PIP4K2A |
| A_23_P123503 | 8.87E-04 | 3.07E-04 |  6.08 | TRIB1 |
| A_23_P212768 | 6.94E-05 | 1.29E-05 | -2.92 | ADD1 |
| A_24_P682285 | 6.08E-05 | 1.08E-05 |  1.87 | HSPA1A |
| A_24_P29401  | 3.47E-03 | 1.52E-03 | -2.39 | PIK3R1 |
| A_24_P344307 | 3.82E-04 | 1.12E-04 | -1.78 | PSME3 |
| A_23_P146990 | 2.20E-05 | 2.35E-02 | -2.67 | C6orf25 |
| A_23_P212768 | 3.73E-02 | 2.03E-02 | -1.61 | SMAP1 |
| A_24_P682285 | 6.94E-05 | 1.29E-05 |  1.87 | HSPA1A |
| A_24_P29401  | 3.47E-03 | 1.52E-03 | -2.39 | PIK3R1 |
| A_24_P344307 | 3.82E-04 | 1.12E-04 | -1.78 | PSME3 |
| A_23_P146990 | 2.20E-05 | 2.35E-02 | -2.67 | C6orf25 |
| A_23_P212768 | 3.73E-02 | 2.03E-02 | -1.61 | SMAP1 |
| A_24_P682285 | 6.94E-05 | 1.29E-05 |  1.87 | HSPA1A |
| A_24_P29401  | 3.47E-03 | 1.52E-03 | -2.39 | PIK3R1 |
| A_24_P344307 | 3.82E-04 | 1.12E-04 | -1.78 | PSME3 |
| A_23_P146990 | 2.20E-05 | 2.35E-02 | -2.67 | C6orf25 |
| A_23_P212768 | 3.73E-02 | 2.03E-02 | -1.61 | SMAP1 |
| A_24_P682285 | 6.94E-05 | 1.29E-05 |  1.87 | HSPA1A |
| A_24_P29401  | 3.47E-03 | 1.52E-03 | -2.39 | PIK3R1 |
| A_24_P344307 | 3.82E-04 | 1.12E-04 | -1.78 | PSME3 |
| A_23_P146990 | 2.20E-05 | 2.35E-02 | -2.67 | C6orf25 |
| A_23_P212768 | 3.73E-02 | 2.03E-02 | -1.61 | SMAP1 |
| A_24_P682285 | 6.94E-05 | 1.29E-05 |  1.87 | HSPA1A |
| A_24_P29401  | 3.47E-03 | 1.52E-03 | -2.39 | PIK3R1 |
| A_24_P344307 | 3.82E-04 | 1.12E-04 | -1.78 | PSME3 |
| A_23_P146990 | 2.20E-05 | 2.35E-02 | -2.67 | C6orf25 |
| A_23_P212768 | 3.73E-02 | 2.03E-02 | -1.61 | SMAP1 |
| A_24_P682285 | 6.94E-05 | 1.29E-05 |  1.87 | HSPA1A |
| A_24_P29401  | 3.47E-03 | 1.52E-03 | -2.39 | PIK3R1 |
| A_24_P344307 | 3.82E-04 | 1.12E-04 | -1.78 | PSME3 |
| A_23_P146990 | 2.20E-05 | 2.35E-02 | -2.67 | C6orf25 |
| A_23_P212768 | 3.73E-02 | 2.03E-02 | -1.61 | SMAP1 |
| A_24_P682285 | 6.94E-05 | 1.29E-05 |  1.87 | HSPA1A |
| A_24_P29401  | 3.47E-03 | 1.52E-03 | -2.39 | PIK3R1 |
| A_24_P344307 | 3.82E-04 | 1.12E-04 | -1.78 | PSME3 |
| A_23_P146990 | 2.20E-05 | 2.35E-02 | -2.67 | C6orf25 |
| A_23_P212768 | 3.73E-02 | 2.03E-02 | -1.61 | SMAP1 |
| A_24_P682285 | 6.94E-05 | 1.29E-05 |  1.87 | HSPA1A |
| A_24_P29401  | 3.47E-03 | 1.52E-03 | -2.39 | PIK3R1 |
| A_24_P344307 | 3.82E-04 | 1.12E-04 | -1.78 | PSME3 |
| A_23_P146990 | 2.20E-05 | 2.35E-02 | -2.67 | C6orf25 |
| A_23_P212768 | 3.73E-02 | 2.03E-02 | -1.61 | SMAP1 |
| A_24_P682285 | 6.94E-05 | 1.29E-05 |  1.87 | HSPA1A |
| A_24_P29401  | 3.47E-03 | 1.52E-03 | -2.39 | PIK3R1 |
| A_24_P344307 | 3.82E-04 | 1.12E-04 | -1.78 | PSME3 |
| A_23_P146990 | 2.20E-05 | 2.35E-02 | -2.67 | C6orf25 |
| A_23_P212768 | 3.73E-02 | 2.03E-02 | -1.61 | SMAP1 |
| Gene ID    | Fold Change | P-Value   | Gene ID    | Fold Change | P-Value   |
|------------|-------------|-----------|------------|-------------|-----------|
| A_24_P231513 | 1.24E-05    | 9.54E-07  | -2.16      | ACTR3       |
| A_24_P936758 | 3.60E-03    | 1.59E-03  | -3.76      | IGF2        |
| A_23_P211985 | 8.64E-03    | 4.33E-03  | 2.07       | SNRK        |
| A_23_P166219 | 3.36E-02    | 2.03E-02  | 4.46       | GABPA       |
| A_32_P57870  | 1.50E-04    | 3.49E-05  | -3.47      | PSMC1       |
| A_24_P82200  | 1.24E-02    | 6.50E-03  | 1.88       | MEI52       |
| A_24_P53595  | 1.43E-03    | 5.40E-04  | 6.05       | GNAS        |
| A_23_P167674 | 7.39E-05    | 1.40E-05  | -2.10      | F12         |
| A_23_P9688   | 5.91E-05    | 3.84E-04  | -2.10      | DYNC1LI2    |
| A_24_P938293 | 4.65E-05    | 7.51E-06  | -2.00      | HES1        |
| A_23_P82929  | 7.74E-06    | 3.68E-07  | -2.97      | NOV         |
| A_23_P65031  | 2.06E-05    | 2.01E-06  | -4.25      | DYNLL1      |
| A_23_P65370  | 1.04E-05    | 7.04E-07  | -3.50      | GLRX5       |
| A_23_P472055 | 4.59E-03    | 2.11E-03  | -2.75      | RNF125      |
| A_23_P213204 | 1.26E-06    | 6.76E-09  | -1.79      | WHSC1       |
| A_23_P76538  | 9.98E-05    | 2.09E-05  | -3.56      | TESC        |
| A_23_P166371 | 8.92E-03    | 4.48E-03  | -2.19      | VPREB3      |
| A_23_P111381 | 5.74E-06    | 1.96E-07  | -2.66      | ATG5        |
| A_32_P170003 | 3.87E-04    | 1.14E-04  | -2.19      | TRAF3IP1    |
| A_32_P162726 | 1.77E-03    | 6.96E-04  | -2.82      | EXOSC6      |
| A_23_P122174 | 4.21E-02    | 2.64E-02  | -2.09      | XRCC4       |
| A_23_P99980  | 6.90E-05    | 1.28E-05  | -3.15      | HMGB1       |
| A_23_P153372 | 2.63E-04    | 7.07E-05  | -2.57      | HSH2D       |
| A_23_P97632  | 7.19E-06    | 3.05E-07  | -2.88      | EPRS        |
| A_24_P236949 | 3.87E-02    | 2.40E-02  | 2.43       | C19orf66    |
| A_23_P159956 | 2.90E-02    | 1.72E-02  | 1.53       | MID2        |
| A_23_P254120 | 1.40E-04    | 3.19E-05  | -3.65      | FBXO9       |
| A_23_P120002 | 4.65E-05    | 7.49E-06  | 2.41       | SP110       |
| A_23_P71624  | 1.97E-02    | 1.11E-02  | -1.86      | PAX5        |
| A_23_P205929 | 9.39E-05    | 1.95E-05  | -2.97      | DPP8        |
| A_32_P210252 | 4.59E-05    | 7.34E-06  | -2.83      | RPL22       |
| A_23_P75453  | 2.32E-04    | 5.96E-05  | -2.49      | MEN1        |
| A_24_P916522 | 4.40E-02    | 2.78E-02  | -2.03      | PAX5        |
| A_23_P637237 | 2.67E-05    | 3.32E-06  | -2.99      | FOXP1       |
| A_23_P134851 | 2.46E-04    | 6.42E-05  | 2.45       | DOK2        |
| A_23_P107351 | 1.34E-04    | 3.03E-05  | -3.31      | NLRP1       |
| A_24_P13381  | 1.16E-03    | 4.21E-04  | 2.51       | TRPV4       |
| A_23_P59426  | 8.87E-04    | 3.07E-04  | -1.72      | PAXIP1      |
| A_24_P935026 | 1.51E-04    | 3.52E-05  | -2.95      | STK4        |
| A_32_P342064 | 1.14E-04    | 2.49E-05  | -5.33      | FTH1        |
| A_23_P8281   | 1.14E-05    | 8.08E-07  | -2.52      | IFNGR1      |
| A_23_P55273  | 7.32E-04    | 2.45E-04  | 4.97       | SBNO2       |
| A_23_P348636 | 1.25E-02    | 6.55E-03  | 1.76       | FOXJ1       |
| A_23_P140648 | 2.81E-04    | 7.69E-05  | -2.03      | CYFIP1      |
| Gene Symbol | Log2 Fold Change | p-value | Description |
|-------------|------------------|---------|-------------|
| LAMP3       | 4.68E-02         | 3.00E-02| -2.01       |
| COL3A1      | 4.70E-05         | 7.65E-06| 3.34        |
| GATA1       | 5.91E-03         | 2.81E-03| 3.68        |
| HERC6       | 8.52E-03         | 4.25E-03| 6.15        |
| FADD        | 1.27E-02         | 6.68E-03| 4.10        |
| YWHAZ       | 4.00E-05         | 6.02E-06| -2.22       |
| PSMA6       | 5.11E-05         | 8.59E-06| -4.01       |
| HIST1H2BK   | 8.65E-04         | 2.97E-04| -2.52       |
| POLR3C      | 9.04E-03         | 3.14E-04| 2.94        |
| LAX1        | 5.91E-03         | 2.81E-03| 3.34        |
| KIF3C       | 1.29E-04         | 2.90E-05| -3.24       |
| TGFBR2      | 9.15E-04         | 3.19E-04| -2.06       |
| MYLPF       | 9.52E-04         | 3.35E-04| 2.60        |
| SLC11A1     | 2.76E-02         | 1.62E-02| -1.87       |
| BCR         | 2.11E-04         | 5.27E-05| -4.01       |
| PLD2        | 5.55E-04         | 1.78E-04| 2.06        |
| DEFB118     | 2.54E-04         | 6.72E-05| 4.16        |
| GOLPH3      | 1.21E-04         | 2.69E-05| -2.81       |
| IFIT1       | 1.44E-05         | 1.20E-06| -3.18       |
| PPP3CA      | 2.51E-05         | 3.06E-06| -3.53       |
| FARPA       | 1.64E-04         | 3.90E-05| 2.62        |
| OLR1        | 2.72E-03         | 1.16E-03| -1.83       |
| MRGPRX4     | 1.34E-02         | 7.10E-03| -2.35       |
| SPTA1       | 1.75E-02         | 9.71E-03| 4.71        |
| ZFPM1       | 1.03E-03         | 3.70E-04| -3.95       |
| CDC42       | 3.61E-05         | 5.25E-06| -2.76       |
| DCTN2       | 1.08E-05         | 7.32E-07| -2.35       |
| UBA52       | 1.44E-05         | 1.22E-06| -3.50       |
| PSMA6       | 9.05E-05         | 1.86E-05| -1.93       |
| HSP90B1     | 2.36E-05         | 2.71E-06| -3.43       |
| BTN3A1      | 5.10E-05         | 8.54E-06| 3.19        |
| SPTB        | 3.08E-05         | 4.10E-06| 1.78        |
| THPO        | 8.52E-05         | 1.71E-05| 12.88       |
| HLA-DOA     | 6.19E-04         | 2.00E-04| 3.75        |
| SPG21       | 1.26E-06         | 9.54E-09| -2.53       |
| A2M         | 4.12E-04         | 1.23E-04| -2.89       |
| ILF2        | 2.46E-05         | 2.92E-06| -2.91       |
| SLAMF6      | 1.91E-04         | 4.66E-05| 3.97        |
| CXCR5       | 2.32E-03         | 9.56E-04| 5.95        |
| TYK2        | 2.45E-03         | 1.02E-03| 3.44        |
| RIPK2       | 4.59E-06         | 1.45E-07| -2.22       |
| NLRC5       | 3.50E-02         | 2.13E-02| -2.21       |
| VAV1        | 8.64E-03         | 4.33E-03| 2.12        |
| PSMA6       | 7.62E-06         | 3.57E-07| -3.50       |
| MSH6        | 3.40E-06         | 7.88E-08| -1.88       |
| ISG15       | 1.44E-03         | 5.44E-04| -1.88       |
| CD27        | 3.02E-04         | 8.42E-05| -2.52       |
| PLA2G2D     | 1.10E-03         | 3.99E-04| 2.29        |
| HCST        | 1.41E-03         | 5.29E-04| -2.61       |
| Gene ID   | Log2 Fold Change | p Value | Adjusted p Value | Gene Name |
|----------|-----------------|---------|------------------|-----------|
| A_23_P219060 | 1.65E-02 | 9.04E-03 | -2.23 | GPSM3 |
| A_23_P356684 | 5.29E-06 | 1.73E-07 | -3.51 | ANLN |
| A_32_P111565 | 1.43E-05 | 1.19E-06 | -3.02 | FTH1 |
| A_32_P880454 | 3.26E-05 | 4.50E-06 | -4.18 | APLF |
| A_23_P162866 | 4.21E-06 | 1.27E-07 | -3.31 | HSP90AA1 |
| A_32_P24581 | 6.58E-04 | 2.17E-04 | 2.03 | PDGFB |
| A_23_P137806 | 3.88E-03 | 1.73E-03 | -2.61 | MPL |
| A_23_P118544 | 3.49E-05 | 5.01E-06 | -3.90 | CLTC |
| A_32_P199252 | 4.45E-04 | 1.36E-04 | -3.43 | HSP90AA1 |
| A_23_P339944 | 6.58E-04 | 2.17E-04 | 2.03 | PDGFB |
| A_23_P171074 | 5.31E-05 | 5.07E-06 | -4.27 | ITM2A |
| A_23_P127842 | 3.53E-06 | 8.79E-08 | -5.02 | RARA |
| A_23_P103398 | 2.24E-04 | 5.69E-05 | -2.65 | PSEN2 |
| A_23_P1119943 | 4.74E-04 | 1.48E-04 | -2.56 | IGFBP2 |
| A_24_P141332 | 6.61E-05 | 1.21E-05 | -2.87 | CAMK2G |
| A_32_P175198 | 1.57E-04 | 3.69E-05 | -3.25 | ACTG1 |
| A_24_P275984 | 1.87E-03 | 7.41E-04 | 7.87 | ZNF616 |
| A_23_P138635 | 2.48E-05 | 2.98E-06 | -5.72 | BNIP3 |
| A_23_P88201 | 2.15E-06 | 3.18E-08 | -2.69 | PPP2R3C |
| A_23_P133245 | 7.74E-06 | 3.70E-07 | -2.10 | IK |
| A_24_P311917 | 6.56E-04 | 2.16E-04 | 2.28 | BTN3A3 |
| A_23_P256473 | 3.12E-04 | 8.76E-05 | -2.41 | SEMA3C |
| A_24_P63019 | 2.60E-03 | 1.09E-03 | 4.54 | IL1R2 |
| A_23_P210100 | 4.29E-05 | 6.66E-06 | -2.64 | CYP26B1 |
| A_23_P502174 | 3.28E-05 | 4.56E-06 | -3.57 | DYNC2L1 |
| A_23_P79732 | 1.35E-04 | 3.06E-05 | -5.38 | RPS27A |
| A_23_P38894 | 2.19E-05 | 2.36E-06 | -2.43 | C19orf66 |
| A_23_P163814 | 3.35E-04 | 9.50E-05 | -3.83 | ATXN1L |
| A_23_P20814 | 6.17E-04 | 2.00E-04 | 1.61 | DDX58 |
| A_24_P340679 | 9.05E-06 | 5.55E-07 | -3.65 | PPIA |
| A_23_P35970 | 2.68E-04 | 7.24E-05 | -1.67 | SLC37A4 |
| A_23_P389919 | 1.44E-02 | 7.76E-03 | -1.81 | WHSC1 |
| A_24_P82106 | 5.89E-04 | 1.89E-04 | 4.73 | MMP14 |
| A_23_P367995 | 7.57E-03 | 3.72E-03 | 3.52 | PSM8 |
| A_23_P146922 | 1.43E-02 | 7.72E-03 | 1.94 | GAS6 |
| A_23_P22444 | 2.55E-02 | 1.48E-02 | 1.68 | CFP |
| A_23_P22378 | 1.33E-04 | 3.01E-05 | 2.96 | SOX11 |
| A_23_P115223 | 1.81E-05 | 1.82E-06 | -3.07 | HAX1 |
| A_24_P373976 | 3.14E-04 | 8.84E-05 | 14.21 | SDC4 |
| A_23_P99771 | 7.53E-05 | 1.44E-05 | -3.81 | PNMA1 |
| A_24_P166431 | 1.71E-03 | 6.72E-04 | -2.70 | TRIM10 |
| A_24_P216165 | 2.09E-04 | 5.23E-05 | -4.75 | CEBPA |
| A_23_P10815 | 9.43E-06 | 6.09E-07 | -3.60 | PUM1 |
| A_32_P186921 | 3.29E-05 | 4.59E-06 | -1.98 | ZNF616 |
| A_23_P29993 | 1.71E-05 | 1.68E-06 | -11.09 | IL15 |
| A_23_P218369 | 2.87E-06 | 5.47E-08 | 7.86 | CCL15 |
| A_24_P154037 | 1.41E-05 | 1.16E-06 | -2.23 | IRS2 |
| Gene Symbol | Standardized T-value | Fold Change | Regulation |
|------------|---------------------|-------------|------------|
| CREB1      | 4.12E-04            | 1.23E-04    | 9.19       |
| PRR5       | 9.50E-05            | 1.97E-05    | -3.61      |
| PRKD1      | 2.56E-04            | 6.84E-05    | -2.34      |
| UBQLN1     | 1.09E-03            | 3.95E-04    | -2.10      |
| TGFBR2     | 1.26E-06            | 8.32E-09    | 1.92       |
| LST1       | 1.78E-02            | 9.88E-03    | 1.90       |
| HDAC9      | 1.57E-02            | 8.56E-03    | -3.41      |
| PPI1       | 1.68E-05            | 1.62E-06    | 1.91       |
| C12orf29   | 4.41E-05            | 6.93E-05    | -4.23      |
| PRR5       | 1.78E-02            | 9.88E-03    | 1.90       |
| PRKD1      | 2.34E-03            | 9.62E-04    | -2.29      |
| CD6        | 4.33E-02            | 2.72E-02    | -1.86      |
| CD177      | 1.79E-02            | 9.96E-03    | -4.14      |
| ACTB       | 2.70E-06            | 4.61E-08    | -2.25      |
| ARHGEF7    | 6.99E-04            | 2.33E-04    | -2.35      |
| RAB10      | 2.49E-05            | 2.99E-06    | -2.47      |
| ADAM9      | 6.14E-03            | 8.67E-06    | -3.73      |
| PSMB4      | 8.40E-06            | 4.55E-07    | -4.94      |
| SOCS6      | 4.85E-02            | 3.12E-02    | -2.55      |
| JARID2     | 6.14E-05            | 1.10E-05    | -1.87      |
| ERAP1      | 1.01E-04            | 2.12E-05    | 4.13       |
| SIVA1      | 1.52E-05            | 1.36E-06    | -2.75      |
| TCF12      | 9.09E-03            | 4.58E-03    | -2.13      |
| RILP       | 8.42E-05            | 1.67E-05    | -3.00      |
| AP1S2      | 6.57E-05            | 1.19E-05    | -2.36      |
| HLA-DPA1   | 1.65E-05            | 1.56E-06    | -2.93      |
| ARF1       | 8.89E-06            | 5.32E-07    | -3.28      |
| PREX1      | 6.00E-06            | 2.20E-07    | -1.89      |
| AXIN1      | 6.21E-04            | 2.01E-04    | 2.78       |
| PSMD5      | 5.55E-04            | 1.78E-04    | -2.48      |
| SPTB       | 1.34E-03            | 4.98E-04    | -3.06      |
| TPD52      | 2.25E-05            | 2.50E-06    | -3.74      |
| CCL24      | 6.56E-03            | 3.17E-03    | -3.02      |
| UBA52      | 3.35E-05            | 4.76E-06    | -3.73      |
| PSMD10     | 1.96E-06            | 2.30E-08    | -3.92      |
| APOBEC3D   | 2.28E-05            | 2.54E-06    | 3.36       |
| LAM1P1     | 1.93E-04            | 4.73E-05    | -3.16      |
| RPL22      | 9.85E-05            | 2.06E-05    | -2.28      |
| RNF41      | 3.40E-03            | 1.49E-03    | -2.63      |
| CRHR1      | 4.28E-04            | 1.29E-04    | -3.28      |
| PRKACA     | 5.08E-04            | 1.60E-04    | -2.14      |
| PTMS       | 7.06E-06            | 2.89E-07    | -5.82      |
| PTPRO      | 1.31E-05            | 1.04E-06    | -3.76      |
| SHMT2      | 2.34E-02            | 1.35E-02    | 1.84       |
| KRAS       | 9.83E-06            | 6.42E-07    | -3.10      |
| IFI6       | 2.14E-03            | 8.63E-04    | -2.03      |
| ATP6V1H    | 6.90E-05            | 1.28E-05    | -2.98      |
| HIST1H2BC  | 3.29E-03            | 1.43E-03    | 2.02       |
| BNIP3L     | 1.33E-05            | 1.07E-06    | -2.45      |
| REL        | 2.16E-02            | 1.24E-02    | 2.57       |
| Gene ID   | Expression 1 | Expression 2 | Fold Change | Gene Name |
|----------|--------------|--------------|-------------|-----------|
| A_23_P501538 | 7.30E-06     | 3.22E-07     | 1.97        | HOXA3     |
| A_23_P69493  | 3.88E-06     | 1.11E-07     | -3.42       | RHOA      |
| A_24_P39759  | 1.41E-05     | 1.17E-06     | 1.64        | RNF135    |
| A_24_P277456 | 1.02E-04     | 2.17E-05     | -3.50       | UBE2K     |
| A_24_P935437 | 4.77E-05     | 7.81E-06     | 1.92        | MBP       |
| A_23_P2097   | 5.73E-04     | 1.84E-04     | -1.79       | TRIM68    |
| A_23_P256561 | 2.05E-04     | 5.13E-05     | 1.64        | TLR6      |
| A_23_P207940 | 5.57E-05     | 9.61E-06     | -1.79       | PTPN2     |

In bold are highlighted candidate genes already known to contribute to ALS susceptibility.
*Gene expression fold-changes are given on a linear scale.*
**Supplementary Table 5. Neuroinflammatory genes differentially expressed in SALS1 and SALS2.**

| Probe ID   | p Value (Corr) | p Value | Fold Change (SALS1/CTRL)* | Fold Change (SALS2/CTRL)* | GENE_SYMBOL |
|------------|----------------|---------|---------------------------|---------------------------|-------------|
| A_23_P89249 | 7.67E-04       | 2.59E-04| 1.99                      | 1.6245594                 | ERBB2       |
| A_23_P309739 | 2.75E-02       | 1.61E-02| -1.46                     | -1.5552287                | ESR1        |
| A_23_P70095 | 1.39E-02       | 7.41E-03| 1.69                      | 2.1040883                 | CD74        |
| A_23_P101992 | 3.31E-02       | 1.99E-02| 2.44                      | 2.9789243                 | MARCO       |
| A_23_P103361 | 1.17E-02       | 6.08E-03| -1.48                     | -1.6601439                | LCK         |
| A_24_P943283 | 1.43E-03       | 5.37E-04| -1.64                     | -2.3417015                | DENND1B     |
| A_24_P254079 | 6.81E-03       | 3.31E-03| 2.10                      | 2.963726                  | ICAM5       |
| A_23_P81912 | 1.39E-02       | 7.41E-03| 1.69                      | 2.1040883                 | ERBB2       |
| A_23_P151294 | 8.17E-03       | 4.15E-04| 1.64                      | -1.6825967                | BRAF        |
| A_23_P140916 | 4.24E-06       | 1.30E-07| 2.17                      | -2.0372417                | GLG1        |
| A_23_P29994 | 8.12E-02       | 4.08E-07| 2.08                      | -2.1532817                | RBPJ        |
| A_24_P42935 | 1.17E-02       | 6.08E-03| 2.10                      | -2.1532817                | TUBB        |
| A_32_P120977 | 8.16E-06       | 1.5E-07 | 1.64                      | -1.6825967                | PRELID1     |
| A_23_P121253 | 1.57E-02       | 8.57E-03| -1.40                     | -1.5319853                | TNFSF10     |
| A_23_P113716 | 7.07E-06       | 2.91E-07| 2.11                      | -2.3847184                | HLA-C       |
| A_23_P130815 | 3.40E-03       | 1.49E-03| -1.84                     | -1.9945887                | KIR2DS2     |
| A_24_P276853 | 1.29E-02       | 4.79E-04| 2.01                      | 2.162412                  | GON4L       |
| A_24_P252078 | 1.81E-02       | 1.01E-02| 1.63                      | 1.7563841                 | BTN3A2      |
| A_24_P766716 | 2.55E-02       | 1.48E-02| 1.72                      | 1.8776253                 | CMKL1R1     |
| A_23_P207582 | 7.09E-06       | 2.99E-07| -3.23                     | 3.2294095                 | CCL16       |
| A_24_P103469 | 4.54E-03       | 2.08E-03| 1.98                      | 2.8276353                 | LST1        |
| A_32_P232865 | 6.76E-03       | 3.28E-03| 3.14                      | 3.7766464                 | BCR         |
| A_23_P25644  | 6.68E-07       | 8.25E-10| 1.69                      | -2.291853                 | PCID2       |
| A_23_P79161  | 3.88E-06       | 1.11E-07| 1.54                      | -1.6402473                | PRELID1     |
| A_23_P56195  | 6.68E-07       | 1.26E-09| 1.58                      | -2.210804                 | UBA52       |
| A_23_P203053 | 2.04E-03       | 8.20E-04| 1.70                      | 2.2072346                 | NCAM1       |
| A_23_P30122  | 4.59E-06       | 1.48E-07| -1.83                     | 2.1090114                 | IL2         |
| A_23_P169331 | 1.37E-02       | 7.28E-03| 1.78                      | 1.5586059                 | TRAF2       |
| A_24_P222655 | 1.03E-02       | 5.29E-03| 2.90                      | 2.3396752                 | C1QA        |
| A_32_P217709 | 4.24E-06       | 1.29E-07| 2.37                      | -2.239976                 | RAC1        |
| A_23_P38346  | 8.68E-06       | 4.99E-07| 1.98                      | -2.0749657                | DDX58       |
| A_23_P31921  | 4.35E-03       | 1.98E-03| 2.69                      | 3.2652416                 | ASS1        |
| A_23_P142380 | 6.68E-07       | 9.44E-10| 1.79                      | -1.8057177                | AKAP8       |
| A_23_P136325 | 6.22E-03       | 2.98E-03| 1.62                      | 2.1003823                 | WIPF2       |
| A_32_P67533  | 6.00E-06       | 2.15E-07| 1.40                      | -1.482858                 | L3MBTL3     |
| A_23_P71268  | 1.55E-03       | 5.97E-04| 2.25                      | 3.2261822                 | AZGP1       |
| A_24_P184031 | 8.21E-06       | 4.26E-07| 2.08                      | -2.0806754                | PHPT1       |
| A_23_P350991 | 5.39E-03       | 2.53E-03| 1.73                      | 1.6670423                 | SMAD3       |
| A_23_P59005  | 1.64E-06       | 1.41E-08| 2.05                      | -2.0266466                | TAP1        |
| A_24_P337592 | 9.84E-03       | 5.01E-03| 1.61                      | 1.8112911                 | BTN2A2      |
| A_23_P115460 | 1.01E-06       | 4.08E-09| 1.75                      | -1.9200194                | RPL22       |
| A_32_P9700   | 2.37E-06       | 3.82E-08| 1.94                      | -2.1930177                | PSMC1       |
| A_23_P171249 | 1.67E-06       | 1.69E-08| 1.98                      | -1.8409251                | IGBP1       |
| A_23_P17560  | 6.07E-03       | 2.90E-03| 3.32                      | 6.287112                  | KIF3B       |
| A_24_P346277 | 7.30E-06       | 3.15E-07| 1.93                      | -2.093793                 | SRF         |
| A_24_P8892   | 4.59E-06       | 1.46E-07| 1.75                      | -1.7740107                | HDAC4       |
| A_23_P119562 | 1.15E-02       | 5.97E-03| 2.46                      | 1.9826583                 | CFD         |
| Gene symbol | log2FoldChange | p-value | q-value | geneM | description |
|-------------|----------------|---------|---------|-------|-------------|
| PSME1       | 1.26E-06       | 7.59E-09| 2.42    | -1.9032911 | A_23_P151610 |
| FKBP1B      | 1.60E-06       | 1.72E-02| 2.53    | 2.2931263  | A_24_P402222 |
| GALNT2      | 4.32E-04       | 1.31E-04| 2.05    | 1.7299206  | A_24_P353794 |
| BDKRB1      | 2.73E-02       | 1.60E-02| -2.15   | -2.1131637 | A_23_P128744 |
| SLC25A6     | 7.09E-06       | 2.98E-07| 2.12    | -2.0164661 | A_24_P682285 |
| HSPA1A      | 6.08E-05       | 1.08E-05| 3.53    | 1.874959  | A_24_P226554 |
| ACTB        | 8.64E-03       | 8.86E-08| 2.64    | -2.288506  | A_23_P211985 |
| SNRK        | 8.64E-03       | 4.33E-03| 1.87    | 2.0685003  | A_24_P022000 |
| MEIS2       | 4.59E-03       | 2.11E-03| -2.14   | -2.749359  | A_24_P472055 |
| RNF125      | 8.92E-03       | 4.48E-03| -1.99   | -2.1929023 | A_23_P166371 |
| PAX5        | 1.24E-02       | 6.50E-03| 1.59    | 1.8813595  | A_24_P822000 |
| FOXJ1       | 8.64E-03       | 4.33E-03| 1.66    | 2.119077   | A_23_P38959  |
| VAV1        | 3.02E-04       | 8.42E-05| -1.64   | -2.5189831 | A_23_P48088  |
| CD27        | 7.74E-06       | 3.70E-07| 1.99    | -2.1024985 | A_23_P133245 |
| IK          | 2.09E-04       | 5.23E-05| -2.49   | -4.746586  | A_24_P216165 |
| CEBPA       | 3.29E-05       | 4.59E-06| -1.42   | -1.9837334 | A_32_P186921 |
| ZNF616      | 1.26E-06       | 8.32E-09| -1.75   | 1.9213755  | A_23_P337242 |
| TGFBR2      | 1.78E-02       | 9.88E-03| 1.88    | 1.896965   | A_24_P94916  |
| LST1        | 2.70E-06       | 4.61E-08| 2.60    | -2.473917  | A_23_P31323  |
| ACTB        | 6.00E-06       | 2.20E-07| 1.78    | -1.890054  | A_23_P43641  |
| PREX1       | 2.34E-02       | 1.35E-02| 1.75    | 1.8354497  | A_23_P158239 |
| SHMT2       | 7.30E-06       | 3.22E-07| -2.04   | 1.9682595  | A_23_P501538 |

*Gene expression fold-changes are given on a linear scale.
### Supplementary Table 6. List of genes included in the SALS1-related PPI network.

| Degree | Node | Gene name |
|--------|------|-----------|
| 157    | UBC  | ubiquitin C |
| 84     | TPS3 | tumor protein p53 |
| 79     | AKT1 | v-akt murine thymoma viral oncogene homolog 1 |
| 66     | MYC  | v-myc myelocytomatosis viral oncogene homolog (avian) |
| 64     | CCND1| cyclin D1 |
| 63     | HSPA8| heat shock protein 90kDa alpha (cytosolic), class A member 1 |
| 62     | JUN  | jun proto-oncogene |
| 61     | EGFR | epidermal growth factor receptor |
| 56     | FO5  | FBJ murine osteosarcoma viral oncogene homolog |
| 56     | MAPK14| mitogen-activated protein kinase 14 |
| 54     | RAC1 | ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) |
| 49     | RHOA | ras homolog family member A |
| 47     | MAPK1| mitogen-activated protein kinase 1 |
| 47     | PIK3R3| phosphoinositide-3-kinase, regulatory subunit 1 (alpha) |
| 46     | MAPK8| mitogen-activated protein kinase 8 |
| 45     | NFkB1| nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 |
| 45     | CTNNB1| catenin (cadherin-associated protein), beta 1, 88kDa |
| 45     | PTEN | protein tyrosine phosphatase, non-receptor type 11 |
| 44     | EP300| E1A binding protein p300 |
| 44     | CREBBP| CREB binding protein |
| 43     | HRAS | v-Ha-ras Harvey rat sarcoma viral oncogene homolog |
| 43     | UBB  | ubiquitin B |
| 43     | EP300| E1A binding protein p300 |
| 41     | ESR2 | erb-2 erythroblast leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian) |
| 40     | MTOR | mechanistic target of rapamycin (serine/threonine kinase) |
| 40     | AR   | androgen receptor |
| 39     | RELA | v-rel reticuloendotheliosis viral oncogene homolog A (avian) |
| 39     | VEGFA| vascular endothelial growth factor A |
| 39     | UBA52| ubiquitin A-52 residue ribosomal protein fusion product 1 |
| 38     | CHD1 | cadherin 1, type 1, E-cadherin (epithelial) |
| 38     | GRB2 | growth factor receptor-bound protein 2 |
| 37     | HIF1A| hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) |
| 36     | CREB1| cAMP responsive element binding protein 1 |
| 36     | CD44 | CD44 molecule (Indian blood group) |
| 35     | NOTCH1| notch 1 |
| 34     | CDKN1B| cyclin-dependent kinase inhibitor 1B (p27, Kip1) |
| 34     | SMAD3| SMAD family member 3 |
| 33     | JAK2 | Janus kinase 2 |
| 33     | NRAS | neuroblastoma RAS viral (v-ras) oncogene homolog |
| 33     | CDC42| cell division cycle 42 (GTP binding protein, 25kDa) |
| 33     | PTK2 | protein tyrosine kinase 2 |
| 32     | NOTCH1| notch 1 |
| 32     | BCL2L1| BCL2-like 1 |
| 32     | Kras | v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog |
| 32     | LYK5 | v-yes-1 Yamaguchi sarcoma viral oncogene homolog |
| 30     | HSPA8| heat shock 70kDa protein 8 |
| 30     | CDK6 | cyclin-dependent kinase inhibitor 1B (p27, Kip1) |
| 30     | SMAD3| SMAD family member 3 |
| 29     | JAK1 | Janus kinase 1 |
| 29     | CREB1| cAMP responsive element binding protein 1 |
| 29     | CD44 | CD44 molecule (Indian blood group) |
| 28     | PLK1 | polo-like kinase 1 |
| 28     | HDAC9| histone deacetylase 9 |
| 27     | KIT  | v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog |
| 27     | CXCL12| chemokine (C-X-C motif) ligand 12 |
| 27     | APP  | amyloid beta (A4) precursor protein |
| 27     | ACTB | actin, beta |
| 26     | MAPK11| mitogen-activated protein kinase 11 |
| 25     | EZR  | ezrin |
| 25     | NOS3 | nitric oxide synthase 3 (endothelial cell) |
| 24     | GAPDH| glyceraldehyde-3-phosphate dehydrogenase |
| 24     | SUMO1| SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae) |
| 24     | TLR4 | toll-like receptor 4 |
| 24     | HLA-DRB1| major histocompatibility complex, class II, DR beta 1 |
| 23     | IKKβ | inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta |
| 22     | F2   | coagulation factor II (thrombin) |
| 21     | JAK3 | Janus kinase 3 |
| 21     | PML  | promyelocytic leukemia |
| 20     | MAPK10| mitogen-activated protein kinase 10 |
|   | Gene Symbol | Gene Name                                      |
|---|-------------|-----------------------------------------------|
|20 | ALB         | albumin                                       |
|19 | BIRC5       | baculoviral IAP repeat containing 5           |
|19 | BCR         | breakpoint cluster region                     |
|19 | CDK4        | cyclin-dependent kinase 4                     |
|19 | PSMAD4      | proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 |
|18 | NCAM1       | neural cell adhesion molecule 1               |
|18 | PSMC5       | proteasome (prosome, macropain) 26S subunit, ATPase, 5 |
|17 | INSR        | insulin receptor                              |
|17 | CCND3       | cyclin D3                                     |
|17 | SMARCA4     | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 |
|16 | TRAF2       | TNF receptor-associated factor 2              |
|16 | HLA-A       | major histocompatibility complex, class I, A |
|16 | PSMID13     | proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 |
|16 | PSMID11     | proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 |
|16 | PSMID9      | proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 |
|16 | PSMID3      | proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 |
|16 | ACTN1       | actinin, alpha 1                              |
|16 | PSMC3       | proteasome (prosome, macropain) 26S subunit, ATPase, 3 |
|16 | TSPO        | translocator protein (18kDa)                 |
|16 | DNMT2       | dynamin 2                                     |
|16 | PSMC1       | proteasome (prosome, macropain) 26S subunit, ATPase, 1 |
|16 | PSMF1       | proteasome (prosome, macropain) inhibitor subunit 1 (PI31) |
|16 | PSMD1       | proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 |
|15 | CLU         | clusterin                                     |
|15 | HLA-C       | major histocompatibility complex, class I, C |
|15 | MYH14       | myosin, heavy chain 14, non-muscle            |
|15 | HLA-B       | major histocompatibility complex, class I, B |
|15 | SQSTM1      | sequestosome 1                                |
|14 | BECN1       | beclin 1, autophagy related                   |
|14 | OASL        | 2'-5'-oligoadenylate synthetase-like          |
|14 | OAS1        | 2'-5'-oligoadenylate synthetase 1, 40/46kDa  |
|14 | ANGPT2      | angiopeitin 2                                 |
|14 | TYK2        | tyrosine kinase 2                             |
|14 | BCL6        | B-cell CLL/lymphoma 6                        |
|13 | NFATC1      | nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 |
|13 | DECR1       | 2,4-dienoyl CoA reductase 1, mitochondrial   |
|13 | PARK2       | parkinson protein 2, E3 ubiquitin protein ligase (parkin) |
|13 | HSPA5       | heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) |
|13 | MSN         | moesin                                        |
|13 | ARNT        | aryl hydrocarbon receptor nuclear translocator |
|13 | CDC37       | cell division cycle 37 homolog (S. cerevisiae) |
|13 | NTRK1       | neurotrophic tyrosine kinase, receptor, type 1 |
|13 | DDX41       | DEAD (Asp-Glu-Ala-Asp) box polypeptide 41    |
|12 | PRDM10      | PR domain containing 10                      |
|12 | CD80        | CD80 molecule                                 |
|12 | TGFBR2      | transforming growth factor, beta receptor II (70/80kDa) |
|12 | BRAF        | v-raf murine sarcoma viral oncogene homolog B1 |
|12 | CYLD        | cylindromatosis (turban tumor syndrome)      |
|12 | ANXA2       | annexin A2                                   |
|12 | SLC3A2      | solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 |
|12 | PDIA3       | protein disulfide isomerase family A, member 3 |
|12 | TSC1        | tuberous sclerosis 1                         |
|12 | AP2M1       | adaptor-related protein complex 2, mu 1 subunit |
|12 | NCF2        | neutrophil cytosolic factor 2                |
| Degree | Node   | Gene name                                      |
|--------|--------|-----------------------------------------------|
| 326    | UBC    | ubiquitin C                                   |
| 131    | AKT1   | v-akt murine thymoma viral oncogene homolog 1 |
| 130    | TP53   | tumor protein p53                              |
| 105    | EGFR   | epidermal growth factor receptor               |
| 99     | RAC1   | ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) |
| 98     | STAT3  | signal transducer and activator of transcription 3 (acute-phase response factor) |
| 97     | MAPK1  | mitogen-activated protein kinase 1             |
| 95     | HSP90AB1 | heat shock protein 90kDa alpha (cytosolic), class A member 1 |
| 90     | JUN    | jun proto-oncogene                             |
| 89     | MYC    | v-myc myelocytomatosis viral oncogene homolog (avian) |
| 88     | CCND1  | cyclin D1                                     |
| 87     | UBB    | ubiquitin B                                   |
| 86     | RPS27A | ribosomal protein 527a                        |
| 81     | HRAS   | v-Ha-ras Harvey rat sarcoma viral oncogene homolog |
| 81     | UBAS2  | ubiquitin A-52 residue ribosomal protein fusion product 1 |
| 79     | MAPK14 | mitogen-activated protein kinase 14           |
| 78     | RHOD   | ras homolog family member A                   |
| 76     | CTNNB1 | catenin (cadherin-associated protein), beta 1, 88kDa |
| 76     | MAPK8  | mitogen-activated protein kinase 8            |
| 75     | PIK3R1 | phosphoinositide-3-kinase, regulatory subunit 1 (alpha) |
| 75     | MAPK3  | mitogen-activated protein kinase 3            |
| 74     | PTPN11 | protein tyrosine phosphatase, non-receptor type 11 |
| 74     | FOS    | FB1 murine osteosarcoma viral oncogene homolog |
| 72     | NFE2L1 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 |
| 70     | GRB2   | growth factor receptor-bound protein 2         |
| 69     | STAT1  | signal transducer and activator of transcription 1, 91kDa |
| 69     | ABL1   | c-abl oncogene 1, non-receptor tyrosine kinase |
| 69     | FYN    | FYN oncogene related to SRC, FGR, YES          |
| 68     | RELA   | v-rel reticuloendotheliosis viral oncogene homolog A (avian) |
| 68     | JAK2   | Janus kinase 2                                |
| 68     | CREBBP | CREB binding protein                          |
| 67     | CDC42  | cell division cycle 42 (GTP binding protein, 25kDa) |
| 67     | VEGFA  | vascular endothelial growth factor A           |
| 66     | EP300  | E1A binding protein p300                      |
| 66     | SOS1   | son of sevenless homolog 1 (Drosophila)       |
| 65     | HSP90A1 | heat shock protein 90kDa protein B            |
| 64     | SHC1   | SHC (Src homology 2 domain containing)         |
| 62     | AGT    | angiotensinogen (serpin peptidase inhibitor, clade A, member B) |
| 61     | PTX2   | PTX2 protein tyrosine kinase 2                |
| 61     | HSPIB  | heat shock 27kDa protein 1                     |
| 60     | CREB1  | cAMP responsive element binding protein 1      |
| 59     | PLCG1  | phospholipase C, gamma 1                      |
| 59     | AR     | androgen receptor                             |
| 58     | RAC3   | ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3) |
| 56     | CDH1   | cadherin 1, type 1, E-cadherin (epithelial)    |
| 56     | EGFR1  | early growth response 1                       |
| 56     | CENP1B | cyclin-dependent kinase inhibitor 1B (p27, Kip1) |
| 55     | NRR1   | neuroblastoma RAS viral (v-ras) oncogene homolog |
| 55     | PRKCA  | protein kinase C, alpha                       |
| 55     | RAF1   | v-raf-1 murine leukemia viral oncogene homolog 1 |
| 55     | HIF1A  | hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) |
| 53     | APP    | amyloid beta (A4) precursor protein            |
| 53     | JAK1   | Janus kinase 1                                |
| 53     | LYN    | v-yes-1 Yamaguchi sarcoma viral related oncogene homolog |
| 52     | ACTB   | actin, beta                                   |
| 52     | NOTCH1 | notch 1                                       |
| 51     | BTRC   | beta-transducin repeat containing E3 ubiquitin protein ligase |
| 51     | SMAD3  | SMAD family member 3                          |
| 51     | IGF1   | insulin-like growth factor 1 (somatomedin C)  |
| 50     | PRKCD  | protein kinase C, delta                       |
| 50     | SKP1   | S-phase kinase-associated protein 1            |
| 50     | MTOR   | mechanistic target of rapamycin (serine/threonine kinase) |
| 50     | NOS3   | nitric oxide synthase 3 (endothelial cell)     |
| 49     | CUL1   | cullin 1                                      |
| 48     | ERBB2  | v-erb-b2 erythroblastoid leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian) |
| 48     | KIT    | v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog |
| 47     | CAV1   | caveolin 1, caveolae protein, 22kDa           |
| 47     | PRKACA | protein kinase, cAMP-dependent, catalytic, alpha |
| 45     | IGF1R  | insulin-like growth factor 1 receptor         |
| 45     | PLK1   | polo-like kinase 1                            |
| 44     | CXCL12 | chemokine (C-X-C motif) ligand 12             |
| 44     | HSP90AB1 | heat shock protein 90kDa alpha (cytosolic), class B member 1 |
PXN  paxillin
NFKBIA nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
PDGFRB platelet-derived growth factor receptor, beta polypeptide
BCL2L1 BCL2-like 1
KRAS v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
PDGFB platelet-derived growth factor beta polypeptide
SMAD4 SMAD family member 4
MET met proto-oncogene (hepatocyte growth factor receptor)
YES1 v-yes-1 Yamaguchi sarcoma viral oncogene homolog
PSMA4 proteasome (prosome, macropain) subunit, alpha type, 4
PSMB1 proteasome (prosome, macropain) subunit, beta type, 1
PSMC2 proteasome (prosome, macropain) 26S subunit, ATPase, 2
RAC2 ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)
PSMD10 proteasome (prosome, macropain) 26S subunit, non-ATPase, 10
PSMD14 proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
PSMD3 proteasome (prosome, macropain) 26S subunit, non-ATPase, 3
MAPK11 mitogen-activated protein kinase 11
PSMC1 proteasome (prosome, macropain) 26S subunit, ATPase, 1
PSMD12 proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
PSMD6 proteasome (prosome, macropain) 26S subunit, non-ATPase, 6
PSMD1 proteasome (prosome, macropain) inhibitor subunit 1 (Pxi1)
F2 coagulation factor II (thrombin)
PSMA5 proteasome (prosome, macropain) subunit, alpha type, 5
PSMA6 proteasome (prosome, macropain) subunit, alpha type, 6
PSMD2 SMAD family member 2
PSMA1 proteasome (prosome, macropain) subunit, alpha type, 1
PSMB4 proteasome (prosome, macropain) subunit, beta type, 4
PSMB5 proteasome (prosome, macropain) subunit, beta type, 5
PSMB2 proteasome (prosome, macropain) subunit, beta type, 2
PSMB3 proteasome (prosome, macropain) subunit, beta type, 3
PSMC6 proteasome (prosome, macropain) 26S subunit, ATPase, 6
TLR4 toll-like receptor 4
PTK2B protein tyrosine kinase 2 beta
PSME3 proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)
PSMB6 proteasome (prosome, macropain) subunit, beta type, 6
PSMB7 proteasome (prosome, macropain) subunit, beta type, 7
ITG1 integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)
PSMD9 proteasome (prosome, macropain) 26S subunit, non-ATPase, 9
PSME4 proteasome (prosome, macropain) activator subunit 4
PRKCB protein kinase C, beta
CASP3 caspase 3, apoptosis-related cysteine peptidase
PRKACB protein kinase, cAMP-dependent, catalytic, beta
LNPEP leucyl/cystinyl aminopeptidase
PPARA peroxisome proliferator-activated receptor alpha
YWHAZ tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
JAK3 Janus kinase 3
PRKCZ protein kinase C, zeta
SUMO1 SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
GAPDH glyceraldehyde-3-phosphate dehydrogenase
GAB2 GRB2-associated binding protein 2
MMP2 matrix metalloptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)
HDAC9 histone deacetylase 9
INSR insulin receptor
AKT2 v-akt murine thymoma viral oncogene homolog 2
ARRB2 arrestin, beta 2
HSPA4 heat shock 70kDa protein 4
PLCB1 phospholipase C, beta 1 (phosphoinositide-specific)
B2M beta-2-microglobulin
FGR Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog
SMARCA4 SWI/SNF-related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
BCR breakpoint cluster region
TRA2 TFN receptor-associated factor 2
CEBPB CCAAT/enhancer binding protein (C/EBP), beta
PML promyelocytic leukemia
DKK4 cyclin-dependent kinase 4
MAP9 mitogen-activated protein kinase 9
HLA-C major histocompatibility complex, class I, C
VAV2 vav 2 guanine nucleotide exchange factor
PRKCE protein kinase C, epsilon
AZM alpha-2-macroglobulin
PDGFR alpha platelet-derived growth factor receptor, alpha polypeptide
NCA M1 neural cell adhesion molecule 1
ALB albumin
MYD88  myeloid differentiation primary response 88
KITLG  KIT ligand
SH3GL2  SH3-domain GRB2-like 2
PLD2  phospholipase D2
BAX  BCL2-associated X protein
dynamin 2
MAP3K5  mitogen-activated protein kinase kinase kinase 5
HMG1B  high mobility group box 1
HSPD1  heat shock 60kDa protein 1 (chaperonin)
PTMA2  proteasome (prosome, macropain) subunit, alpha, type 2
PTAFR  platelet-activating factor receptor
RET  ret proto-oncogene
AB1  abl-interactor 1
RPS6KA3  ribosomal protein S6 kinase, 90kDa, polypeptide 3
ITCH  itchy E3 ubiquitin protein ligase
calcium/calmodulin-dependent protein kinase II delta
IGF2  insulin-like growth factor 2 (somatomedin A)
SPTBN2  spectrin, beta, non-erythrocytic 2
TYK2  tyrosine kinase 2
ARHGFE7  Rho guanine nucleotide exchange factor (GEF) 7
IFNB1  interferon, beta 1, fibroblast
calcium/calmodulin-dependent protein kinase II gamma
SNCA  synuclein, alpha (non A4 component of amyloid precursor)
DECR1  2,4-dienoyl CoA reductase 1, mitochondrial
HSPA5  heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
MAPK13  mitogen-activated protein kinase 13
HS900B1  heat shock protein 90kDa beta (Grp94), member 1
MAP2K4  mitogen-activated protein kinase kinase 4
MITF  microphthalmia-associated transcription factor
SO2  son of sevenless homolog 2 (Drosophila)
ADRM1  adhesion regulating molecule 1
CALM1  calmodulin 1 (phosphorylase kinase, delta)
CD74  CD74 molecule, major histocompatibility complex, class II invariant chain
FGFR2  fibroblast growth factor receptor 2
PSEN1  presenilin 1
TSP1  translocator protein (18kDa)
DCTN1  dynactin 1
CSF1R  colony stimulating factor 1 receptor
SUMO2  SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae)
RPS6KA5  ribosomal protein S6 kinase, 90kDa, polypeptide 5
CANX  calnexin
RIPK1  receptor (TNFRSF)-interacting serine-threonine kinase 1
ZAP70  zeta-chain (TCR) associated protein kinase 70kDa
GNA5  GNAS complex locus
MYH14  myosin, heavy chain 14, non-muscle
OAS1  2'-5'-oligoadenylate synthetase 1, 40/46kDa
DYNL1  dynein, light chain, LCB-type 1
NCB1  neutrophil cytosolic factor 1
UBEZD2  ubiquitin-conjugating enzyme E2D 2
WWP1  WW domain containing E3 ubiquitin protein ligase 1
ACT3  ARP3 actin-related protein 3 homolog (yeast)
ITGA6  integrin, alpha 6
SIN3A  SIR3 transcription regulator homolog A (yeast)
syndecan 4
calreticulin
ACT1A  ARP1 actin-related protein 1 homolog A, centrinactin alpha (yeast)
PARP1  poly (ADP-ribose) polymerase 1
OASL  2'-5'-oligoadenylate synthetase-like
transforming growth factor, beta receptor II (70/80kDa)
OAS3  2'-5'-oligoadenylate synthetase 3, 100kDa
PARK2  parkinson protein 2, E3 ubiquitin protein ligase (parkin)
MAP7  mitogen-activated protein kinase 7
BRAF  v-raf murine sarcoma viral oncogene homolog B1
PAFAH1B1  platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)
STK11  serine/threonine kinase 11
ARPC2  actin related protein 2/3 complex, subunit 5, 16kDa
ARPC2  actin related protein 2/3 complex, subunit 2, 34kDa
ARPC3  actin related protein 2/3 complex, subunit 3, 21kDa
ITPR1  inositol 1,4,5-trisphosphate receptor, type 1
BECN1  beclin 1, autophagy related
TRAF3  TNF receptor-associated factor 3
EPAS1  endothelial PAS domain protein 1
PSEN2  presenilin 2 (Alzheimer disease 4)
DCTN2  dynactin 2 (p50)
CYP2P  cytoplasmic FMR1 interacting protein 2
NCKAP1  NCK-associated protein 1
HNRNPK  heterogeneous nuclear ribonucleoprotein K
RNF41  ring finger protein 41
SOX9  SRY (sex determining region Y)-box 9
KLL3  kallikrein-related peptidase 3
ATM  ataxia telangiectasia mutated
DYNCI2  dynein, cytoplasmic 1, intermediate chain 2
GBP2  guanylate binding protein 2, interferon-inducible
TFRC  transferrin receptor (p90, CD71)
DCTN3  dynactin 3 (p22)
APOE  apolipoprotein E
RARA  retinoic acid receptor, alpha
| Gene Symbol | Gene Name |
|-------------|-----------|
| RPS14       | ribosomal protein S14 |
| RPS19       | ribosomal protein S19 |
| GNRH1       | gonadotropin-releasing hormone 1 (luteinizing-releasing hormone) |
| RPS24       | ribosomal protein S24 |
| IFI6        | interferon, alpha-inducible protein 6 |
| ELMO1       | engulfment and cell motility 1 |
| EFNB2       | ephrin-B2 |
| FGF10       | fibroblast growth factor 10 |
| SLC3A2      | solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 |
| MX2         | myxovirus (influenza virus) resistance 2 (mouse) |
| SOD2        | superoxide dismutase 2, mitochondrial |
| SAR1B       | SAR1 homolog B (S. cerevisiae) |
| EPRS        | glutamyl-prolyl-tRNA synthetase |
| PLA2G6      | phospholipase A2, group VI (cytosolic, calcium-independent) |
| JAG1        | jagged 1 |
| DUSP3       | dual specificity phosphatase 3 |
| CLTA        | clathrin, light chain A |
| UBE203      | ubiquitin-conjugating enzyme E2D 3 |
| TICAM1      | toll-like receptor adaptor molecule 1 |
| OGT         | O-linked N-acetylglucosamine (GlcNAc) transferase |
| AP1G1       | adaptor-related protein complex 1, gamma 1 subunit |
| UBQLN1      | ubiquilin 1 |
| RPS17       | ribosomal protein S17 |
| FTH1        | ferritin, heavy polypeptide 1 |
| SEC31A      | SEC31 homolog A (S. cerevisiae) |
| GAL         | galanin/GMAP prepropeptide |
| SCARB1      | scavenger receptor class B, member 1 |
| THPO        | thrombopoietin |
| UBE2V1      | ubiquitin-conjugating enzyme E2 variant 1 |
| EPS8        | epidermal growth factor receptor pathway substrate 8 |
| API1S2      | adaptor-related protein complex 1, sigma 2 subunit |
| RICTOR      | RPTOR independent companion of MTOR, complex 2 |
| ADORA3      | adenosine A3 receptor |
| #     | Maps                                                                 | SALS1/CTRL+ | SALS2_CTRL |
|-------|----------------------------------------------------------------------|-------------|------------|
| 1     | Immune response_Classical complement pathway                          | 1.384E-17   | 1.082E-14  |
| 2     | Immune response_Role of FPR in stress-induced antiviral cell response | 8.973E-17   | 8.318E-15  |
| 3     | Immune response инвестиции complement pathway                         | 9.264E-14   | 9.264E-14  |
| 4     | Immune response_HMGBl/RAGE signaling pathway                          | 1.427E-15   | 1.203E-13  |
| 5     | SLE genetic marker-specific pathways in T cells                       | 2.990E-15   | 2.133E-13  |
| 6     | Oxidative stress_Activation of NADPH oxidase                         | 3.036E-15   | 2.133E-13  |
| 7     | PDE4 regulation of cyto/chemokine expression in inflammatory skin diseases | 3.221E-15  | 2.133E-13  |
| 8     | Immune response_B cell antigen receptor (BCR) pathway                 | 8.304E-15   | 5.132E-13  |
| 9     | Development_VEGF signaling via VEGFR2 - generic cascades             | 2.129E-14   | 2.129E-14  |
| 10    | Immune response_Antigen presentation by MHC class I, classical pathway | 2.835E-14   | 1.546E-12  |
| 11    | Immune response_Platelet activating factor/ PAFR pathway signaling   | 4.701E-14   | 2.293E-12  |
| 12    | Immune response_T cell receptor signaling path                        | 4.701E-14   | 2.293E-12  |
| 13    | Development_EGFR signaling path                                       | 7.271E-14   | 3.120E-12  |
| 14    | Role of Tissue factor in cancer independent of coagulation proteinases signaling | 1.408E-13   | 1.408E-13  |
| 15    | Aberrant production of IL-2 and IL-17 in SLE T cells                   | 1.978E-13   | 7.978E-12  |
| 16    | Immune response_CD16 signaling in NK cells                            | 2.733E-12   | 1.056E-11  |
| 17    | Development_c-Kit ligand signaling pathway during hemopoiesis         | 7.479E-13   | 7.778E-13  |
| 18    | Immune response_IL-3 signaling via ERK and PI3K                      | 1.157E-12   | 4.117E-11  |
| 19    | Development_Cytokine-mediated regulation of megakaryopoiesis          | 1.199E-12   | 4.117E-11  |
| 20    | Immune response_ICOS signaling protein in T helper cell               | 1.722E-12   | 5.700E-11  |
| 21    | Signal transduction_Additional pathways of NF-kB activation (in the cytoplasm) | 1.873E-13   | 5.986E-11  |
| 22    | Immune response_CCL2 signaling                                        | 2.954E-12   | 8.557E-11  |
| 23    | Immune response_Role of DAP12 receptors in NK cells                   | 4.601E-12   | 4.601E-12  |
| 24    | Immune response_TLR2 and TLR4 signaling pathways                      | 1.078E-11   | 2.848E-10  |
| 25    | Immune response_IL-15 signaling                                       | 1.415E-11   | 3.451E-10  |
| 26    | Cell adhesion_Chemokines and adhesion                                 | 2.272E-11   | 5.137E-10  |
| 27    | SLE genetic marker-specific pathways in B cells                       | 2.272E-11   | 5.137E-10  |
| 28    | Immune response_IL-4 signaling pathway                                | 2.480E-11   | 5.473E-10  |
| 29    | Immune response_HSP60 and HSP70/TLR signaling pathway                 | 2.692E-11   | 5.802E-10  |
| 30    | Immune response_IL-18 signaling                                       | 3.571E-11   | 6.962E-10  |
| 31    | Apoptosis and survival_NSF/TrkA PI3K-mediated signaling               | 3.605E-11   | 6.962E-10  |
| 32    | Immune response_IL-5 signaling via PI3K, MAPK and NF-kB               | 3.605E-11   | 6.962E-10  |
| 33    | Cytoskeleton remodeling_Cytoskeleton remodeling                       | 3.888E-11   | 7.356E-10  |
| 34    | Development_Non-genomic action of Retinoic acid in cell differentiation | 4.070E-11   | 7.397E-10  |
| 35    | Immune response_P-3 epsilon RI pathway                                | 4.070E-11   | 7.397E-10  |
| 36    | Development_Adenosine A2B receptor signaling                          | 4.361E-11   | 7.774E-10  |
| 37    | Immune response_IL-6 signaling pathway via JAK/STAT                   | 4.751E-11   | 8.310E-10  |
| 38    | Development_PDGF signaling via STATs and NF-kB                       | 6.419E-11   | 1.102E-09  |
| 39    | Cytoskeleton remodeling_TGF, WNT and cytoskeletal remodeling           | 7.224E-11   | 1.218E-09  |
| 40    | Signal transduction_mTORC2 downstream signaling                       | 8.608E-11   | 1.425E-09  |

Supplementary Table 8. Pathway enrichment analyses on the list of statistically deregulated neuroinflammatory genes in SALS patients.
127 Th17 cells in CF
128 Immune response: Role of HMGBl in dendritic cell maturation and migration
129 B cell signaling in hematological malignancies
130 Signal transduction: PTMs in IL-17-induced CKS-dependent MAPK signaling pathways
131 Role of cell adhesion in vaso-occlusion in Sickle cell disease
132 Tissue Factor signaling in cancer via PAR1 and PAR2
133 Immune response: Bacterial infections in normal airways
134 Blood coagulation: GPVI-dependent platelet activation
135 Glucocorticoid-induced elevation of intraocular pressure as glaucoma risk factor
136 Development: EGF signaling via small GTPases
137 Immune response: Innate immune response to RNA viral infection
138 Development: Angiotensin signaling via PFK2
139 Nociception: Expression and role of Nociceptin in immune system
140 Influence of smoking on activation of EGF signaling in lung cancer cells
141 Development: GM-CSF signaling
142 Immune response: CIsa signaling
143 Immune response: Gastrin in inflammatory response
144 Apoptosis and survival: APRIL and BAFF signaling
145 Immune response: IFN alpha/beta signaling pathway
146 Immune response: TNF-R2 signaling pathways
147 Development: EPO-induced MAPK pathway
148 Signal transduction: PTMs in BAFF-induced signaling
149 Immune response: NFAT in immune response
150 Pacap (gfl B)
151 Role of B cells in SLE
152 Signal transduction: PTMs in IL-17-induced CKS-independent signaling pathways
153 Development: Role of IL-8 in angiogenesis
154 Muscle contraction: Regulation of eNOS activity in endothelial cells
155 Ovarian cancer (main signaling cascades)
156 NF-AT signaling in cardiac hypertrophy
157 Immune response: Oncostatin M signaling via MAPK in mouse cells
158 Immune response: T cell subsets: secreted signals
159 Development: Thyroid stimulating hormone binding
160 Apoptosis and survival: TNF-alpha-induced ROS-dependent Caspase-3 signaling
161 Immune response: Regulation of T cell function by CTLA-4
162 G protein signaling: RAC1 in cellular process
163 CRC12_cancer_2
164 Membrane-bound ESR1: interaction with G-proteins signaling
165 Neurophysiological process: Dynin-dynactin motor complex in axonal transport in neurons
166 Role of IL-23/ IL-17 pathogenic axis in psoriasis
167 Immune response: Neurotensin-induced activation of IL-8 in colonocytes
168 Immune response: Murine NGK2D signaling
169 Immune response: PIP3 signaling in B lymphocytes
| ID  | Description                                                                 | Value   |
|-----|-----------------------------------------------------------------------------|---------|
| 213 | Development, Melanocyte development and pigmentation                        | 4.315E-06 |
| 214 | Th17 cells in CF (mouse model)                                               | 4.315E-06 |
| 215 | Development, EPO-induced PI3K/AKT pathway and Ca2+ influx                    | 4.743E-06 |
| 216 | Chemotaxis, CCL16, CCL20, CXCL16- and CCL25-mediated cell migration         | 4.743E-06 |
| 217 | Development, Adenosine A2A receptor signaling                              | 4.743E-06 |
| 218 | Chemotaxis, CCL2-induced chemotaxis                                         | 4.779E-06 |
| 219 | Neuroprotective action of lithium                                            | 4.944E-06 |
| 220 | Apoptosis and survival, hTRIL signaling                                     | 5.610E-06 |
| 221 | Development, Ligand-independent activation of ESR1 and ESR2                | 6.303E-06 |
| 222 | Development, Transcription regulation of granulocyte development             | 6.399E-06 |
| 223 | Development, Angiotensin signaling via STATs                                | 6.399E-06 |
| 224 | Development, SDF-1 signaling in hematopoietic stem cell homing              | 6.545E-06 |
| 225 | Apoptosis and survival, Anti-apoptotic action of membrane-bound ESR1        | 6.645E-06 |
| 226 | Development, Gastrin in differentiation of the gastric mucosa               | 6.654E-06 |
| 227 | Some pathways of EMT in cancer cells                                        | 7.238E-06 |
| 228 | Regulation of lipid metabolism, Stimulation of Arachidonic acid production by ACM receptors | 7.334E-06 |
| 229 | Development, Regulation of cytoskeleton proteins in oligodendrocyte differentiation and myelination | 7.662E-06 |
| 230 | Immune response, PGE2 signaling in immune response                          | 8.299E-06 |
| 231 | Development, Adiponectin signaling                                         | 8.299E-06 |
| 232 | Cytoskeleton remodeling, ESR1 action on cytoskeleton remodeling and cell migration | 8.725E-06 |
| 233 | Transcription, Receptor-mediated HIF regulation                           | 9.002E-06 |
| 234 | Development, PACAP signaling in neural cells                                | 9.002E-06 |
| 235 | G-protein signaling, Regulation of p38 and JNK signaling mediated by G-proteins | 9.002E-06 |
| 236 | Immune response, Antiviral actions of Interferons                           | 9.272E-06 |
| 237 | Immune response, FGf gamma R-mediated phagocytosis in macrophages          | 1.083E-05 |
| 238 | PGF signaling in pancreatic cancer                                          | 1.083E-05 |
| 239 | Cell adhesion, Integrin inside-out signaling in T cells                     | 1.086E-05 |
| 240 | Signal transduction, PTMs in IL-17-induced CIKS-dependent NF-kB signaling and mRNA stabilization | 1.149E-05 |
| 241 | Immune response, Cytokine receptor-mediated modulation of effector T cell and NK cell functions | 1.180E-05 |
| 242 | Cell cycle, Influence of Ras and Rho proteins on G1/S Transition           | 1.180E-05 |
| 243 | Immune response, IL-17 signaling pathways                                     | 1.200E-05 |
| 244 | Apoptosis and survival, NGF activation of NF-kB                             | 1.205E-05 |
| 245 | Signal transduction, Erk Interactions: Inhibition of Erk                    | 1.246E-05 |
| 246 | Immune response, CXCR4 signaling via second messenger                       | 1.246E-05 |
| 247 | Immune response, JCB-induced phagocytosis via alpha-M/beta-2 integrin       | 1.489E-05 |
| 248 | Immune response, Immunological synapse formation                            | 1.568E-05 |
| 249 | Immune response, CD117 signaling in immune cell                            | 1.645E-05 |
| 250 | Development, Growth hormone signaling via STATs and PLC/IP3                 | 1.702E-05 |
| 251 | Immune response, C3a signaling                                              | 1.801E-05 |
| 252 | Immune response, IL-16 signaling pathway                                     | 1.872E-05 |
| 253 | Cell adhesion, Integrin inside-out signaling in neutrophils                 | 1.902E-05 |
| 254 | Cytoskeleton remodeling, Role of PDGFs in cell migration                    | 2.018E-05 |
| 255 | Development, Melanocyte development and pigmentation                        | 2.018E-05 |
Immune response_IL-4-responsive genes in type 2 immunity

Androgen receptor activation and downstream signaling in Prostate cancer

Immune response_Differentiation of natural regulatory T cells

Development_Adenosine A3 receptor signaling

Immune response_IL-22 signaling pathway

Development_G-CSF-induced myeloid differentiation

Immune response_Substance P-stimulated expression of proinflammatory cytokines via MAPKs

Development_MEMO1 and ACM4 activation of ERK

Development_ACM2 and ACM4 activation of ERK

Development_ACM2 and ACM4 activation of ERK

Development_ACM2 and ACM4 activation of ERK

Development_ACM2 and ACM4 activation of ERK

Immune response_IL-7 signaling in T lymphocytes

Development_Angiotensin signaling via beta-Arrestin

Development_ACM2 and ACM4 activation of ERK

Development_ACM2 and ACM4 activation of ERK

Development_ACM2 and ACM4 activation of ERK

Immune response_CD40 signaling

Signal transduction_mTORC1 upstream signaling

Immune response_HTR2A-induced activation of cPLA2

Hyaluronic acid_CD44 signaling in cancer

Cell adhesion_integrin outside-in signaling

Immune response_IL-7 signaling in T lymphocytes

Substance_P-mediated inflammation and pain in Sickle cell disease

Cell adhesion_integrin outside-out signaling

Development_Growth factors in regulation of oligodendrocyte precursor cell proliferation

Development_ERBB-family signaling

Immune response_Generation of memory CD4+ T cells

Development_Activation of Erk by ACM1, ACM3 and ACM5

Neurophysiological process_Constitutive and regulated NMDA receptor trafficking

Cytoskeleton remodeling_integrin outside-in signaling

Modulation of tumor response to cytotoxic T cells by hypoxia in tumors

TGF-beta-dependent CFTR expression

Immune response_CD40 signaling

G-protein signaling_N-RAS regulation pathway

Immune responseilla_L-1_0.jpg

Development_Role of HDAC and calcium/calmodulin-dependent kinase (CaMK) in proliferation

Development_Membrane-bound ESR1: Interaction with growth factors signaling

Immune responseILERK12 signaling pathway

Signal transduction, mTORC1 upstream signaling

Cell adhesion_Histamine H1 receptor signaling in the interruption of cell barrier integrity

Immune response_5TLP signaling

Immunoregulatory response_CD40 signaling

Immune response_CD40 signaling

Signal transduction_Erk1/2 signaling pathway

Immune response_TLR3 signaling

Translation_Regulation of Erk4F activity

Development_Role of HDAC and calcium/calmodulin-dependent kinase (CaMK) in control of skeletal myogenesis

Development_G-protein-mediated regulation of MAPK-ERK signaling

Immune response_TH1 and TH2 cell differentiation

G-protein signaling_N-RAS regulation pathway

Development_G-protein-mediated regulation of MAPK-ERK signaling

Immune response_TH1 and TH2 cell differentiation

G-protein signaling_N-RAS regulation pathway

Development_G-protein-mediated regulation of MAPK-ERK signaling

Immune response_TH1 and TH2 cell differentiation

G-protein signaling_N-RAS regulation pathway
| Pathway Description | Gene Symbol | Fold Change | Log2 Fold Change | p-value | Adjusted p-value |
|---------------------|-------------|-------------|-----------------|---------|-----------------|
| Development_S1P1 signaling pathway | | 1.745E-04 | 4.245E-04 | 1.936E-01 | 1.745E-04 |
| LRK2 and immune function in Parkinson’s disease | | 1.866E-04 | 2.280E-03 | 1.866E-04 | 2.830E-03 |
| Ligand-independent activation of Androgen receptor in Prostate Cancer | | 1.910E-04 | 4.634E-04 | 2.748E-04 | 9.100E-04 |
| Development_Activation of ERK by Kappa-type opioid receptor | | 1.989E-04 | 4.401E-04 | 5.494E-01 | 1.989E-04 |
| Development_Transactivation of PDGFR in non-neuronal cells by Dopamine D2 Receptor | | 1.989E-04 | 4.401E-04 | 1.850E-02 | 1.989E-04 |
| Cytoskeleton remodeling_Thyroliberin in cytoskeleton remodeling | | 2.137E-04 | 5.118E-04 | 3.537E-04 | 2.137E-04 |
| G-protein signaling_TC21 regulation pathway | | 2.137E-04 | 5.118E-04 | 4.742E-01 | 2.137E-04 |
| G-protein signaling_R-RAS regulation pathway | | 2.137E-04 | 5.118E-04 | 3.134E-01 | 2.137E-04 |
| Development_Activation of ERK by Alpha-1 adrenergic receptors | | 2.165E-04 | 5.140E-04 | 8.595E-01 | 2.165E-04 |
| Cell adhesion_Ephrin signaling | | 2.165E-04 | 5.140E-04 | 1.053E-01 | 2.165E-04 |
| Role of alpha-6/beta-4 integrins in carcinoma progression | | 2.165E-04 | 5.140E-04 | 2.669E-02 | 2.165E-04 |
| Development_G-protein alpha-12 signaling pathway | | 2.173E-04 | 5.140E-04 | 1.516E-02 | 2.173E-04 |
| Signal transduction_Cyclic AMP signaling | | 2.173E-04 | 5.140E-04 | 6.238E-01 | 2.173E-04 |
| Development_TGF-beta-dependent induction of EMT via SMADs | | 2.196E-04 | 5.292E-03 | 2.196E-04 | 9.216E-03 |
| Nociception_Nociceptin receptor signaling | | 2.227E-04 | 5.253E-01 | 4.347E-02 | 2.227E-04 |
| Translation_Translation regulation by Alpha-1 adrenergic receptors | | 2.463E-04 | 5.795E-01 | 3.904E-01 | 2.463E-04 |
| Putative pathways for stimulation of fat cell differentiation by Bisphenol A | | 2.596E-04 | 6.093E-01 | 4.656E-02 | 2.596E-04 |
| Putative pathways for stimulation of fat cell differentiation by Bisphenol A | | 2.596E-04 | 6.093E-01 | 4.656E-02 | 2.596E-04 |
| High shear stress-induced platelet activation | | 2.667E-04 | 6.150E-04 | 1.066E-01 | 2.667E-04 |
| Chemotaxis_Lipoxin inhibitory action on Formyl-Met-Leu-Phe-induced neutrophil chemotaxis | | 2.667E-04 | 6.150E-04 | 5.920E-03 | 2.418E-02 |
| Development_Angiotensin inhibitory action on Formyl-Met-Leu-Phe-induced neutrophil chemotaxis | | 2.667E-04 | 6.150E-04 | 4.442E-01 | 2.667E-04 |
| Neurophysiological process_ACM regulation of nerve impulse | | 2.667E-04 | 6.150E-04 | 6.939E-01 | 2.667E-04 |
| Regulation of GSK3 beta in bipolar disorder | | 2.667E-04 | 6.150E-04 | 3.260E-01 | 2.667E-04 |
| Signal transduction_Calcium signaling | | 2.667E-04 | 6.150E-04 | 1.066E-01 | 2.667E-04 |
| Cell adhesion_PLAU signaling | | 2.741E-04 | 6.290E-04 | 7.553E-02 | 2.741E-04 |
| Immune response_Differentiation and clonal expansion of CD8+ T cells | | 2.741E-04 | 6.290E-04 | 4.056E-04 | 2.741E-04 |
| Development_TGF-beta-induction of EMT via ROS | | 2.864E-04 | 6.556E-04 | 9.024E-02 | 2.864E-04 |
| G-protein signaling_Ras family GTPases in kinase cascades (schema) | | 2.898E-04 | 6.601E-04 | 4.289E-04 | 6.601E-04 |
| Development_Hedgehog signaling | | 3.264E-04 | 7.379E-04 | 1.606E-01 | 3.264E-04 |
| Development_Leptin signaling via PI3K-dependent pathway | | 3.264E-04 | 7.379E-04 | 1.606E-01 | 3.264E-04 |
| Development_Angiotensin activation of ERK | | 3.350E-04 | 7.537E-04 | 5.721E-01 | 3.350E-04 |
| Cytoskeleton remodeling_Thyroliberin in cytoskeleton remodeling | | 3.350E-04 | 7.537E-04 | 5.721E-01 | 3.350E-04 |
| Development_Role of Activin A in cell differentiation and proliferation | | 3.428E-04 | 7.675E-04 | 8.019E-02 | 3.428E-04 |
| Apoptosis and survival_Ceramides signaling pathway | | 3.428E-04 | 7.675E-04 | 2.693E-01 | 3.428E-04 |
| PGE2 pathways in cancer | | 3.557E-04 | 7.945E-04 | 1.269E-01 | 3.557E-04 |
| Transport_Cathepsin-coated vesicle cycle | | 3.615E-04 | 8.055E-04 | 2.075E-03 | 3.615E-04 |
| Neurophysiological process_Activity-dependent synaptic AMPA receptor removal | | 3.658E-04 | 8.133E-04 | 2.148E-02 | 3.658E-04 |
| Apoptosis and survival_Anti-apoptotic TNF/s/NF-kB/IAP pathway | | 3.867E-04 | 8.555E-04 | 1.489E-01 | 3.867E-04 |
| HCV-dependent regulation of membrane receptors signaling in HCC | | 3.867E-04 | 8.555E-04 | 3.016E-02 | 3.867E-04 |
| Multiple sclerosis (general schema) | | 4.038E-04 | 8.911E-04 | 9.813E-02 | 4.038E-04 |
| Airway smooth muscle contraction in asthma | | 4.242E-04 | 9.216E-04 | 7.635E-01 | 4.242E-04 |
| Muscle contraction_ACM regulation of smooth muscle contraction | | 4.242E-04 | 9.216E-04 | 7.635E-01 | 4.242E-04 |
| Development_Growth hormone-releasing hormone (GH-RH) signaling | | 4.252E-04 | 9.216E-04 | 2.790E-01 | 4.252E-04 |
| TLR2-induced platelet activation | | 4.252E-04 | 9.216E-04 | 2.790E-01 | 4.252E-04 |
| Pathway                                                                 | Expression Values |
|------------------------------------------------------------------------|-------------------|
| Immune response_PGE2 common pathways                                   | 1.338E-03         |
| Regulation of lipid metabolism_Insulin signaling; generic cascades      | 1.338E-03         |
| Development_Beta-adrenergic receptor-induced regulation of ERK          | 1.338E-03         |
| Signal transduction_INK pathway                                         | 1.338E-03         |
| Development_WNT5A signaling                                            | 1.338E-03         |
| Development_HGF signaling pathan                                 | 1.338E-03         |
| Apoptosis and survival_Endoplasmic reticulum stress response pathway    | 1.338E-03         |
| Tau pathology in Alzheimer disease                                     | 1.338E-03         |
| Signal transduction_mTORC2 upstream signaling                          | 1.353E-03         |
| Blood coagulation_Platelet microparticle generation                    | 1.379E-03         |
| miRNA and delta5SO-CFTR traffic / Claudin coated vesicles formation (normal and CF) | 1.421E-03 |
| Development_WNT signaling pathway, Part 1. Degradation of beta-catenin in the absence WNT signaling | 1.461E-03 |
| Translation_IL-2 regulation of translation                             | 1.461E-03         |
| Development_YAP/TAZ-mediated co-regulation of transcription            | 1.563E-03         |
| Development_Activation of astroglial cells proliferation by ACM3       | 1.660E-03         |
| Cell adhesion_Cadherin-mediated cell adhesion                          | 1.676E-03         |
| Cal(2+)-dependent NF-AT signaling in cardiac hypertrophy               | 1.816E-03         |
| Development_Regression of lung epithelial progenitor cell differentiation| 1.832E-03         |
| Immune response_Oncostatin M signaling via JAK-Stat in mouse cells     | 1.964E-03         |
| Immune response_Sialic-acid receptors (Siglecs) signaling              | 1.997E-03         |
| G-protein signaling_Regulation of RAC1 activity                        | 1.999E-03         |
| Immune response_inflammasome in inflammatory response                  | 2.039E-03         |
| G-protein signaling_Rhoa regulation pathway                            | 2.039E-03         |
| Development_S1P1 receptor signaling via beta-арестин                  | 2.039E-03         |
| Immune response_TLR ligands                                           | 2.039E-03         |
| Development_Epigenetic and transcriptional regulation of oligodendrocyte precursor cell differentiation and myelination | 2.039E-03 |
| G-protein signaling_Rhoa regulation pathway                            | 2.039E-03         |
| Apoptosis and survival_Cytoplasmal/mitochondrial transport of proapoptotic proteins Bid, Bim and Bim | 2.039E-03 |
| Development_Role of cell-cell and ECM-cell interactions in oligodendrocyte differentiation and myelination | 2.039E-03 |
| G-protein signaling_G-Protein alpha-i signaling cascades              | 2.127E-03         |
| Immune response_inhibitory action of lipoxins on superoxide production induced by IL-8 and Leukotriene B4 in neutrophils | 2.192E-03 |
| Transcription_Role of the non-genomic action of Retinoic acid and phosphorylation of Retinoic acid receptors in the initiation of transcription | 2.483E-03 |
| Oxidative stress_NOX and DUOX families of NAPDH oxidases               | 2.483E-03         |
| Cell cycle_Regulation of G1/S transition (part 1)                       | 2.555E-03         |
| Chemokinin_Inhibitory action of lipoxins on IL-8- and Leukotriene B4-induced neutrophil migration | 2.558E-03 |
| Development_Role of HGF in hematopoietic stem cell mobilization        | 2.588E-03         |
| Transcription_Role of Akt in hypoxia induced HIF1 activation           | 2.588E-03         |
| Development_S1P3 receptor signaling pathway                            | 2.599E-03         |
| Chemotaxis_C5a-induced chemotaxis                                      | 2.599E-03         |
| Development_Notch Signaling Pathway                                    | 2.599E-03         |
| Development_Mu-type opioid receptor regulation of proliferation        | 2.667E-03         |
| Development_Regulation of CDK5 in CNS                                  | 2.667E-03         |
| Transcription_PS3 signaling pathway                                    | 2.871E-03         |

**Note:** The expression values (column 2) are not explicitly stated in the provided text and are assumed to be placeholders for actual values. The text contains some terms not fully defined in the context provided.
| Page | Section                                                                 | Value 1   | Value 2   | Value 3   | Value 4   | Value 5   | Value 6   |
|------|------------------------------------------------------------------------|-----------|-----------|-----------|-----------|-----------|-----------|
| 557  | Neurophysiological process: Synaptic vesicle fusion and recycling in nerve terminals | 2.775E-02 | 4.183E-02 | 3.814E-01 | 4.954E-01 | 2.775E-02 | 4.183E-02 |
| 558  | Immune response: T cell subsets: cell surface markers                  | 2.775E-02 | 4.183E-02 | 7.378E-01 | 7.714E-01 | 2.775E-02 | 4.183E-02 |
| 559  | Cytoskeleton remodeling: Neurofilaments                                | 2.787E-02 | 4.193E-02 | 1.314E-01 | 2.304E-01 | 2.787E-02 | 4.193E-02 |
| 560  | Transport: cAMP/ Ca(2+) dependent insulin secretion                     | 2.910E-02 | 4.372E-02 | 6.939E-01 | 7.111E-01 | 2.910E-02 | 4.372E-02 |
| 561  | Chemotaxis: CCR4-induced chemotaxis of immune cells                    | 2.946E-02 | 4.05E-02  | 5.830E-01 | 6.494E-01 | 2.946E-02 | 4.05E-02  |
| 562  | Mechanism of action of CCR4 antagonists in asthma and atopic dermatitis | 2.946E-02 | 4.05E-02  | 5.830E-01 | 6.494E-01 | 2.946E-02 | 4.05E-02  |
| 563  | CCR4-dependent immune cell chemotaxis in asthma and atopic dermatitis  | 2.946E-02 | 4.05E-02  | 5.830E-01 | 6.494E-01 | 2.946E-02 | 4.05E-02  |
| 564  | ENaC regulation in normal and CF airways                               | 3.075E-02 | 4.590E-02 | 1.507E-01 | 2.567E-01 | 3.075E-02 | 4.590E-02 |
| 565  | Cell adhesion: Plasmin signaling                                       | 3.351E-02 | 4.963E-02 | 2.223E-01 | 3.382E-01 | 3.351E-02 | 4.963E-02 |
| 566  | Development: Regulation of telomere length and cellular immortalization| 3.351E-02 | 4.963E-02 | 5.817E-02 | 1.315E-01 | 3.351E-02 | 4.963E-02 |
| 567  | Neurophysiological process: EphB receptors in dendritic spine morphogenesis and synaptogenesis | 3.351E-02 | 4.963E-02 | 5.817E-02 | 1.315E-01 | 3.351E-02 | 4.963E-02 |
| 568  | Beta-adrenergic-dependent CFTR expression                              | 3.371E-02 | 4.984E-02 | 3.704E-01 | 4.835E-01 | 3.371E-02 | 4.984E-02 |
| 569  | Development: Regulation of telomere length and cellular immortalization| 3.371E-02 | 4.984E-02 | 3.704E-01 | 4.835E-01 | 3.371E-02 | 4.984E-02 |
| 570  | Epigenetics: Default                                                   | 3.662E-02 | 5.388E-02 | 2.962E-01 | 4.182E-01 | 3.662E-02 | 5.388E-02 |
| 571  | DeltaF508-CFTR traffic / Sorting endosome formation in CF             | 4.337E-02 | 6.272E-02 | 5.133E-01 | 6.081E-01 | 4.337E-02 | 6.272E-02 |
| 572  | DeltaF508-CFTR traffic / Sorting endosome formation in CF             | 4.337E-02 | 6.272E-02 | 5.133E-01 | 6.081E-01 | 4.337E-02 | 6.272E-02 |
| 573  | DeltaF508-CFTR traffic / Sorting endosome formation in CF             | 4.337E-02 | 6.272E-02 | 5.133E-01 | 6.081E-01 | 4.337E-02 | 6.272E-02 |
| 574  | DeltaF508-CFTR traffic / Sorting endosome formation in CF             | 4.337E-02 | 6.272E-02 | 5.133E-01 | 6.081E-01 | 4.337E-02 | 6.272E-02 |
| 575  | DeltaF508-CFTR traffic / Sorting endosome formation in CF             | 4.337E-02 | 6.272E-02 | 5.133E-01 | 6.081E-01 | 4.337E-02 | 6.272E-02 |
| 576  | DeltaF508-CFTR traffic / Sorting endosome formation in CF             | 4.337E-02 | 6.272E-02 | 5.133E-01 | 6.081E-01 | 4.337E-02 | 6.272E-02 |
| 577  | DeltaF508-CFTR traffic / Sorting endosome formation in CF             | 4.337E-02 | 6.272E-02 | 5.133E-01 | 6.081E-01 | 4.337E-02 | 6.272E-02 |
| 578  | DeltaF508-CFTR traffic / Sorting endosome formation in CF             | 4.337E-02 | 6.272E-02 | 5.133E-01 | 6.081E-01 | 4.337E-02 | 6.272E-02 |
| 579  | DeltaF508-CFTR traffic / Sorting endosome formation in CF             | 4.337E-02 | 6.272E-02 | 5.133E-01 | 6.081E-01 | 4.337E-02 | 6.272E-02 |
| 580  | DeltaF508-CFTR traffic / Sorting endosome formation in CF             | 4.337E-02 | 6.272E-02 | 5.133E-01 | 6.081E-01 | 4.337E-02 | 6.272E-02 |
| 581  | DeltaF508-CFTR traffic / Sorting endosome formation in CF             | 4.337E-02 | 6.272E-02 | 5.133E-01 | 6.081E-01 | 4.337E-02 | 6.272E-02 |
| 582  | DeltaF508-CFTR traffic / Sorting endosome formation in CF             | 4.337E-02 | 6.272E-02 | 5.133E-01 | 6.081E-01 | 4.337E-02 | 6.272E-02 |
| 583  | DeltaF508-CFTR traffic / Sorting endosome formation in CF             | 4.337E-02 | 6.272E-02 | 5.133E-01 | 6.081E-01 | 4.337E-02 | 6.272E-02 |
| 584  | DeltaF508-CFTR traffic / Sorting endosome formation in CF             | 4.337E-02 | 6.272E-02 | 5.133E-01 | 6.081E-01 | 4.337E-02 | 6.272E-02 |
| 585  | DeltaF508-CFTR traffic / Sorting endosome formation in CF             | 4.337E-02 | 6.272E-02 | 5.133E-01 | 6.081E-01 | 4.337E-02 | 6.272E-02 |