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Ampelopsin facilitates diabetic wound healing and keratinocyte cell progression by inhibiting the NLRP3 inflammasome pathway in macrophages

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Abstract. Ampelopsin (AMP) had a wound-healing effect in rat skin wounds with or without purulent infection. However, the role of AMP in diabetic wound healing remains poorly defined. Wounds were created on the dorsal skin of type 2 diabetic mouse model, and the histological features of wounds were examined by hematoxylin and eosin (HE) staining. Caspase-1 activity and the secretion of inflammatory cytokines were detected by enzyme-linked immunosorbent assay (ELISA). Cell viability and migration were examined through cell counting kit-8 (CCK-8) and wound healing assays, respectively. AMP facilitated wound healing *in vivo*. AMP notably facilitated platelet endothelial cell adhesion molecule-31 (CD31), collagen type I alpha 1 chain (COL1A1), and alpha-smooth muscle actin (α-SMA), and inhibited matrix metallopeptidase 9 (MMP9) and cyclooxygenase 2 (Cox2) expression in diabetic wounds. The inflammasome pathway was implicated in skin injury. AMP inhibited pro-inflammatory factor secretions and NLR family pyrin domain containing 3 (NLRP3) inflammasome pathway in diabetic wounds and high glucose-treated THP-1 macrophages. AMP-mediated NLRP3 inflammasome inhibition in THP-1 macrophages increased cell viability and migratory capacity in HaCaT cells. AMP facilitated diabetic wound healing and increased keratinocyte cell viability and migratory ability by inhibiting the NLRP3 inflammasome pathway in macrophages.

Key words: Ampelopsin — Wound — Diabetes — Macrophage — Keratinocyte

Introduction

Wounds can influence millions of people globally (Cowin 2019; Bowers and Franco 2020). Wound healing is a complex process involving three or more overlapping and sequential stages: inflammation, proliferation, and remodeling (Baron et al. 2020). During the inflammatory phase, pro-inflammatory factors and inflammatory cells including macrophages were notably increased (Patel et al. 2019). The proliferative stage is characterized by the proliferation and migration of keratinocytes, synthesis of extracellular matrix (ECM) proteins (e.g. collagens I and III and α-SMA), granulation formation, angiogenesis, and re-epithelialization (Baron et al. 2020; Bowers and Franco 2020; Potekaev et al. 2021). The reconstruction of the ECM is the major feature of the remodeling stage (Baron et al. 2020; Potekaev et al. 2021). The disruption of the above-mentioned wound healing processes including persistent inflammation, keratinocyte migration impairment, and excessive ECM can result in the failure or delay of wound healing, skin injury, and the formation of chronic trophic ulcers and cicatrices (Baron et al. 2020; Potekaev et al. 2021).

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Diabetes mellitus is the fifth leading cause of death globally (Khan et al. 2019). More than 400 million people are living with diabetes and the prevalence rate of diabetes is continuously raised worldwide (Khan et al. 2019; Saeedi et al. 2019; Lovic et al. 2020). Moreover, approximately 20–30% of patients with diabetes develop diabetic wounds globally (Patel et al. 2019; Burgess et al. 2021; Chang and Nguyen 2021). The recurrence rate of diabetic wounds was extremely high with a one-year recurrence rate of approximately 40% and a five-year recurrence rate of approximately 65% (Armstrong et al. 2017). Additionally, diabetic wounds are the major cause of amputations and even deaths (Perez-Favila et al. 2019; Jalilian et al. 2020).

Recent studies have shown that some phytochemicals possess potential pharmacological activities in wound healing (El-Ashram et al. 2021). For instance, the extract of Ampelopsis japonica root tuber could facilitate the scald wound repair in scald Sprague-Dawley rats (Lee et al. 2015). Ampelopsin (AMP), also named dihydromyricetin, is the major flavonol compound of the *Ampelopsis grossedentata* and *Hovenia dulcis* (Tong et al. 2020; Sferrazza et al. 2021). AMP has numerous biological functions and pharmacological properties such as anti-inflammatory, anti-microbial, anti-angiogenic, antioxidant, and metabolic regulation activities (Tong et al. 2020; Sferrazza et al. 2021). Moreover, AMP has potential preventive and therapeutic effects on multiple metabolic disorders including diabetes mellitus (Tong et al. 2020; Wang et al. 2022). Additionally, Shevelev et al. demonstrated that AMP could noticeably accelerate perifocal oedema disappearance, granulation, edge epithelialization, and wound closure in rat skin wounds infected with or without *Staphylococcus aureus*, *Candida albicans* or *Pseudomonas aeruginosa* (Shevelev et al. 2020). However, the knowledge of the effect of AMP on diabetic wound healing is lacking.

Previous studies have shown that AMP can exert its functions by suppressing the NLR family pyrin domain containing 3 (NLRP3) inflammasome pathway in doxorubicin-induced cardiotoxicity (Sun et al. 2020), sepsis-induced acute lung injury (Wang YC et al. 2019), and Alzheimer's disease (Feng et al. 2018). Moreover, NLRP3 inflammasome pathway was involved in the regulation of diabetic wound healing (Wang T et al. 2018; Liu et al. 2019; Zhao et al. 2021). Thus, we further investigated whether AMP could modulate diabetic wound healing by the NLRP3 inflammasome pathway.

Given the crucial role of macrophage-mediated inflammation and sustained NLRP3 inflammasome activity in macrophages in diabetic wound healing, we further explored the effect of AMP on the NLRP3 inflammasome pathway in high glucose-treated THP-1 macrophages. Additionally, we further examined whether the AMP-modulated secretions in high glucose-treated THP-1 macrophages could influence the biological behaviors of keratinocyte cells (a vital cell player in diabetic wound healing).

Materials and Methods

Mice experiments

The animal experiments were conducted with the approval of the Animal and Care Committee of our institution and the procedures were consistent with NIH guidelines. The type 2 diabetic mouse model was induced in Kunming mice (male, 18–22 g) by high-fat diet and Streptozotocin (STZ; Sigma-Aldrich, St. Louis, MO, USA) injection (Kintoko et al. 2018; Liang T et al. 2019). Mice were maintained under controlled environmental condition (temperature 22–25°C; 12-h light/12-h darkness cycle) and were provided with standard rodent chow and water *ad libitum*. The mice were fed with high-fat diet for a month and received an intravenous injection of 80 mg/kg STZ in saline-1% Tween 80 after a 12 h fast. After 72 h, mice with fasting blood glucose level exceeding 11.1 mM were classified as diabetic mice. The model mice (n = 10) were randomized to control (Con) and AMP groups. Each group contained 5 mice. Hair at the surgical sites were removed. The next day, the mice were anesthetized with isoflurane, and wounds were made on the dorsal skin of mice using a sterile 6-mm punch biopsy. Wounds were covered with Tegaderm (3 M) until euthanasia to avoid contamination and infection. After creating wounds, mice were individually caged to avoid biting and interference with the wounds. Mice in the AMP group were administered with AMP (500 mg/kg body weight) orally each day for 14 days (He et al. 2019). Wound regions were imaged at the indicated time points and wound area alterations were presented as the percentages of the initial wound area. About 2-mm tissues surrounding the injured sites were collected using scissors. A part of wound tissues was stored at −80°C for the following real time quantitative polymerase chain reaction (RT-qPCR), Western blot, and enzyme-linked immunosorbent assay (ELISA) analyses. For hematoxylin and eosin (HE) and immunofluorescence (IF) analysis, the wound tissues were fixed with 4% paraformaldehyde and embedded in paraffin. No mice dead during the whole experimental process. After 14-day experiment, mice were euthanized by CO_2-inhalation, and the death was verified by the absence of respiration or heartbeat.

HE staining

The paraffin-embedded sections were dewaxed and then stained with HE solutions. After dehydrating, the sections were sealed and imaged.

Cell culture

THP-1 cells were obtained from Procell Life Science Technology Co., Ltd. (Wuhan, China) and maintained in RPMI-1640 medium (Thermo Scientific, Waltham, MA, USA) containing 10% fetal bovine serum (FBS; Thermo Scientific) and 1% penicillin-streptomycin solution (Thermo Scientific). THP-1 cells were treated with phorbol myristate acetate (PMA, 300 ng/ml) for 72 h. THP-1 cells in the high glucose group were cultured in complete medium containing 30 mM glucose for 24 h (Dai et al. 2019). HaCaT human skin keratinocyte cells were purchased from China Center for Type Culture Collection (Wuhan, China) and cultured in DMEM medium (Thermo Scientific) containing 10% FBS (Thermo Scientific), and 1% penicillin-streptomycin solution (Thermo Scientific).

IF assay

IF assay was performed using the experimental procedures of IF assay as previously described (Wang T et al. 2019; Zhao et al. 2020). Briefly, after dewaxing, antigen retrieval, endogenous peroxidase blockade, and non-specific protein signal blockade, the slides were incubated with primary antibody, horseradish peroxidase (HRP)-labeled secondary antibody, and fluorescent dye-labeled tyramide. Next, cell nucleus was counterstained with DAPI solution. After mounting, slides were imaged.

Western blot assay

Protein was extracted from skin wound tissues, THP-1 cells, or HaCaT cells using RIPA lysis buffer (Beyotime, Shanghai, China) supplemented with protease inhibitor (Thermo Scientific). Protein was quantified by BCA assay kit (Thermo Scientific). After the separation of protein (35 μg) by SDS-PAGE electrophoresis, protein on the gels was transferred onto nitrocellulose membranes (Millipore, Bedford, MA, USA). After the blockade of non-specific signals on the membranes by the skimmed milk, the membranes were immunoblotted with specific primary antibody against Cox2 (1:500, GB11077-2, Servicebio), NLRP3 (1:500, 19771-1-AP, Proteintech), cleaved caspase-1 (1:1000, CST #4199, Cell signaling Technology) and HRP-labelled secondary antibody. Protein bands were examined by ECL reagent (Beyotime).

Bioinformatics analysis

The GSE98105 dataset was downloaded from the NCBI GEO database. Genes associated with skin wound were obtained from the DisGENET database. The gene lists were compared using the jvenn online website (http://jvenn.toulouse.inra.fr/app/index.html). The protein-protein interaction (PPI) network was established by the String database (https://cn.string-db.org/).

RT-qPCR

Total RNA was extracted from skin tissues using the TRIzol Reagent (Thermo Scientific). RNA was reversely transcribed into cDNA using the RevertAid First Strand cDNA Synthesis Kit (Thermo Scientific). Genes expression levels were examined using the specific primers and SYBR Select Master Mix (Thermo Scientific) on a real-time PCR instrument (Thermo Scientific) and calculated using the $2^{-\Delta\Delta Ct}$ method.

ELISA

Tumor necrosis factor-α (TNF-α), interleukin-1β (IL-1β) and IL-6 in the THP-1 cell medium or mouse skin tissue homogenates were measured using corresponding human or mouse ELISA kits according to the manufacturer's protocols (Lianke Biotechnology). Caspase-1 activity was tested using the Caspase-1 Activity Assay Kit. The ELISA kits were purchased from the Beyotime Biotechnology Co., Ltd.

Co-culture experiments

The medium of untreated and treated THP-1 cells was collected at 24 h after AMP treatment and mixed with HaCaT complete medium at a 1:1 ratio. The mixed medium was named conditioned medium. HaCaT cells were cultured in the conditioned medium for another 24 h. Next, cell viability and migratory ability were examined by cell counting kit 8 (CCK-8) and wound healing assays, respectively.

CCK-8 assay

HaCaT cells were plated into 96-well plates and cultured in the above-mentioned conditioned medium. At 24 h after incubation, 10 μl/well of CCK-8 solution (Beyotime Biotechnology) was added to microplates and incubated for 1 h at 37°C. Next, the absorbance was measured at 450 nm.

5-ethynyl-2'-deoxyuridine (Edu) assay

Cell proliferation activity was assessed using EdU cell proliferation assay kit (Servicebio, Wuhan, China) according the manufacturer's instructions. Briefly, cells were seeded in 24-well plates and treated with high glucose or AMP for 24 h, followed by the incubation with 10 μM EdU solution for 2 h. After that, cells were fixed and incubated with 0.5% Triton X-100 solution for 15 min. Then cells were incubated with EdU click buffer for 30 min. Cell nuclei were labeled using DAPI (Beyotime). Stained cells

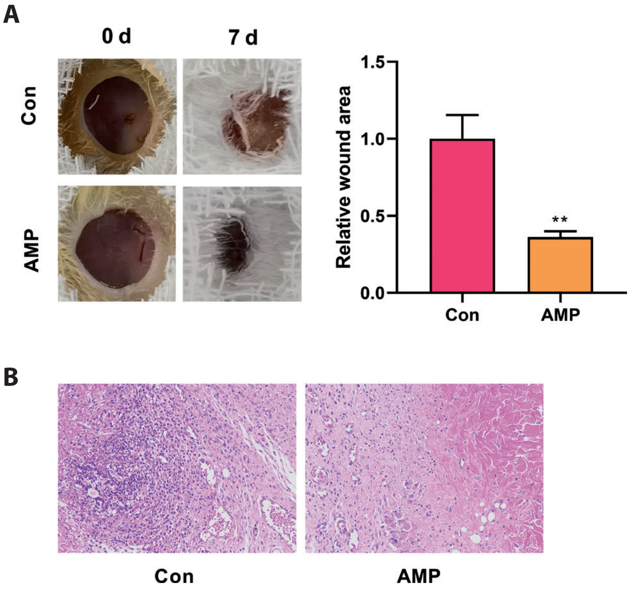

Figure 1. Ampelopsin facilitated diabetic wound healing. **A.** The images of mouse wound sites. The percentage of wound area was calculated as follows: wound area (%) = wound area/initial wound area. **B.** Hematoxylin and eosin staining images of wound tissues. AMP, mice administered with ampelopsin (500 mg/kg body weight) orally each day for 14 days; Con, control group. ** $p < 0.01$ *vs.* Con.

were observed using a fluorescence microscope (Olympus, Japan). Cell proliferation was represented *via* the ratio of EdU-positive cells.

Wound healing assay in vitro

HaCaT cells were seeded onto 24-well plates at the density of 0.5×10^6 cells/ml and were allowed to grow to 100% confluence. The scratch wound was created using a 200 μl pipette tip. Cell debris and detached cells were removed by washing with PBS (phosphate buffer saline) three times. THP-1 cells were cultured in the high glucose condition containing 1% FBS with or without AMP (50 μM) for 24 h. Next, the conditioned medium was collected to incubate with HaCaT cells for 16 h. The wound regions were photographed at 0 and 16 h after scratching, and the scratch area was analyzed using ImageJ software. The migratory distance = [wound area (0 h) − wound area (16 h)]/wound area (0 h) × 100%, and the migratory distances in glucose group and glucose+AMP groups were normalized to that of control group.

Statistical analysis

Statistical analysis was conducted using the GraphPad Prism software version 7 (La Jolla, CA, USA) and the outcomes were shown as mean ± standard deviation. Comparisons among groups were conducted using the one-way or two-way analysis of variance (ANOVA) and Tukey test. Significant differences were defined at p-value < 0.05.

Results

AMP facilitated wound healing in diabetic mice

As presented in Figure 1A, the wound area was markedly reduced in the type 2 diabetic mouse model treated with AMP relative to the untreated group. Histopathological analysis showed that AMP-treated type 2 diabetic mouse model group presented lower serious histological lesions in the wound sites such as severe cell injury and fewer blood vessels compared to the control group (Fig. 1B).

IF and Western blot assays disclosed that the expression levels of platelet endothelial cell adhesion molecule-31 (CD31, a vascularization marker), collagen type I alpha 1 chain (COL1A1, an ECM protein), alpha-smooth muscle actin (α-SMA, an ECM protein) were notably elevated and the expression levels of matrix metallopeptidase 9 (MMP9, an ECM-degrading protein) and cyclooxygenase 2 (Cox2, an inflammatory mediator) were markedly reduced in the wound sites of AMP-treated type 2 diabetic mice relative to the untreated group (Fig. 2). These data suggested that AMP promoted diabetic wound healing.

The identification of the inflammasome pathway implicated in skin injury by bioinformatics analysis

Venn analysis showed that 103 genes were differentially expressed in wounded skin specimens relative to the unwounded group (|Log2 Fold Change| > 1, $p < 0.05$) (Table S1 in Supplementary material) and closely correlated with skin injury (Table S2; Fig. 3A). Functional annotation analysis revealed that these 103 genes might play vital roles in inflammation (Fig. 3B). Among 103 genes, 46 genes were highly significant differential expression (|Log2 Fold Change| > 2, $p < 0.01$). Next, the PPI networks of the above-mentioned 46 genes were established and inflammasome pathway-related factors NLRP3 and IL-1β were screened out from the PPI network (Fig. 3C).

AMP inhibited the NLRP3 inflammasome pathway in wound sites of type 2 diabetic mouse model

RT-qPCR and Western blot assays showed that NLRP3 expression level was lower in wound tissues of AMP-treated type 2 diabetic mice than in the untreated group (Fig. 4A,B). ELISA assay also disclosed that AMP inhibited the secretions of IL-1β, IL-6, and TNF-α and reduced the

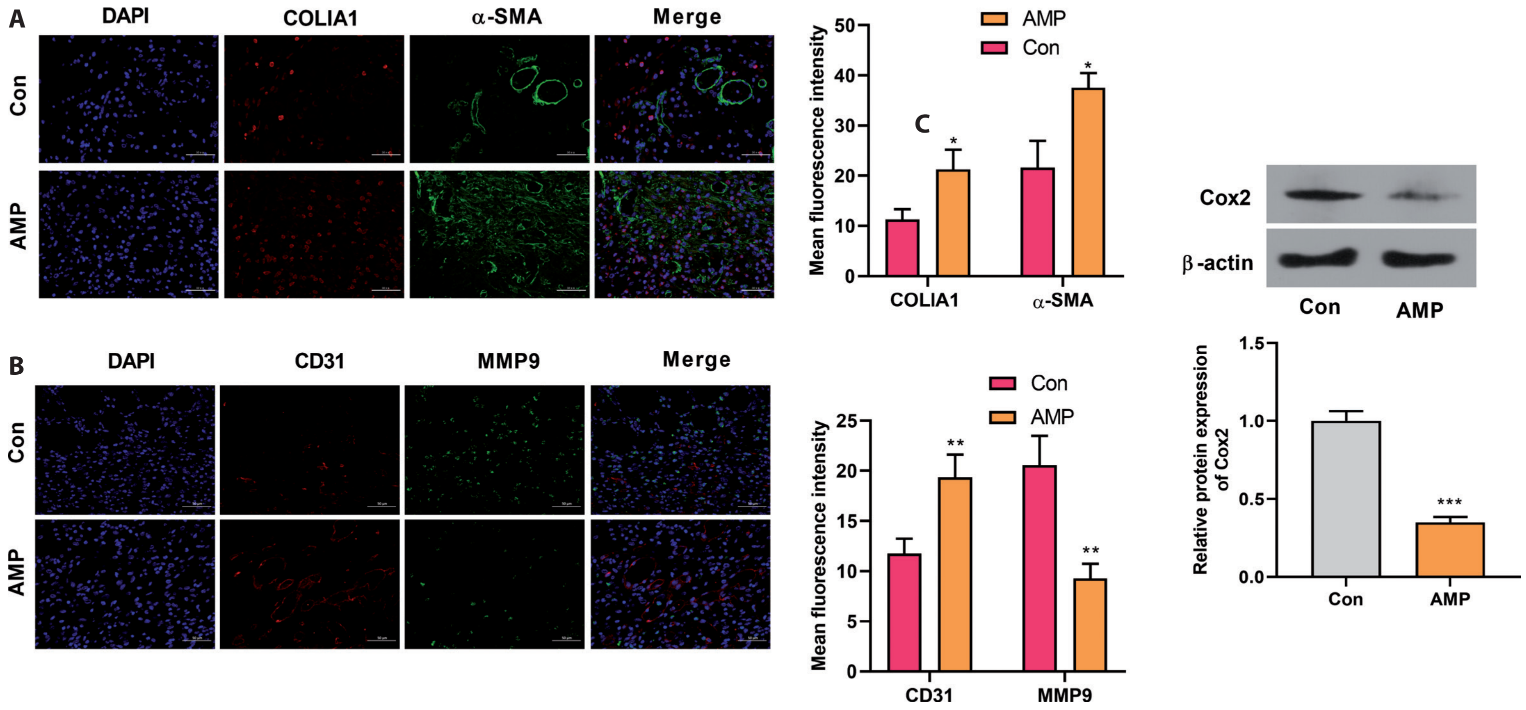

Figure 2. Ampelopsin promoted ECM synthesis and inhibited Cox2. Immunofluorescence analysis of COL1A1, α-SMA (**A**) and CD31, MMP9 (**B**) in wound tissues. **C.** Western blot analysis of Cox2 protein level in wound tissues. ECM, extracellular matrix; Cox2, cyclooxygenase 2; COLIA1, collagen type I alpha 1 chain; α-SMA, alpha-smooth muscle actin; CD31, platelet endothelial cell adhesion molecule-31; MMP9, matrix metallopeptidase 9. For other abbreviations see Figure 1. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ *vs.* Con.

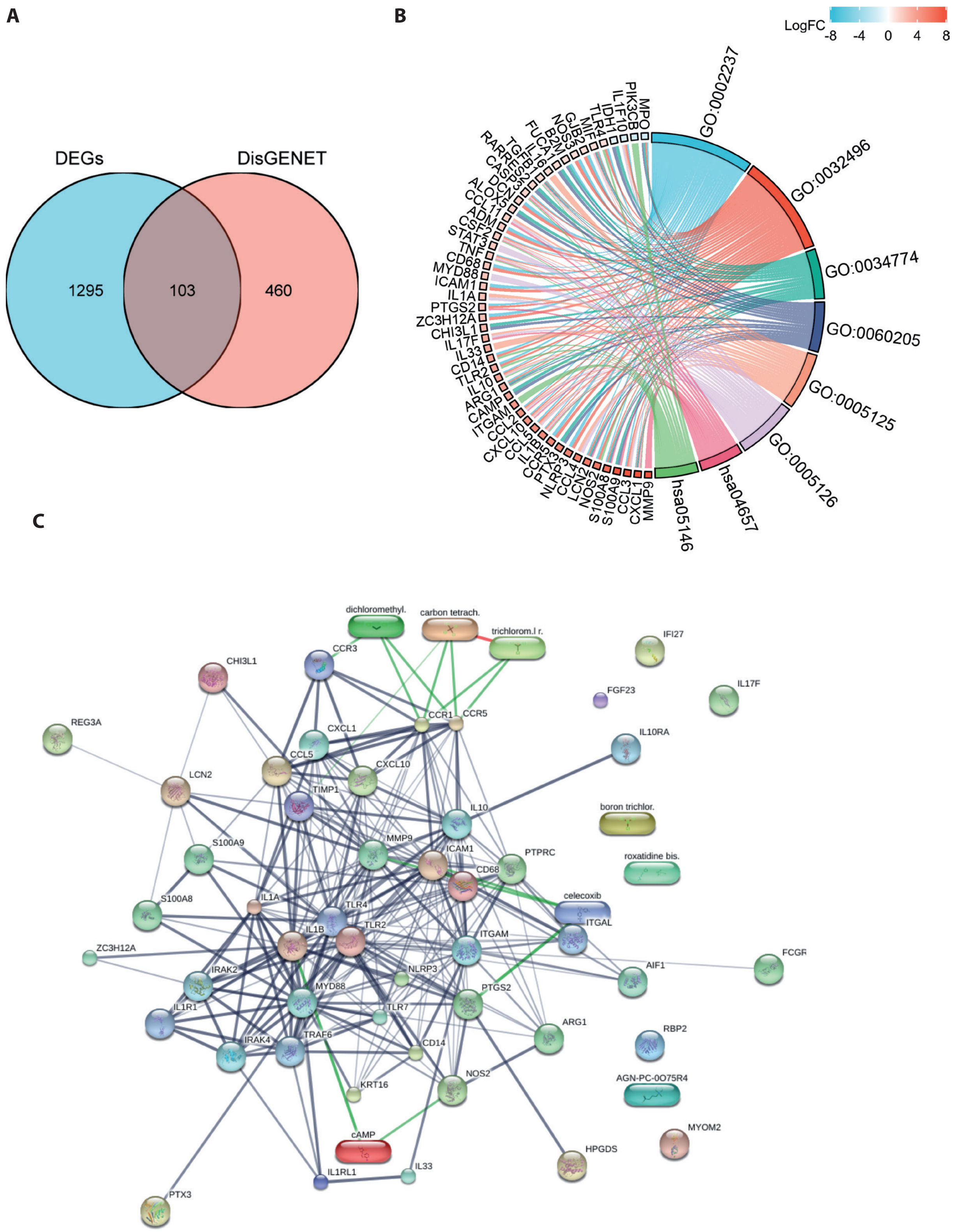

Figure 3. The identification of the inflammasome pathway implicated in wound healing by bioinformatics analysis. **A.** Venn analysis for genes listed in Table S1 and Table S2 (see Supplementary material). **B.** Circos plot showing the functional annotations on the 103 genes. **C.** PPI network of 46 genes.

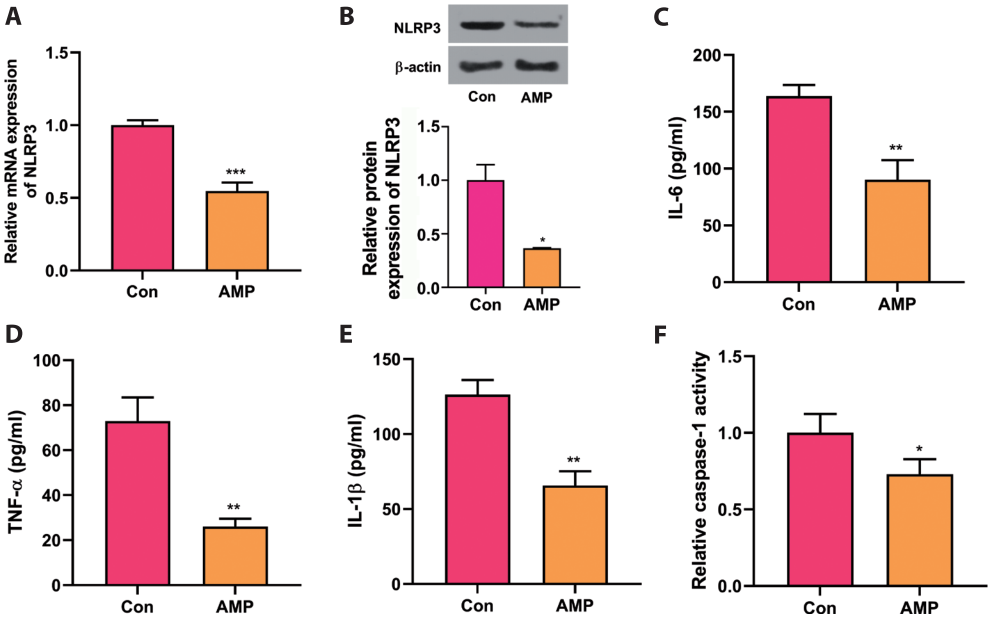

Figure 4. Ampelopsin inhibited the NLRP3 inflammasome pathway in wound sites of type 2 diabetic mouse model. The mRNA (**A**) and protein (**B**) levels of NLRP3 was measured by RT-qPCR and Western blot in wound tissues of type 2 diabetic mice treated with or without ampelopsin. The secretion levels of IL-6 (**C**), TNF-α (**D**), IL-1β (**E**) and activity of caspase-1 (**F**) were examined by ELISA assay in wound tissue homogenates of type 2 diabetic mice treated with or without ampelopsin. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ *vs.* Con group. For abbreviations see Figure 1.

activity of caspase-1 in wound tissues of type 2 diabetic mouse model (Fig. 4C–F). These outcomes suggested that AMP suppressed the NLRP3 inflammasome pathways in diabetic wounds.

AMP suppressed the NLRP3 inflammasome pathway in high glucose-treated THP-1 cells

Next, we demonstrated that high glucose could active the inflammasome pathway in THP-1 cells, as evidenced by the notable increase of IL-6, TNF-α, IL-1β secretion level, caspase 1 activity, NLRP3 protein expression, and cleaved-caspase 1 protein level in THP-1 cells exposed to high glucose *versus* untreated cells (Fig. 5). The administration of AMP reduced IL-6, TNF-α, IL-1β secretion and caspase 1 activity and inhibited NLRP3 and cleaved-caspase 1 expressions in high glucose-treated THP-1 cells in a dose-dependent manner (Fig. 5). These outcomes suggested that AMP dose-dependently inhibited the activation of the NLRP3 inflammasome pathway in THP-1 cells.

AMP-mediated NLRP3 inflammasome pathway inhibition in THP-1 cells might increase HaCaT cell viability and migratory ability

Next, our study showed that the addition of high glucose-treated THP-1 cell medium noticeably weakened the viability and migratory ability of HaCaT cells (Fig. 6). Moreover, cell viability and migratory activity were markedly enhanced in HaCaT cells co-cultured with THP-1 cell supernatants treated with AMP than in cells co-incubated with THP-1 cell medium treated with high glucose alone (Fig. 6). Combined with the above-mentioned outcomes, we supposed that AMP-mediated NLRP3 inflammasome pathway inhibition in THP-1 cells might increase HaCaT cell viability and facilitate HaCaT cell migration.

Discussion

In this study, we demonstrated that AMP reduced skin wound area percentage in diabetic mice. Moreover, wound tissues of diabetic mice treated with AMP presented more blood vessels compared with the untreated diabetic mouse group, which were the features of proliferative stage of wound healing. These data showed that AMP promoted diabetic wound healing.

CD31, a multifunctional molecule, functions as a crucial player in the maintenance and restoration of vascular permeability barrier (Lertkiatmongkol et al. 2016). Moreover, CD31 has been used to assess angiogenesis and vascularization in the wounds (Liang Y et al. 2019; Guo et al. 2020; Shukla et al. 2021). Our present study demonstrated that CD31 expression was notably increased in wound tissues of diabetic mice after AMP treatment, suggesting that AMP could facilitate the vascularization in the diabetic wounds, which was consistent with our histopathological outcomes.

Extracellular matrix is mainly composed of several classes of macromolecules including fibrous proteins (collagens) and glycoproteins (e.g. proteoglycans and fibronectins) (Potekaev et al. 2021). It has been found that ECM proteins participate in the regulation of wound healing by controlling multiple processes including cell migration, proliferation, and adhesion (Rousselle et al. 2019; Arenas Gómez et al. 2020; Potekaev et al. 2021). Matrix metalloproteinases (MMPs) are a family of endopeptidases that can degrade almost all ECM components (Cabral-Pacheco et al. 2020). MMP9, a member of MMPs family, also has been reported to be involved in the regulation of wound healing and keratinocyte migration (Zhang C et al. 2017; Wang W et al. 2018). Our data showed that two ECM proteins (COL1A1 and α-SMA) were highly expressed and MMP9 was low expressed in wound tissues of AMP-treated diabetic mice relative to the untreated group. The synthesis of ECM proteins is a vital feature of the proliferative stage during wound healing. Thus, we believed that AMP could facilitate wound healing progress. Cox2 is a vital mediator of inflammation (Cui and Jia 2021). The inhibition of Cox2 contributed to the repair of diabetic wound tissues (Davis et al. 2020). Our data disclosed that AMP inhibited Cox2 expression in wound tissues, further suggesting the beneficial effect of AMP on diabetic wound healing.

Our bioinformatics analysis showed that NLRP3 inflammasome pathway was related to skin injury. Also, previous studies have shown that NLRP3 inflammasome pathway functions as a crucial player in skin wound healing and the sustained activation of NLRP3 pathway hindered wound healing related to diabetes (Wang T et al. 2018; Zhao et al. 2021; Cavalcante-Silva and Koh 2022). In this study, we demonstrated that AMP could inhibit the NLRP3 inflammasome pathway in diabetic wound tissues and high glucose-treated THP-1 cells, suggesting that AMP might accelerate diabetic wound healing by inhibiting the NLRP3 inflammasome pathway.

It has been reported that the macrophage-mediated inflammation plays a vital role in normal and diabetic skin wound healing (Boniakowski et al. 2017; Aitcheson et al. 2021). NLRP3 inflammasome pathway was sustainedly activated in macrophages isolated from diabetic wounds and the sustained activation of NLRP3 inflammasome in macrophages hampered wound healing in diabetic human and

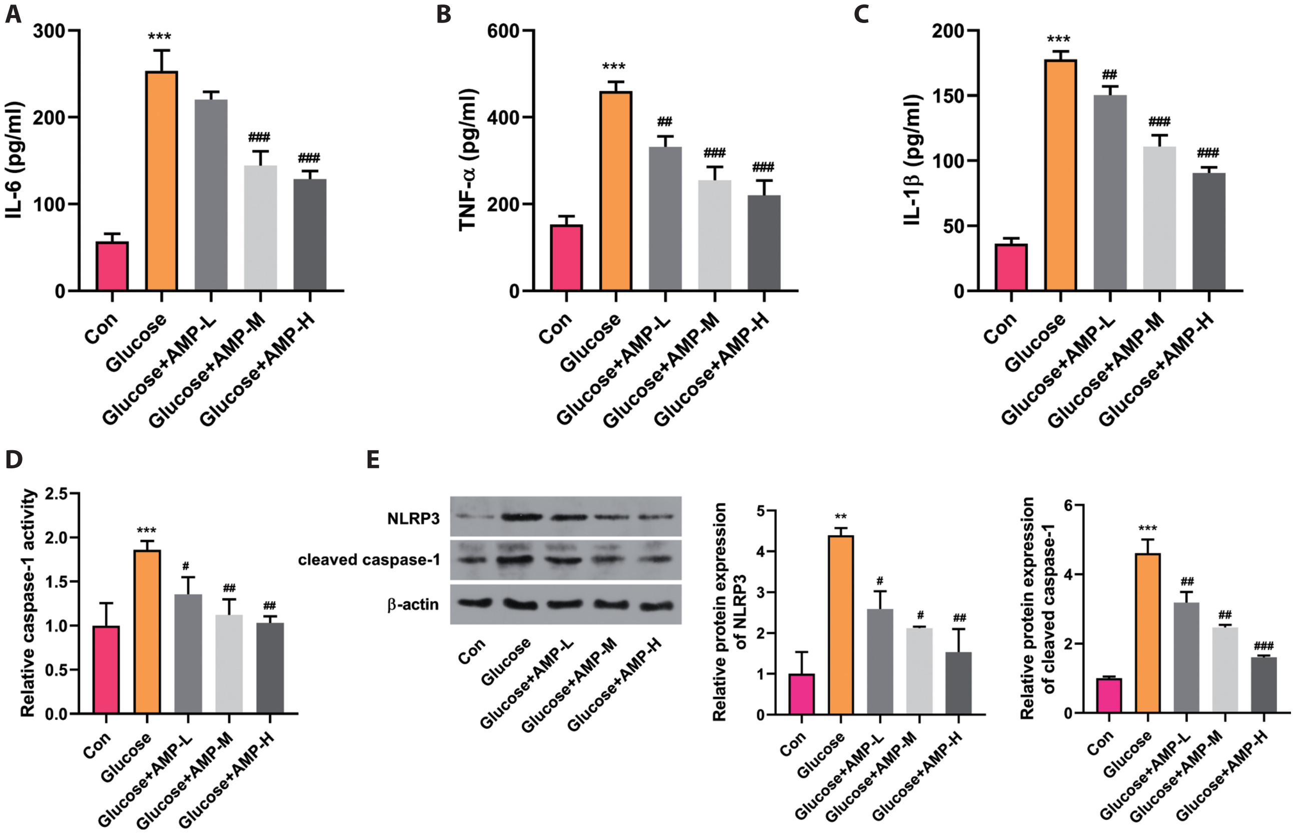

Figure 5. Ampelopsin suppressed the NLRP3 inflammasome pathway in high glucose-treated THP-1 cells. THP-1 cells cultured in high glucose medium were treated with or without different concentrations of ampelopsin: 25 μM (Glucose+AMP-L), 50 μM (Glucose+AMP-M), 100 μM (Glucose+AMP-H) for 24 h (Zeng et al 2018). IL-6 (**A**), TNF-α (**B**), IL-1β (**C**) secretion level and caspase-1 activity (**D**) were measured using corresponding kits. **E.** NLRP3 and cleaved caspase-1 protein levels were measured by Western blot. Con, control group; Glucose, THP-1 cells cultured in medium containing 30 mM glucose for 24 h. ** $p < 0.01$, *** $p < 0.001$ *vs.* Con; $^{\#}$ $p < 0.05$, $^{\#\#}$ $p < 0.01$, $^{\#\#\#}$ $p < 0.001$ *vs.* Glucose.

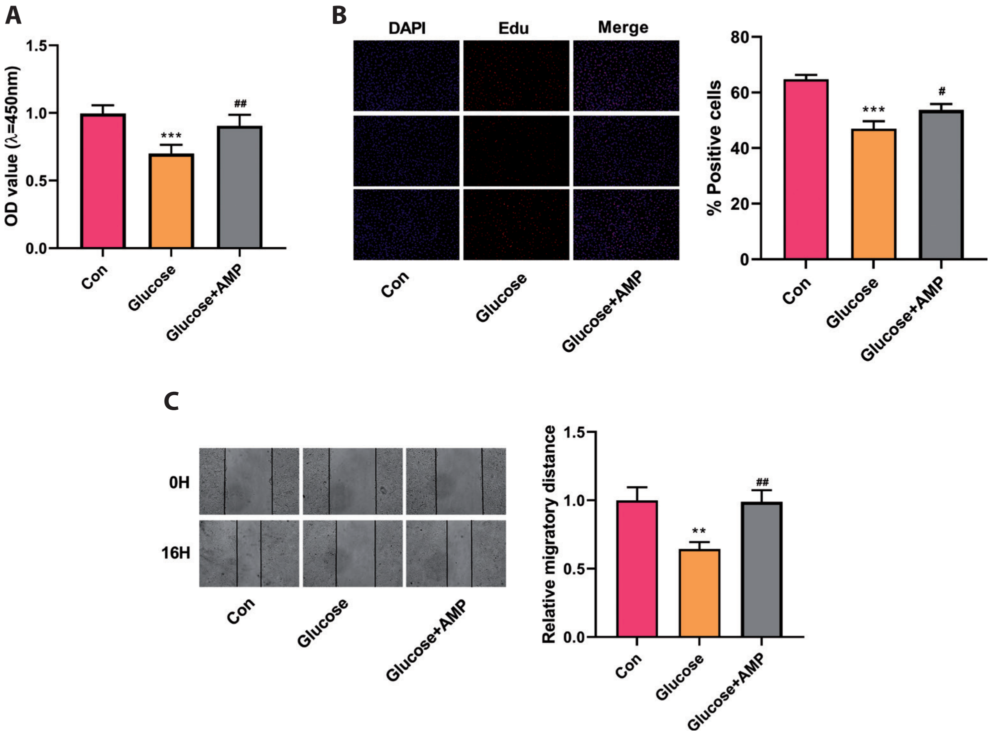

Figure 6. Ampelopsin-mediated NLRP3 inflammasome pathway inhibition in THP-1 cells might increase HaCaT cell viability and migratory ability. THP-1 cells cultured in the high glucose condition were treated with 50 μM ampelopsin (Glucose+AMP) or without ampelopsin (Glucose) for 24 h. Next, cell medium was collected and co-incubated with HaCaT cells for 24 h. **A.** Cell viability was measured by CCK-8 assay. **B.** Cell proliferation activity was assessed by Edu assay. **C.** Cell migratory ability was examined by wound healing assay. Con, control group ** $p < 0.01$, *** $p < 0.001$ *vs.* Con; $^{\#}$ $p < 0.05$, $^{\#\#}$ $p < 0.01$ *vs.* Glucose.

mice (Mirza et al. 2014). Prior studies also disclosed that high glucose could activate the NLRP3 inflammasome pathway in THP-1-derived macrophages (Zhang X et al. 2017; Dai et al. 2019). Thus, we further examined the effect of AMP on NLRP3 inflammasome pathway in high glucose-stimulated THP-1 cells. Consistent with previous reports (Zhang X et al. 2017; Dai et al. 2019), our study also demonstrated that NLRP3 inflammasome pathway was activated in THP-1 subjected to high glucose treatment. Moreover, we demonstrated that AMP inhibited the activation of NLRP3 inflammasome pathway induced by high glucose in THP-1 cells.

It has been well documented that macrophages can secrete some factors including NLRP3 inflammasome pathway-related molecules to regulate biological behaviors (e.g. proliferation and migration) of multiple cells including keratinocytes in diabetic wounds (Huang et al. 2019; Aitcheson et al. 2021). Keratinocytes is the main cell type in skin and the disturbances of keratinocyte functions (e.g. the impairment of keratinocyte proliferation and migration) can curb diabetic wound healing (Hosseini Mansoub 2021). Thus, we further investigated whether AMP could modulate some secretion substances in macrophages to influence the viability and migration of HaCaT cells. Our data showed that factors that were secreted by THP-1 cells treated with high glucose could notably reduce cell viability, inhibit cell migration, in HaCaT cells. The conditioned medium from THP-1 cells treated with high glucose and AMP notably increased cell viability and migratory ability in HaCaT cells compared to the conditioned medium of THP-1 cells treated with high glucose alone. In combination with our outcomes, we supposed that AMP-mediated NLRP3 inflammasome pathway inhibition in THP-1 macrophages might improve HaCaT keratinocyte cell viability and migratory capacity.

In conclusion, our data showed that AMP facilitated diabetic wound healing by promoting the expression of CD31, COL1A1 and α-SMA and inhibiting the expression of MMP9 and Cox2 in diabetic wound sites. Moreover, AMP could inhibit the NLRP3 inflammasome pathway in diabetic wounds and high glucose-treated THP-1 macrophage cells. Additionally, AMP-mediated inflammasome inhibition in high glucose-treated THP-1 macrophage cells increased cell viability, facilitated cell migration in HaCaT cells. Our data could deepen our understanding of the roles and biological basis of AMP in diabetic wound healing and suggested the potential therapeutic value of AMP for diabetic wounds. Given the great harm of diabetic wounds to the health and life of people with diabetes, the identification of a potential therapeutic drug AMP is of great importance to the clinical treatment of patients with diabetes.

Conflict of interest. The authors declare that they have no financial conflicts of interest.

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Supplementary Material

Ampelopsin facilitates diabetic wound healing and keratinocyte cell progression by inhibiting the NLRP3 inflammasome pathway in macrophages

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Supplementary Tables

Table S1. The differentially expressed genes in wounded skin specimens relative to the unwounded group from GSE98105 dataset.

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30008189	1,85E-10	1,14E-14	35	22,59614	10	Mmp12
ENSRNOG00000011483	7,9E-10	1,35E-13	29,1	20,75677	7,5	S100a9
Rn30002489	7,9E-10	1,62E-13	28,7	20,61264	7,91	Cxcl1
Rn30010572	7,9E-10	2,75E-13	27,6	20,19341	8,44	S100a9
Rn30013264	7,9E-10	3,16E-13	27,3	20,081	7,47	Krt16
R001406_01	7,9E-10	3,41E-13	27,1	20,01769	7,5	Ccl3
Rn30010640	9,35E-10	5,14E-13	26,3	19,68239	6,53	S100a8
R001461_01	9,8E-10	6,65E-13	25,8	19,46952	8,11	Mmp9
ENSRNOG00000011557	2,09E-09	1,55E-12	24,2	18,75699	7,13	S100a8
ENSRNOG00000014441	3,31E-09	2,66E-12	23,2	18,29407	7,29	Ka11,Krt16
R003960_01	6,12E-09	6,04E-12	21,8	17,57407	5,63	Csf3
R003673_01	1,81E-08	2,23E-11	19,8	16,39825	8,13	Mmp8
Rn30007967	2,11E-08	2,86E-11	19,4	16,17245	5,49	Csf3r
ENSRNOG00000005825	2,11E-08	2,86E-11	19,4	16,17014	5,29	Lyz2
Rn30008195	2,27E-08	3,23E-11	19,2	16,06094	8,84	Mmp12
R003775_01	2,66E-08	3,94E-11	18,9	15,87579	5,82	Fcnb
R001188_01	5,01E-08	8,34E-11	17,9	15,17826	4,77	Il1b
Rn30009083	5,89E-08	1,02E-10	17,6	14,99102	7,47	Mmp8
ENSRNOG00000002792	6,11E-08	1,09E-10	17,5	14,92425	8,49	Cxcl2
ENSRNOG00000009342	7,23E-08	1,38E-10	17,2	14,70186	6,17	Fcnb
Rn30001094	7,42E-08	1,51E-10	17,1	14,61807	4,85	Itgb2
R001475_01	7,93E-08	1,76E-10	16,9	14,4729	10,9	Cxcl2
ENSRNOG00000037097	8,61E-08	1,97E-10	16,7	14,36911	7,23	Expi
R000393_01	8,66E-08	2,03E-10	16,7	14,33841	5,16	Pglyrp1
ENSRNOG00000002916	0,000000098	2,51E-10	16,4	14,13712	5,76	Car4
Rn30004468	0,000000098	2,52E-10	16,4	14,13096	4,73	Upp1
ENSRNOG00000019854	0,000000098	2,54E-10	16,4	14,12426	5,64	Napsa
ENSRNOG00000010208	0,000000108	2,88E-10	16,2	14,00561	4,19	Timp1
Rn30005109	0,000000114	3,18E-10	16,1	13,91173	4,22	Mgp
ENSRNOG00000036673	0,000000114	3,18E-10	16,1	13,91069	4,83	Sectm1b
R004746_01	0,000000141	4E-10	15,8	13,69011	5,99	Fgf23

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
ENSRNOG00000008478	0,000000151	4,53E-10	15,7	13,56955	4,96	Mmp13
R002282_01	0,000000151	4,65E-10	15,6	13,54437	4,98	Fgr
ENSRNOG00000006306	0,000000153	4,98E-10	15,6	13,47956	4,4	Gip
ENSRNOG00000004972	0,000000153	5,03E-10	15,6	13,46994	4,39	Upp1
ENSRNOG00000005695	0,000000153	5,11E-10	15,5	13,45393	3,79	Mgp
R002882_01	0,000000153	5,28E-10	15,5	13,42307	3,95	Timp1
ENSRNOG00000008525	0,000000153	5,37E-10	15,5	13,40699	5,98	Csf3
ENSRNOG00000013395	0,000000153	5,47E-10	15,5	13,38917	4,82	Pglyrp1
Rn30002732	0,000000163	5,95E-10	15,4	13,30761	3,82	Bst1
ENSRNOG00000017539	0,000000172	6,39E-10	15,3	13,23876	6,32	Mmp9
R002022_01	0,000000207	7,94E-10	15	13,02764	4,14	Hp
Rn30015013	0,000000341	1,36E-09	14,4	12,50203	4,18	Pstpip1
R003655_01	0,000000341	1,37E-09	14,4	12,4983	6,7	Cxcl6
ENSRNOG00000007059	0,000000341	1,39E-09	-14,4	12,48162	-3,47	Atp1b4
R002220_01	0,00000036	1,49E-09	14,3	12,4143	4,69	Reg3a
ENSRNOG00000000419	0,000000373	1,63E-09	14,2	12,32821	3,75	Cfb
Rn30002615	0,000000373	1,63E-09	14,2	12,32496	4,43	Socs3
ENSRNOG00000018570	0,000000377	1,68E-09	-14,2	12,29919	-3,57	C1qtnf3
Rn30026566	0,000000409	1,84E-09	14,1	12,20616	5,73	Sectm1b
Rn30008190	0,000000414	1,89E-09	14	12,18041	4,07	Mmp3
R001657_01	0,000000423	1,96E-09	14	12,14584	3,78	Il4ra
Rn30006757	0,000000426	0,000000002	14	12,12697	3,63	Serping1
ENSRNOG00000002843	0,000000475	2,26E-09	13,8	12,00726	4,9	Cxcl6
Rn30026248	0,000000493	2,38E-09	13,8	11,95748	6,31	Cxcl3
R002806_01	0,000000517	2,52E-09	-13,7	11,89937	-3,64	Igsf1
ENSRNOG00000011406	0,000000537	2,69E-09	13,6	11,83599	5,46	Ccl4
ENSRNOG00000010203	0,000000563	2,85E-09	13,6	11,77847	4,56	Clec4e
Rn30000308	0,000000597	3,12E-09	13,5	11,68942	3,29	Cfb
ENSRNOG00000000187	0,000000597	3,16E-09	13,5	11,67661	3,11	Csf2rb
ENSRNOG00000018598	0,000000597	3,19E-09	13,5	11,66603	4,75	Ankrd1
ENSRNOG00000013794	0,000000597	3,21E-09	13,5	11,66228	3,25	Rbp1
Rn30018159	0,000000608	3,3E-09	13,4	11,63341	4,08	Itgam
ENSRNOG00000000239	0,000000609	3,35E-09	13,4	11,61909	4,67	Ccl7
ENSRNOG00000009907	0,000000657	3,65E-09	13,3	11,53379	5,79	Mmp8
Rn30002157	0,000000664	3,73E-09	13,3	11,51292	3,61	Prg4
Rn30026019	0,000000711	4,04E-09	13,2	11,43348	4,1	Lilrb4
ENSRNOG00000020090	0,000000736	4,25E-09	13,2	11,38251	4,34	Ceacam1,Ceacam10
ENSRNOG00000002776	0,000000736	4,4E-09	13,1	11,34824	5,42	Sell
ENSRNOG00000006151	0,000000751	4,54E-09	13,1	11,31769	5,72	Reg3b
Rn30000137	0,00000084	5,22E-09	12,9	11,1805	3,1	Csf2rb
Rn30007316	0,00000084	5,24E-09	12,9	11,1765	4,44	Plscr1
R002843_01	0,000000888	5,65E-09	12,9	11,10196	3,91	Gda
Rn30009402	0,000000902	5,79E-09	12,8	11,07711	3,36	Cd163
Rn30010157	0,000000955	6,19E-09	12,8	11,01062	5,92	Nos2
ENSRNOG00000006715	0,000000975	6,41E-09	12,7	10,97572	3,59	Ccr1
ENSRNOG00000009734	0,000000975	6,46E-09	12,7	10,96781	3,63	Akr1b8
ENSRNOG00000012280	0,000000975	6,56E-09	12,7	10,95351	4,95	Ptx3
ENSRNOG00000026644	0,000000975	6,56E-09	12,7	10,95341	4,35	Glipr1
R003495_01	0,00000102	6,96E-09	12,7	10,89431	3,38	Cd14
R003209_01	0,00000103	7,15E-09	12,6	10,86801	3,54	Ccr1
R000846_01	0,00000119	8,44E-09	12,5	10,70224	3,11	Ripk3

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30009682	0,00000119	8,48E-09	12,5	10,69849	6,7	Serpina3n
ENSRNOG00000002946	0,00000122	8,77E-09	12,4	10,66416	3,59	Socs3
ENSRNOG00000014835	0,00000128	9,36E-09	12,4	10,59946	4,1	Il1rl1
ENSRNOG00000031927	0,00000146	1,07E-08	12,2	10,46365	2,93	Klk6
Rn30009006	0,00000151	1,12E-08	12,2	10,41929	3,43	Tlr2
ENSRNOG00000028616	0,00000153	1,14E-08	-12,2	10,40162	-3,75	Pck1
Rn30014939	0,00000171	1,29E-08	12	10,283	3,41	Uox
ENSRNOG00000004649	0,00000172	0,000000013	12	10,26803	4,09	Il1b
ENSRNOG00000020845	0,00000181	1,39E-08	12	10,2072	3,15	Tyrobp
ENSRNOG00000007545	0,00000186	1,44E-08	11,9	10,17123	3,23	Angptl4
R000887_01	0,00000195	1,53E-08	11,9	10,10936	4,65	Ccl5
Rn30000166	0,00000201	0,000000016	11,8	10,06409	5,8	Ccl12
ENSRNOG00000003138	0,00000201	0,000000016	11,8	10,06109	5,61	Fcgr2a
Rn30013644	0,00000211	1,69E-08	-11,8	10,0065	-3,51	Ogn
Rn30016019	0,00000229	1,85E-08	11,7	9,91624	3,29	Irf7
Rn30004672	0,00000233	0,000000019	11,7	9,89215	4,28	Plek
R003712_01	0,00000234	1,92E-08	11,7	9,88168	2,98	Chrna1
Rn30011246	0,00000236	1,95E-08	11,6	9,86387	3,59	Itgb7
R000330_01	0,00000243	2,03E-08	11,6	9,82778	3,85	Fetub
ENSRNOG00000017874	0,00000245	2,06E-08	11,6	9,81141	3,66	Cd53
Rn30002173	0,00000248	0,000000021	11,6	9,79287	3,21	Hcls1
ENSRNOG00000036837	0,00000249	2,12E-08	11,6	9,78058	3,09	Nfe2
ENSRNOG00000033557	0,00000252	2,16E-08	11,6	9,76097	2,8	Stfa2l1
Rn30020978	0,00000255	0,000000022	11,5	9,74307	5,64	Cd177
Rn30006438	0,00000257	2,24E-08	11,5	9,72671	3,2	Myo1g
ENSRNOG00000019587	0,00000258	2,26E-08	11,5	9,71787	4,7	Ptprn
Rn30002801	0,0000026	0,000000023	11,5	9,7005	3,8	Fcgr2a
ENSRNOG00000014504	0,00000265	2,38E-08	11,5	9,6672	4,14	Il1r1
Rn30020063	0,00000265	2,38E-08	11,5	9,66492	3,28	Clec4a1
Rn30000016	0,00000274	2,48E-08	11,4	9,62314	3,73	Steap1
ENSRNOG00000019855	0,00000287	2,63E-08	11,4	9,56532	5,98	Fgf23
R005067_01	0,00000287	2,64E-08	-11,4	9,5624	-2,9	Rpl3l
Rn30002011	0,00000305	2,83E-08	11,3	9,49244	3,63	Plac8
Rn30015012	0,00000312	2,91E-08	11,3	9,46506	4,4	Pstpip1
R002918_01	0,00000314	2,94E-08	11,3	9,45232	3,75	Gch1
ENSRNOG00000017819	0,00000325	3,09E-08	11,2	9,40318	3,27	Cd14
Rn30020145	0,00000326	3,12E-08	11,2	9,39409	6,26	Isg15
R003454_01	0,00000343	0,000000033	-11,2	9,33703	-2,84	Akap12
Rn30009092	0,00000347	3,37E-08	11,1	9,31679	5,27	Irg1
ENSRNOG00000011205	0,00000417	4,17E-08	11	9,1018	5,48	Ccl3
Rn30001237	0,00000417	4,17E-08	11	9,10058	4,61	Oas1a
Rn30012735	0,00000417	0,000000042	10,9	9,09514	4,17	Ankrd2
ENSRNOG00000024159	0,00000426	4,32E-08	10,9	9,06651	2,8	Fcer1g
ENSRNOG00000016339	0,00000426	4,34E-08	10,9	9,0606	3	Uox
Rn30015312	0,0000044	4,51E-08	-10,9	9,02159	-2,92	Nrap
ENSRNOG00000002802	0,00000444	4,58E-08	10,9	9,00662	6,32	Cxcl1
ENSRNOG00000004197	0,00000447	4,63E-08	-10,9	8,99542	-3,23	Asb12
R004362_01	0,00000449	4,69E-08	10,8	8,98336	5,49	Car4
R000055_01	0,00000461	4,86E-08	10,8	8,94704	2,99	Pdpn
ENSRNOG00000015117	0,00000461	4,87E-08	-10,8	8,94549	-3,13	Lrrc39
ENSRNOG00000013932	0,00000462	4,91E-08	10,8	8,93704	2,51	Rbp2

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30009463	0,00000511	5,48E-08	10,7	8,82474	3,42	Lcp1
Rn30017177	0,00000529	5,72E-08	10,7	8,78281	6,6	Rptn
Rn30016464	0,00000546	5,93E-08	10,6	8,74596	2,98	Adam8
Rn30011973	0,00000589	6,47E-08	10,6	8,65724	4,43	Mthfs
ENSRNOG00000037198	0,00000605	6,68E-08	10,5	8,6252	3,75	Usp18
Rn30002484	0,00000606	6,74E-08	10,5	8,61632	4,04	Selp
ENSRNOG00000020465	0,00000606	6,77E-08	10,5	8,61124	2,95	Ripk3
R000644_01	0,00000614	6,89E-08	10,5	8,59346	4,36	Ccl2
Rn30023425	0,00000615	6,95E-08	10,5	8,58496	3,35	Lilrb3l
Rn30021148	0,00000618	7,02E-08	10,5	8,57492	6,53	Ifit3
ENSRNOG00000007113	0,00000642	7,33E-08	10,5	8,53142	3,86	Myo1g
Rn30005224	0,00000645	7,41E-08	10,4	8,52009	4,18	Lyz2
R000075_01	0,00000654	7,55E-08	10,4	8,50128	2,83	Rbp1
Rn30004797	0,00000655	0,000000076	-10,4	8,4948	-2,7	Pamr1
ENSRNOG00000031162	0,00000697	8,18E-08	-10,4	8,4205	-3,01	Ccl24
ENSRNOG00000018822	0,00000701	8,28E-08	10,4	8,40846	2,73	Slc5a5
Rn30024363	0,00000701	8,31E-08	10,3	8,40422	4,69	F5
ENSRNOG00000005214	0,00000702	0,000000084	10,3	8,39319	4,41	Plek
ENSRNOG00000021357	0,00000724	8,72E-08	10,3	8,35545	5,65	Slfn3,Slfn4
Rn30017083	0,00000737	8,91E-08	-10,3	8,33313	-3,18	C1qtnf3
Rn30019719	0,00000739	8,99E-08	10,3	8,32453	5,52	Slfn3,Slfn4
ENSRNOG00000009912	0,00000745	9,11E-08	10,3	8,31118	4,33	Fgr
Rn30001777	0,0000075	9,21E-08	10,3	8,29982	3,52	Retnlg
Rn30006390	0,00000758	9,35E-08	-10,2	8,2844	-3,45	Atp1b4
Rn30001242	0,00000762	9,46E-08	10,2	8,27284	5,53	Oas1k
Rn30017526	0,00000817	0,000000102	10,2	8,19743	2,81	Sod2
Rn30002851	0,0000082	0,000000103	10,2	8,18927	2,95	Fmnl1
ENSRNOG00000012208	0,00000844	0,000000106	10,1	8,15427	2,53	Itgb7
Rn30009494	0,00000851	0,000000108	10,1	8,13574	2,67	Ear11
ENSRNOG00000006930	0,00000851	0,000000108	-10,1	8,13532	-3,04	Casq1
Rn30022563	0,00000851	0,000000109	10,1	8,13194	2,84	Plaur
R001187_01	0,00000862	0,000000111	10,1	8,11334	3,51	Il10
Rn30006415	0,0000087	0,000000112	10,1	8,09906	2,34	Lgmn
Rn30018495	0,00000875	0,000000113	10,1	8,08878	3,79	Ceacam10
ENSRNOG00000007600	0,00000911	0,000000119	-10	8,04314	-4,61	Igsf1
R002279_01	0,00000921	0,000000121	10	8,02738	2,51	Fosl1
ENSRNOG00000030183	0,00000976	0,000000129	9,98	7,95854	3,09	Plod2
R002359_01	0,0000101	0,000000135	9,94	7,91443	3,73	Cd38
R001157_01	0,0000103	0,000000138	9,92	7,89199	2,72	Rbp2
ENSRNOG00000028548	0,0000104	0,00000014	9,91	7,8746	5,89	Ccl9
R001593_01	0,0000108	0,000000147	9,87	7,82809	5,6	Oas1k,Oas1a
Rn30015118	0,0000112	0,000000153	9,84	7,78796	2,91	Susd3
Rn30005642	0,0000112	0,000000154	9,83	7,77819	2,49	Ptges
Rn30015053	0,0000112	0,000000154	9,83	7,77631	3,28	Il33
Rn30002798	0,0000112	0,000000155	9,83	7,77304	3,84	Fcgr2a
Rn30012197	0,0000113	0,000000156	9,82	7,76271	4,73	Olfm4
ENSRNOG00000013407	0,0000115	0,00000016	-9,8	7,74272	-2,5	Slc5a11
ENSRNOG00000001187	0,0000115	0,00000016	9,8	7,73922	4,69	Oasl
Rn30003193	0,0000117	0,000000164	-9,78	7,71718	-2,64	Itgb1bp2
Rn30017635	0,0000119	0,000000168	-9,76	7,68916	-2,94	Kcne1l
Rn30002325	0,0000121	0,000000171	9,74	7,66906	2,25	Serpinb3a

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
R000458_01	0,0000122	0,000000174	9,73	7,65584	2,84	Lgals3bp
Rn30011035	0,0000124	0,000000177	9,72	7,63707	2,99	C1s
Rn30002227	0,0000126	0,000000181	9,7	7,61157	3,92	Ifi47
Rn30012770	0,0000126	0,000000183	9,69	7,60506	4,11	Slpi
Rn30019436	0,0000127	0,000000185	9,68	7,59169	2,24	Fxyd5
R001319_01	0,0000127	0,000000185	9,68	7,5901	2,39	Mvp
Rn30012810	0,0000137	0,0000002	9,62	7,51348	2,38	Rbp2
Rn30002852	0,0000137	0,000000202	9,61	7,50231	2,69	Fmnl1
ENSRNOG00000000907	0,0000139	0,000000206	9,6	7,48162	2,28	Alox5ap
R004778_01	0,0000143	0,000000214	9,56	7,44211	5,72	Prok2
R001077_01	0,0000145	0,000000217	9,55	7,42758	6,17	Reg3b
Rn30020443	0,000015	0,000000226	9,52	7,39011	2,75	Gjb6
R001881_01	0,0000154	0,000000232	9,5	7,36054	2,65	Il1r2
ENSRNOG00000007350	0,0000161	0,000000244	9,46	7,30922	3	Rac2
ENSRNOG00000028814	0,0000163	0,000000249	9,44	7,28943	3,54	Oasl2
Rn30012529	0,0000165	0,000000252	9,44	7,27768	2,12	Myd88
Rn30000168	0,0000168	0,000000259	9,41	7,24792	6,13	Ccl12
R003972_01	0,0000169	0,000000262	-9,41	7,23916	-2,63	Btc
R002572_01	0,0000171	0,000000266	9,39	7,22365	2,82	Slc15a3
ENSRNOG00000008141	0,0000177	0,000000277	9,36	7,18171	2,09	Nppb
Rn30007703	0,000018	0,000000283	9,34	7,16079	4,91	Mmp13
Rn30019331	0,0000184	0,00000029	9,32	7,13257	2,86	Ms4a7
ENSRNOG00000021199	0,0000187	0,000000295	9,31	7,11611	3,9	Fcgr1a
ENSRNOG00000031445	0,0000191	0,000000305	9,28	7,08139	2,77	Ear11
ENSRNOG00000002728	0,0000191	0,000000308	-9,28	7,07361	-2,56	Btc
ENSRNOG00000006360	0,0000191	0,000000309	9,27	7,07091	4,35	Reg3a
Rn30017467	0,0000192	0,00000031	-9,27	7,0652	-2,36	Fndc1
ENSRNOG00000030021	0,0000195	0,000000317	9,25	7,04223	3,04	Ccl6
R003344_01	0,0000197	0,000000323	9,24	7,02463	5,75	Ccl4
Rn30010078	0,0000197	0,000000324	9,24	7,01965	2,17	Tifa
ENSRNOG00000007159	0,0000201	0,000000333	9,22	6,99301	6,53	Ccl2
ENSRNOG00000015441	0,0000208	0,000000346	9,18	6,95342	3,65	Il4ra
Rn30006231	0,0000209	0,000000348	-9,18	6,94911	-2,9	Casq1
Rn30024525	0,0000211	0,000000353	9,17	6,93456	4,17	Hk3
Rn30018760	0,0000212	0,000000357	9,16	6,92337	2,88	Tmem8a
R000450_01	0,0000215	0,000000362	9,15	6,90656	2,19	Slc2a1
Rn30006833	0,0000219	0,000000371	9,13	6,88315	2,58	Angptl4
R002190_01	0,000022	0,000000373	9,13	6,87626	2,96	Adora2a
Rn30007734	0,000022	0,000000375	9,12	6,87118	3,01	Tmem45b
Rn30021553	0,0000231	0,000000394	9,08	6,82036	2,6	Ear11
R003473_01	0,0000247	0,000000426	9,02	6,74109	2,19	Il8rb
R000310_01	0,000025	0,000000432	9,01	6,72739	2,45	Cd37
ENSRNOG00000000569	0,0000255	0,000000442	9	6,70379	2,68	MGC112715
Rn30000127	0,0000255	0,000000444	8,99	6,699	2,53	Sqrdl
R003632_01	0,000026	0,000000453	8,98	6,67802	3,98	Tnfrsf1b
R003618_01	0,0000268	0,000000472	8,95	6,6364	2,84	Slc2a3
ENSRNOG00000000853	0,0000273	0,000000482	8,93	6,6162	2,49	Aif1
Rn30016445	0,0000273	0,000000483	8,93	6,61348	3,22	Cd53
Rn30022466	0,0000276	0,000000491	8,92	6,5971	2,77	Fcer1g
Rn30011009	0,0000283	0,000000505	8,89	6,56768	3,96	Snx10
Rn30019109	0,0000287	0,000000514	8,88	6,54962	3,55	Camp

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30021287	0,0000289	0,000000523	8,87	6,53218	2,67	Nfam1
Rn30018278	0,0000289	0,000000523	8,87	6,53177	3,2	Napsa
ENSRNOG00000012172	0,0000289	0,000000524	8,87	6,53012	2,66	Sfpi1
Rn30006808	0,0000292	0,000000531	-8,86	6,51623	-2,15	Smtnl1
Rn30014956	0,0000293	0,000000536	-8,85	6,50764	-2,26	Plcd4
ENSRNOG00000011971	0,0000295	0,000000542	8,84	6,49656	2,9	C1s
ENSRNOG00000014964	0,0000295	0,000000544	8,84	6,4923	3,21	Hp
Rn30017741	0,0000296	0,000000548	-8,83	6,48362	-1,97	Fsd2
Rn30026821	0,0000304	0,000000565	-8,81	6,45252	-4,22	Pck1
Rn30013465	0,0000304	0,000000567	-8,81	6,44985	-2,12	Cox8b
Rn30017594	0,0000309	0,000000579	8,79	6,42873	2,49	Bcl3
ENSRNOG00000017637	0,0000313	0,000000588	-8,78	6,41201	-2,26	Fbp2
Rn30010766	0,0000313	0,000000589	8,78	6,41088	2,07	Fes
Rn30008196	0,0000317	0,000000599	8,77	6,39395	4,86	Mmp3,Mmp10
ENSRNOG00000036827	0,0000321	0,000000609	-8,75	6,37734	-2,69	Ppp1r1a
Rn30008444	0,0000321	0,00000061	8,75	6,37506	2,24	Ifi27
ENSRNOG00000006774	0,0000321	0,000000612	8,75	6,37134	4,91	Ccr5
Rn30000114	0,0000323	0,000000617	-8,74	6,36265	-2,21	Cdo1
Rn30016270	0,0000324	0,000000621	8,74	6,35633	2,43	Unc93b1
Rn30006787	0,0000326	0,000000628	8,73	6,34441	2,12	Ube2l6
R003409_01	0,0000343	0,000000664	8,69	6,28858	2,55	Ltb4r
ENSRNOG00000015086	0,0000343	0,000000667	-8,68	6,28394	-2,22	Plin
Rn30006648	0,0000343	0,000000667	8,68	6,2832	2,79	Rac2
ENSRNOG00000013330	0,0000345	0,000000675	8,67	6,27095	2,6	Pcdh21
Rn30007437	0,0000353	0,000000695	8,65	6,24145	2,25	Lyn
Rn30024809	0,0000353	0,0000007	-8,65	6,2339	-2,12	Dhrs7c
R004860_01	0,0000353	0,000000701	8,65	6,23308	3,08	Coro1a
Rn30000351	0,0000353	0,000000702	8,65	6,23081	2,54	Psmb9
Rn30017105	0,0000356	0,000000711	8,64	6,2186	3,91	Ankrd1
ENSRNOG00000017277	0,0000356	0,000000713	8,63	6,21583	3,81	Igsf6
ENSRNOG00000019728	0,0000361	0,000000726	8,62	6,19677	5,06	Itgam
ENSRNOG00000001414	0,0000369	0,000000746	8,6	6,16876	2,98	Serpine1
Rn30001796	0,0000373	0,000000758	8,59	6,15282	5,13	Mx2
Rn30006391	0,0000391	0,000000799	8,55	6,09861	2,26	Adfp
Rn30004711	0,0000398	0,000000816	-8,53	6,07747	-2,56	Srl
ENSRNOG00000013973	0,0000401	0,000000828	8,52	6,06256	5,75	Lcn2
R001101_01	0,0000419	0,00000087	-8,49	6,0121	-2,18	Ppp1r1a
Rn30007636	0,0000431	0,000000904	8,46	5,97234	2,59	Myo1f
Rn30008290	0,0000435	0,000000915	8,45	5,95956	2,78	Pon3
Rn30021789	0,0000444	0,00000094	8,43	5,93277	2,15	Parp9
R004693_01	0,0000446	0,000000946	-8,43	5,92582	-2,39	Serpinb7
Rn30019564	0,0000464	0,000000991	8,39	5,87791	3,29	Fcgr1a
ENSRNOG00000032472	0,0000465	0,000000996	-8,39	5,87339	-1,96	Gpr64
ENSRNOG00000033017	0,0000476	0,00000102	8,37	5,8467	4,07	Pilra
Rn30014099	0,0000476	0,00000103	8,37	5,84351	2,16	Arid5a
R004525_01	0,0000476	0,00000103	8,36	5,83999	2,73	Psmb8
Rn30005886	0,0000482	0,00000105	8,35	5,82214	2,15	Hpgds
R000657_01	0,0000482	0,00000105	-8,35	5,81911	-2,26	Fez1
Rn30016609	0,0000487	0,00000106	8,34	5,80463	3,28	F2rl2
Rn30007313	0,0000487	0,00000107	8,34	5,80286	3,76	Slamf9
Rn30008321	0,0000487	0,00000107	8,34	5,79956	2,31	Zc3h12a

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
ENSRNOG00000030712	0,0000489	0,00000108	8,33	5,79234	2,27	RT1-A2
Rn30003750	0,0000494	0,00000109	-8,32	5,77948	-2,15	Asb12
ENSRNOG00000020552	0,0000495	0,0000011	8,32	5,77505	2,7	Fosl1
R001814_01	0,0000497	0,00000111	8,31	5,76658	2,47	P2ry6
Rn30005924	0,0000499	0,00000111	8,31	5,75951	2,15	Cd302
R000807_01	0,0000525	0,00000118	8,26	5,69684	2,23	Pf4
R002276_01	0,0000528	0,00000119	8,26	5,68742	5,53	Lcn2
ENSRNOG00000026605	0,0000529	0,0000012	8,25	5,6845	2,07	Ifi27l2b
ENSRNOG00000002794	0,0000531	0,00000121	8,25	5,67456	3,86	Selp
Rn30006408	0,0000545	0,00000124	8,23	5,64519	2,37	Xdh
R001662_01	0,0000545	0,00000125	8,22	5,63997	2,15	Ptprc
ENSRNOG00000032626	0,0000546	0,00000126	8,22	5,63423	4,54	Mmp3
Rn30011676	0,0000552	0,00000127	8,21	5,62059	2,45	Lgals9
ENSRNOG00000006108	0,0000555	0,00000129	8,2	5,60849	1,99	Gngt2
R004465_01	0,0000555	0,00000129	8,2	5,6046	3,19	Pcdh21
ENSRNOG00000003312	0,0000555	0,0000013	8,2	5,60378	2,7	Chi3l1
Rn30015878	0,0000555	0,0000013	8,2	5,60368	3,2	Igsf6
ENSRNOG00000019430	0,0000577	0,00000135	8,17	5,56201	2,6	Coro1a
Rn30009669	0,0000577	0,00000135	8,17	5,55971	3,04	Tfpi2
Rn30008505	0,0000581	0,00000137	8,16	5,54961	2,16	Hck
ENSRNOG00000007089	0,0000595	0,0000014	8,14	5,52249	2,12	Lgmn
Rn30021790	0,0000601	0,00000142	8,13	5,50825	2,03	Parp9
R003956_01	0,0000603	0,00000143	8,13	5,50235	3,3	Cyp7b1
ENSRNOG00000013304	0,0000616	0,00000146	8,11	5,47851	3,54	Arg1
ENSRNOG00000001959	0,0000618	0,00000148	8,1	5,47074	4,81	Mx1
R003520_01	0,0000618	0,00000148	-8,1	5,46986	-1,96	Lin7b
R000632_01	0,0000628	0,00000151	8,09	5,44998	1,91	Crispld2
ENSRNOG00000010319	0,0000643	0,00000155	8,07	5,41858	3,2	Lcp1
R001746_01	0,0000661	0,0000016	8,05	5,38802	4,36	Cxcl10
ENSRNOG00000030210	0,0000674	0,00000163	-8,03	5,36544	-3,03	Fndc1
ENSRNOG00000007284	0,0000687	0,00000167	8,02	5,34319	2,5	Slc2a1
ENSRNOG00000009263	0,0000697	0,0000017	8	5,32508	2,46	Ifi27
Rn30001791	0,0000718	0,00000176	7,98	5,29203	5,12	Mx1
Rn30013145	0,0000729	0,00000179	7,97	5,27389	2,69	Oscar
ENSRNOG00000007060	0,0000746	0,00000183	7,95	5,24843	2,2	Adfp
R002652_01	0,0000748	0,00000184	7,95	5,24267	1,98	Ifngr1
Rn30002471	0,0000757	0,00000187	7,94	5,22759	5,08	Sell
ENSRNOG00000038881	0,0000758	0,00000188	7,93	5,22371	3,54	Hcls1
ENSRNOG00000011901	0,0000776	0,00000193	7,92	5,19704	2,7	Rrad
ENSRNOG00000020399	0,0000776	0,00000193	7,91	5,19517	2,77	Ltb4r
Rn30009356	0,0000787	0,00000196	7,9	5,17791	4,88	Clec4e
Rn30000541	0,00008	0,00000201	7,89	5,15584	3,58	Ptprc
Rn30013656	0,0000804	0,00000202	-7,88	5,14829	-2,64	Synpo2
R002400_01	0,0000809	0,00000204	7,88	5,13917	2,23	Il1a
Rn30000728	0,0000813	0,00000205	7,87	5,13188	2,33	Aif1
ENSRNOG00000026647	0,0000842	0,00000214	7,84	5,08848	2,02	Cxcl16
Rn30002575	0,0000852	0,00000218	-7,83	5,07136	-3,73	Alb
Rn30017863	0,0000854	0,00000219	-7,83	5,06582	-2,72	Lipk
Rn30003809	0,000088	0,00000226	-7,8	5,03346	-1,83	Cobl
ENSRNOG00000014269	0,000089	0,00000229	7,79	5,0191	4,56	Il8rb
Rn30010953	0,0000906	0,00000234	7,78	4,99801	2,35	Rrad

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
ENSRNOG00000019048	0,0000908	0,00000235	7,78	4,99413	2,96	Sod2
ENSRNOG00000021644	0,0000925	0,0000024	7,76	4,97193	2,62	Slc15a3
ENSRNOG00000008144	0,0000945	0,00000246	7,75	4,94527	2,07	Irf1
Rn30005112	0,000097	0,00000253	-7,73	4,91556	-1,83	Nsg1
Rn30010858	0,0000975	0,00000255	7,72	4,90867	1,86	C1r
Rn30021709	0,0000979	0,00000257	7,71	4,89979	3,58	Ly6c
ENSRNOG00000014961	0,0000979	0,00000257	7,71	4,89975	2,32	Pdpn
R001373_01	0,0001	0,00000264	-7,7	4,87353	-2,96	Adrb3
ENSRNOG00000001369	0,000101	0,00000266	7,69	4,86509	3,76	Oas1a
Rn30000362	0,000101	0,00000267	7,69	4,86351	2,27	RT1-A2
Rn30006050	0,000103	0,00000274	7,67	4,83543	1,79	Tgm3
Rn30007430	0,000103	0,00000274	7,67	4,83494	2,67	Plod2
R002312_01	0,000105	0,0000028	7,66	4,81466	2,75	Pla2g2a
R004138_01	0,000106	0,00000284	7,65	4,79958	1,71	Cd200r1
Rn30006068	0,000107	0,00000286	7,64	4,79061	2,55	Cst7
ENSRNOG00000001302	0,000107	0,00000288	7,64	4,78454	2,92	Adora2a
ENSRNOG00000020922	0,000107	0,00000289	-7,63	4,77936	-2,37	Hspb6
Rn30013737	0,000108	0,00000292	7,63	4,77161	3,82	Slc11a1
ENSRNOG00000020679	0,00011	0,00000298	7,61	4,75093	2,16	Icam1
Rn30007108	0,00011	0,00000299	-7,61	4,74714	-2,02	Slc16a7
R004305_01	0,00011	0,000003	7,61	4,7433	1,96	Cygb
ENSRNOG00000011754	0,000112	0,00000306	-7,6	4,72286	-2,61	Myom2
ENSRNOG00000000655	0,000112	0,00000306	7,6	4,72098	2,43	Ptprc
ENSRNOG00000017414	0,000114	0,00000313	7,58	4,6996	2,87	Irf7
Rn30006245	0,000114	0,00000315	7,58	4,69327	2,36	Arhgap9
ENSRNOG00000002470	0,000114	0,00000315	7,58	4,69085	2,76	Ifi47
ENSRNOG00000031134	0,000115	0,00000318	7,57	4,68362	4,71	Serpinb3
Rn30006185	0,000118	0,00000328	-7,55	4,65221	-1,86	Msx1
ENSRNOG00000009730	0,000118	0,00000329	7,55	4,64908	3,69	Cyp7b1
Rn30011774	0,000119	0,00000332	7,54	4,63811	3,82	Msr1
R002604_01	0,00012	0,00000337	7,53	4,62291	2,22	Alox5ap
Rn30008906	0,00012	0,00000337	7,53	4,62166	3,08	Akr1b8
Rn30003789	0,000121	0,00000339	7,53	4,61654	2,85	Tlr7
ENSRNOG00000011365	0,000124	0,0000035	7,5	4,58393	2,6	Emb
ENSRNOG00000000580	0,000125	0,00000351	-7,5	4,58005	-2,15	Fam26d
R001297_01	0,000126	0,00000356	7,49	4,56804	2,28	Apobec1
Rn30013144	0,000126	0,00000357	7,49	4,56233	2,94	Oscar
Rn30024903	0,000127	0,00000363	7,48	4,54737	1,72	Cxcl16
Rn30003212	0,000129	0,00000368	7,47	4,53131	2,41	Cybb
Rn30018261	0,000129	0,00000369	7,47	4,52965	2	Gmfg
ENSRNOG00000021062	0,000129	0,0000037	7,47	4,5266	2,64	Fxyd5
ENSRNOG00000020035	0,000129	0,00000371	-7,46	4,52386	-3,95	Cyp17a1
Rn30000470	0,000129	0,00000372	7,46	4,52222	2,04	MGC112715
ENSRNOG00000008376	0,000132	0,0000038	7,45	4,49964	2,59	Slc2a3
R001116_01	0,000133	0,00000384	7,44	4,48859	2,31	C3ar1
Rn30013844	0,000133	0,00000385	-7,44	4,48646	-2,07	Plin
Rn30005440	0,000133	0,00000387	7,44	4,4811	1,77	Tfec
Rn30012686	0,000133	0,00000388	-7,44	4,4787	-2,13	C1qtnf9
R001889_01	0,000134	0,00000391	7,43	4,47074	2,45	Itgb7
Rn30011308	0,000134	0,00000392	7,43	4,46878	3,84	Ptx3
Rn30008759	0,000135	0,00000396	-7,42	4,45619	-2,48	Lce1m

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
R001295_01	0,000136	0,00000398	7,42	4,45098	2,58	Cyp11b2
Rn30001956	0,000137	0,00000402	7,41	4,44119	3,25	Tlr6
ENSRNOG00000029508	0,000137	0,00000403	-7,41	4,43799	-2,06	Slpil2
ENSRNOG00000005935	0,000138	0,00000408	7,4	4,42627	2,74	A3galt2
Rn30012432	0,000139	0,00000413	-7,39	4,41528	-1,74	Rnf180
ENSRNOG00000029810	0,000141	0,00000419	7,38	4,39968	1,85	Tspan4
Rn30021164	0,000144	0,00000428	7,37	4,37818	4,47	Trem1
Rn30018177	0,000144	0,00000431	-7,36	4,37078	-2,82	Actn3
ENSRNOG00000010938	0,000144	0,00000431	-7,36	4,36908	-2,1	Slc7a10
Rn30000167	0,000145	0,00000433	7,36	4,36582	4,2	Ccl7
ENSRNOG00000015078	0,000146	0,00000438	7,35	4,3531	1,93	Ifitm3
ENSRNOG00000010897	0,000147	0,00000444	7,34	4,34021	1,76	Nek6
Rn30020918	0,000149	0,00000449	7,34	4,32844	2,27	Agbl1
ENSRNOG00000002911	0,000152	0,0000046	-7,32	4,30282	-2,25	Alb
ENSRNOG00000016456	0,000152	0,00000463	7,32	4,29645	3,14	Il33
ENSRNOG00000012674	0,000152	0,00000463	-7,32	4,29629	-2,65	Adrb3
Rn30013833	0,000159	0,00000487	7,28	4,24425	1,66	Ifitm3
ENSRNOG00000022282	0,00016	0,00000489	-7,28	4,23979	-1,96	Col2a1
Rn30020870	0,000164	0,00000504	7,26	4,20996	2,28	Lrrc25
Rn30011419	0,000168	0,00000517	-7,24	4,18354	-3,17	Thrsp
Rn30002820	0,00017	0,00000527	-7,23	4,16455	-1,94	Mpz
R000009_01	0,000174	0,00000538	7,22	4,14274	3,52	Enpp3
R005107_01	0,000174	0,00000541	7,21	4,13591	3,8	Ctrc
Rn30015761	0,000174	0,00000542	7,21	4,13566	2,29	Pfkp
Rn30012435	0,000175	0,00000545	-7,21	4,12959	-2,45	Pgam2
Rn30019585	0,000175	0,00000547	7,21	4,12469	3,3	Cpxm1
R002677_01	0,000177	0,00000554	7,2	4,11259	2,92	Nkg7
ENSRNOG00000002520	0,000178	0,00000558	7,19	4,1051	1,98	Litaf
ENSRNOG00000013262	0,000178	0,00000561	-7,19	4,09981	-2,4	Myl1_v2
ENSRNOG00000001571	0,000186	0,00000589	-7,16	4,0491	-2,48	Cldn8
Rn30002819	0,00019	0,00000602	7,14	4,02616	5,23	Nlrp3
Rn30003601	0,00019	0,00000603	7,14	4,02567	2,51	Glipr1
Rn30020680	0,00019	0,00000605	-7,14	4,02229	-1,78	Dsg4
R003194_01	0,000193	0,00000615	-7,13	4,00465	-2,6	Alb
Rn30012182	0,000195	0,00000624	-7,12	3,9902	-1,88	Myl1_v2
Rn30017604	0,000196	0,00000627	7,12	3,98529	2	Ch25h
Rn30005483	0,000196	0,0000063	7,11	3,98016	1,97	Gngt2
Rn30009014	0,000196	0,00000631	7,11	3,97805	2,98	Slc39a14
ENSRNOG00000013791	0,000197	0,00000635	7,11	3,97122	3,55	Enpp3
Rn30002288	0,000198	0,00000641	7,1	3,96247	2,01	Rhoh
Rn30022690	0,000204	0,00000662	7,08	3,92871	4,97	Fcgr3a
R004337_01	0,000204	0,00000665	7,08	3,92441	1,7	Litaf
R000556_01	0,000204	0,00000667	7,08	3,9221	1,96	Nppb
Rn30013417	0,000208	0,00000678	-7,06	3,90436	-2,56	Dhx36
Rn30006778	0,00021	0,00000686	7,06	3,89202	1,76	Ehf
ENSRNOG00000018286	0,000216	0,00000709	7,04	3,85807	2,13	Chrna1
R000716_01	0,000218	0,00000715	-7,03	3,85072	-2	Gstm7
ENSRNOG00000039839	0,000219	0,00000722	-7,02	3,84034	-2,24	Trdn
R001392_01	0,000222	0,0000073	-7,02	3,8282	-1,73	Col2a1
ENSRNOG00000012972	0,000227	0,0000075	7	3,80034	1,61	Alox5
Rn30022297	0,000228	0,00000754	7	3,79607	1,88	Rab20

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30022292	0,000232	0,00000772	6,98	3,77116	2,31	Stfa2l2
ENSRNOG00000012881	0,000235	0,00000783	6,97	3,75686	1,9	Fgl2
R001525_01	0,000235	0,00000787	-6,97	3,75113	-2,02	Pxmp2
Rn30002327	0,000235	0,00000789	6,97	3,74917	1,52	Parm1
Rn30006692	0,000237	0,00000794	6,96	3,7417	2,02	Nfkbia
ENSRNOG00000013745	0,000237	0,00000798	6,96	3,7371	3,21	Ctrc
Rn30017860	0,00024	0,0000081	-6,95	3,72121	-1,84	Zfp61
ENSRNOG00000023991	0,000245	0,00000828	6,94	3,69975	1,91	Rab20
Rn30007552	0,000245	0,00000828	-6,93	3,69858	-2,49	Stra6
Rn30017443	0,000245	0,00000829	-6,93	3,69828	-2,07	Col4a5
Rn30014857	0,000247	0,00000839	6,93	3,68547	2,2	Cotl1
ENSRNOG00000003217	0,000249	0,00000846	6,92	3,67708	2,07	Lgals3bp
Rn30003533	0,00025	0,00000852	6,92	3,67001	1,72	Dusp1
ENSRNOG00000020300	0,00025	0,00000852	6,92	3,66947	2,44	Lsp1
ENSRNOG00000014117	0,000251	0,00000858	6,91	3,6625	1,9	Hmox1
ENSRNOG00000012772	0,000251	0,00000858	6,91	3,66213	1,75	Nqo1
ENSRNOG00000006320	0,000251	0,00000863	6,91	3,65696	2,53	Ptges
Rn30005451	0,000253	0,00000872	6,9	3,64547	3,2	Steap2
ENSRNOG00000024923	0,000253	0,00000872	-6,9	3,6454	-2,72	Nnat
ENSRNOG00000008048	0,000253	0,00000878	6,9	3,63921	3,49	Plscr1
ENSRNOG00000000456	0,000254	0,0000088	6,9	3,63626	2,41	Psmb8
Rn30026753	0,000258	0,00000897	6,88	3,61634	2,62	Ccl9
ENSRNOG00000008609	0,000258	0,00000901	-6,88	3,61289	-1,98	Capn3
Rn30026819	0,00027	0,00000943	-6,85	3,56568	-2	Adamts18
R001527_01	0,000271	0,0000095	-6,85	3,55787	-1,6	Orm1
Rn30010523	0,000277	0,00000973	6,83	3,53328	1,83	Smap2
Rn30007899	0,00028	0,00000984	-6,82	3,52176	-1,99	Myoz1
ENSRNOG00000003104	0,00028	0,00000986	6,82	3,51982	2,07	Trpv2
Rn30003090	0,00028	0,00000989	6,82	3,51653	2,27	Ifi204
R004629_01	0,00028	0,00000991	6,82	3,51468	2,12	Serpinb10
Rn30004477	0,000283	0,00001	6,81	3,50115	1,89	Gsdmc
R000800_01	0,000283	0,0000101	6,81	3,49914	1,64	C1qb
ENSRNOG00000025297	0,000285	0,0000101	6,8	3,49022	1,67	Gpr171
R001639_01	0,000293	0,0000105	6,79	3,45887	3,07	Gip
ENSRNOG00000013634	0,000295	0,0000106	6,78	3,44691	1,94	Myd88
Rn30026013	0,000295	0,0000106	6,78	3,44436	2,7	Lilrb4
ENSRNOG00000010633	0,000297	0,0000107	-6,77	3,43586	-1,62	Acsl1
Rn30000731	0,000298	0,0000108	6,77	3,43018	4,04	Lst1
ENSRNOG00000011796	0,000298	0,0000108	6,77	3,43014	2,85	C1r
Rn30002218	0,000306	0,0000111	6,75	3,3991	1,95	Serpinb2
ENSRNOG00000010265	0,000307	0,0000111	6,75	3,39432	2,2	Ada
Rn30012641	0,000309	0,0000112	6,74	3,38821	2,58	Trem3
Rn30005257	0,000313	0,0000114	6,73	3,36984	1,68	Hsd11b1
ENSRNOG00000009761	0,000313	0,0000114	-6,73	3,36923	-1,63	Tmod1
Rn30013839	0,000315	0,0000115	-6,73	3,36331	-2,19	Nlrp10
Rn30012843	0,000315	0,0000115	6,72	3,35851	1,63	Blnk
Rn30000608	0,000317	0,0000117	6,72	3,34676	1,88	RT1-CE1
Rn30012989	0,000317	0,0000117	6,72	3,34589	1,92	Ogfrl1
ENSRNOG00000000837	0,000318	0,0000117	6,71	3,34254	1,9	Tnf
ENSRNOG00000017749	0,000319	0,0000118	6,71	3,33566	1,9	Nkg7
Rn30002799	0,00032	0,0000118	6,71	3,33342	4,51	Fcgr2a

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30021958	0,00032	0,0000119	6,71	3,32861	2,28	Tmem106a
Rn30000283	0,00032	0,0000119	6,7	3,32704	2,45	Srgn
Rn30014079	0,00032	0,0000119	6,7	3,32539	1,9	Neurl3
R000261_01	0,00033	0,0000123	-6,68	3,29182	-1,76	Aldh6a1
ENSRNOG00000000459	0,000333	0,0000124	6,68	3,28231	1,97	Psmb9
ENSRNOG00000009037	0,000337	0,0000127	6,66	3,26316	1,99	Sulf1
Rn30005054	0,000343	0,0000129	6,65	3,24313	2,21	Lcp2
ENSRNOG00000007546	0,000344	0,000013	6,65	3,23855	1,62	Asns
ENSRNOG00000027264	0,000347	0,0000131	-6,64	3,22798	-1,59	Dagla
ENSRNOG00000001943	0,000359	0,0000136	6,62	3,19071	2,85	Retnlg
Rn30003285	0,000359	0,0000136	6,62	3,18871	2,26	Bmx
R000231_01	0,000361	0,0000137	6,61	3,18124	1,6	Ppap2a
Rn30005925	0,000369	0,000014	6,6	3,15668	2,02	Cd302
Rn30002682	0,000374	0,0000142	-6,59	3,14255	-2,17	Myh2
R004277_01	0,000375	0,0000144	6,59	3,13369	1,71	Tmem49
Rn30009968	0,000375	0,0000144	-6,59	3,13337	-1,82	Pdgfrl
ENSRNOG00000007918	0,000375	0,0000144	6,58	3,132	2,59	Tbxas1
ENSRNOG00000015904	0,000379	0,0000146	-6,58	3,11872	-1,95	Wfdc1
Rn30019773	0,000379	0,0000146	6,57	3,1155	1,97	Slfn8
ENSRNOG00000020182	0,000379	0,0000146	6,57	3,11366	1,73	Mvp
Rn30016861	0,000382	0,0000148	6,57	3,10311	1,75	Vwa1
Rn30003602	0,000382	0,0000148	6,57	3,10289	4	Glipr1
Rn30013778	0,000383	0,0000149	-6,56	3,09748	-1,5	Fam189a2
ENSRNOG00000000457	0,000384	0,0000149	6,56	3,09347	1,73	Tap1
ENSRNOG00000001963	0,000384	0,0000149	6,56	3,09192	4,99	Mx2
ENSRNOG00000008161	0,000384	0,000015	6,56	3,08962	2,36	Pdzk1ip1
ENSRNOG00000000441	0,000386	0,0000151	6,56	3,08361	2,19	Gpsm3
R000168_01	0,000399	0,0000156	6,53	3,04773	1,51	Glrx1
Rn30026887	0,0004	0,0000157	-6,53	3,04064	-1,67	Hoxc13
Rn30016557	0,0004	0,0000157	6,53	3,04	1,9	Nckap1l
Rn30001053	0,0004	0,0000158	-6,53	3,03571	-2,06	Cbs
ENSRNOG00000009686	0,0004	0,0000158	-6,53	3,03534	-2,72	Aqp7
ENSRNOG00000020949	0,0004	0,0000158	-6,53	3,03445	-2,09	Hsd17b14
Rn30011309	0,0004	0,0000158	-6,53	3,0342	-2,05	Adh6a
Rn30019644	0,000413	0,0000164	-6,5	2,99363	-1,95	Hmcn1
ENSRNOG00000002643	0,000413	0,0000165	6,5	2,99116	1,78	Ugdh
Rn30024585	0,000417	0,0000167	-6,49	2,97798	-2,27	Lrrn4cl
Rn30016782	0,000423	0,0000169	6,48	2,96331	3,31	Dhx58
Rn30018690	0,000431	0,0000173	6,47	2,93925	2,36	Lsp1
Rn30016210	0,000434	0,0000175	-6,46	2,92893	-2,33	Fbp2
Rn30008522	0,000435	0,0000175	6,46	2,92716	1,69	Arhgap25
ENSRNOG00000038455	0,00044	0,0000178	6,45	2,90995	1,45	Gpx2
Rn30015019	0,00044	0,0000178	-6,45	2,90952	-1,53	Pdlim5
R005508_01	0,00044	0,0000179	-6,45	2,90887	-1,88	Abhd1
ENSRNOG00000030689	0,000444	0,0000181	6,44	2,89713	1,82	Ms4a6b
Rn30021788	0,000446	0,0000182	6,44	2,89198	1,99	Parp9
R002231_01	0,000448	0,0000183	6,44	2,88481	1,69	Nqo1
Rn30014492	0,000452	0,0000185	6,43	2,87503	1,47	Dnajc22
ENSRNOG00000012439	0,000452	0,0000185	6,43	2,87342	2,1	Bid
R000442_01	0,000461	0,0000189	6,41	2,84897	1,82	Hmox1
Rn30019218	0,000463	0,000019	6,41	2,84386	2,89	Tyrobp

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30005829	0,000464	0,0000191	-6,41	2,83886	-1,98	Sema3c
Rn30003511	0,000464	0,0000192	6,41	2,83544	1,6	Il2rg
Rn30008493	0,000464	0,0000192	-6,4	2,83419	-2,28	Ivl
R000773_01	0,000466	0,0000193	-6,4	2,82802	-1,72	Tst
ENSRNOG00000011541	0,000469	0,0000195	6,4	2,81977	1,72	Cygb
Rn30020847	0,00047	0,0000195	6,4	2,81775	1,9	Trex1
Rn30003087	0,000472	0,0000196	6,39	2,81079	1,84	Ifi204
ENSRNOG00000004437	0,000476	0,0000198	-6,39	2,80121	-1,58	Map2k6
Rn30014972	0,000483	0,0000202	-6,37	2,78348	-1,83	Fgfr2
ENSRNOG00000003171	0,000483	0,0000202	-6,37	2,78223	-1,68	Mpz
ENSRNOG00000019838	0,000489	0,0000204	6,37	2,76969	1,99	Gmfg
Rn30010659	0,00049	0,0000206	6,36	2,76417	3,33	Phf11
R002437_01	0,000491	0,0000206	-6,36	2,76053	-3,03	Tm4sf4
Rn30018310	0,000497	0,0000209	6,35	2,74847	1,99	Folr2
ENSRNOG00000012956	0,00051	0,0000215	6,34	2,7193	1,75	Tgm2
ENSRNOG00000007351	0,000515	0,0000217	-6,33	2,70816	-1,76	Ggh
ENSRNOG00000024577	0,000518	0,0000219	-6,32	2,69977	-1,45	Gamt
ENSRNOG00000021412	0,000528	0,0000223	6,31	2,67877	1,67	Slfn8
Rn30026245	0,000532	0,0000225	6,31	2,67018	4,1	Serpinb3
Rn30020062	0,000533	0,0000226	6,3	2,66501	2,14	Clec4a1
Rn30007820	0,000533	0,0000227	-6,3	2,66439	-1,8	Capn3
Rn30015819	0,000533	0,0000227	6,3	2,66437	1,9	Tcirg1
R004666_01	0,000544	0,0000232	-6,29	2,6393	-1,75	Slc36a2
Rn30024005	0,000551	0,0000235	6,28	2,62498	1,92	Pla2g7
ENSRNOG00000001806	0,000576	0,0000248	6,25	2,57067	2,33	Fetub
Rn30014126	0,000576	0,0000249	-6,25	2,56864	-1,96	Aspn
ENSRNOG00000017833	0,000576	0,0000249	-6,25	2,56845	-1,65	Actn2
Rn30025010	0,000578	0,000025	-6,24	2,56439	-2,15	Mypn
Rn30001533	0,000585	0,0000253	6,24	2,55006	1,59	Runx1
R001416_01	0,000587	0,0000255	6,23	2,54282	1,52	Ace
Rn30016778	0,000596	0,0000259	-6,22	2,52634	-1,72	Ank1
ENSRNOG00000008960	0,000605	0,0000263	-6,21	2,51016	-1,54	Fgf22
ENSRNOG00000032717	0,000611	0,0000266	6,21	2,49847	2,82	Mcpt10
ENSRNOG00000019372	0,000611	0,0000267	-6,2	2,49635	-1,58	Pc
ENSRNOG00000018659	0,000611	0,0000267	6,2	2,49598	1,55	Csf1
Rn30005214	0,000622	0,0000272	6,19	2,47558	2,3	Arhgdib
R004431_01	0,000622	0,0000273	-6,19	2,47338	-1,53	Selenbp1
Rn30002621	0,000631	0,0000278	6,18	2,45271	1,7	Pgs1
Rn30017489	0,000636	0,0000281	-6,17	2,44398	-2,03	Mt4
Rn30009414	0,000641	0,0000284	6,17	2,43345	2,05	Hdc
Rn30011330	0,000644	0,0000286	-6,16	2,42625	-2,27	Apobec2
Rn30000331	0,000644	0,0000286	6,16	2,42547	2,44	Gpsm3
Rn30017212	0,000647	0,0000288	-6,16	2,41854	-1,81	Zfp278
Rn30024110	0,000648	0,0000289	6,16	2,41527	1,73	Cfp
Rn30010540	0,00065	0,000029	6,15	2,41069	1,48	Tpd52
ENSRNOG00000018669	0,000653	0,0000292	6,15	2,4043	1,59	Jak3
R002645_01	0,000666	0,0000298	-6,14	2,38176	-1,37	Usp2
R004405_01	0,000676	0,0000303	6,13	2,36451	1,51	Ada
Rn30010076	0,000687	0,0000309	-6,12	2,34625	-1,55	Slc7a10
Rn30000481	0,000694	0,0000312	-6,11	2,33382	-1,85	Fam26d
Rn30004218	0,0007	0,0000315	-6,1	2,3243	-1,81	Angptl1

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
ENSRNOG00000006075	0,000701	0,0000317	-6,1	2,31988	-1,58	Fez1
R002900_01	0,000713	0,0000323	-6,09	2,30074	-1,52	Tnmd
R003898_01	0,000733	0,0000334	6,07	2,26582	2,04	Bid
Rn30012290	0,000736	0,0000336	-6,07	2,25998	-1,38	Hey2
R002663_01	0,000737	0,0000337	-6,06	2,25726	-1,48	Hspb3
Rn30007220	0,000738	0,0000338	-6,06	2,25348	-1,96	Rgn
Rn30000704	0,000738	0,0000338	6,06	2,25187	1,61	Ier3
ENSRNOG00000024382	0,000738	0,0000339	6,06	2,24985	3,81	Fcgr3a
Rn30016777	0,000748	0,0000344	-6,05	2,23539	-2,07	Ank1
ENSRNOG00000015410	0,00075	0,0000345	-6,05	2,2306	-1,87	Aspn
R002625_01	0,000755	0,0000349	6,04	2,22159	2,33	Jak2
ENSRNOG00000011821	0,000756	0,000035	6,04	2,21859	1,55	S100a4
R004970_01	0,000768	0,0000355	-6,03	2,20132	-1,9	Creg1
ENSRNOG00000019776	0,000776	0,000036	-6,02	2,18781	-1,61	Sh3gl3
Rn30000352	0,000776	0,000036	6,02	2,18776	1,34	RT1-DMa
R001785_01	0,000777	0,0000361	6,02	2,18427	1,61	Ccl11
Rn30003804	0,000777	0,0000362	-6,02	2,18293	-1,61	Egfl6
Rn30009787	0,00078	0,0000363	-6,02	2,17855	-1,52	Acsl1
Rn30001244	0,00078	0,0000364	6,02	2,17719	2,56	Oas1b
ENSRNOG00000022210	0,000788	0,000037	-6,01	2,16107	-1,51	Alox12b
ENSRNOG00000004536	0,000799	0,0000376	-6	2,14464	-2,72	Bbox1
ENSRNOG00000012404	0,0008	0,0000377	-6	2,14183	-3,8	Thrsp
ENSRNOG00000014079	0,0008	0,0000377	6	2,14112	2,62	Stat4
Rn30012330	0,0008	0,0000378	-5,99	2,13849	-2,16	Slc5a11
ENSRNOG00000007457	0,0008	0,0000378	5,99	2,13799	2,92	Serping1
ENSRNOG00000009628	0,000802	0,0000379	-5,99	2,13457	-1,52	Pfkm
Rn30019222	0,000822	0,000039	5,98	2,10502	1,52	Hcst
ENSRNOG00000008292	0,000825	0,0000392	5,97	2,09995	1,58	Hif1a
R000002_01	0,000832	0,0000396	5,97	2,09071	1,87	Tgm2
ENSRNOG00000031497	0,000838	0,00004	-5,96	2,08111	-1,64	Myh2
Rn30006075	0,000841	0,0000401	5,96	2,07646	1,48	Mmp19
Rn30006888	0,000841	0,0000402	5,96	2,07537	1,49	Igsf8
Rn30013780	0,000841	0,0000402	-5,96	2,07428	-1,6	Fam189a2
Rn30012217	0,000842	0,0000404	5,96	2,07098	2,03	Arg1
Rn30003752	0,000844	0,0000405	-5,95	2,06727	-1,72	Golsyn
ENSRNOG00000017226	0,000848	0,0000407	-5,95	2,06108	-1,92	Slc2a4
Rn30007510	0,00085	0,0000409	-5,95	2,05681	-1,57	Mfap2
Rn30020152	0,000877	0,0000423	5,93	2,02134	1,67	Gpx3
Rn30008593	0,000878	0,0000424	5,93	2,01905	1,87	Tf
ENSRNOG00000010262	0,00088	0,0000426	5,92	2,01596	2,42	Hdc
Rn30004092	0,000884	0,0000428	5,92	2,00938	2,62	Il1a
ENSRNOG00000028015	0,00089	0,0000433	5,91	1,99899	1,61	Pf4
ENSRNOG00000016243	0,00089	0,0000433	-5,91	1,99872	-1,33	Casq2
R003600_01	0,000905	0,0000441	-5,9	1,98024	-2,53	Ivl
ENSRNOG00000015616	0,000905	0,0000441	5,9	1,979	1,67	Rgs14
R001476_01	0,000905	0,0000442	5,9	1,97742	1,72	Adm
ENSRNOG00000014956	0,000907	0,0000444	5,9	1,97351	3,03	Slc11a1
ENSRNOG00000008245	0,00091	0,0000445	5,9	1,96983	3,33	Ptgis
Rn30017768	0,000912	0,0000447	5,9	1,96581	1,89	Tspan4
Rn30014252	0,000916	0,000045	5,89	1,96	1,58	Jak2
Rn30014979	0,000927	0,0000456	-5,88	1,94636	-1,6	Pik3cb

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
ENSRNOG00000014378	0,000932	0,0000459	5,88	1,93805	2,29	Il1r2
ENSRNOG00000020744	0,000932	0,0000459	5,88	1,93794	1,66	Adar
Rn30005630	0,000951	0,0000469	-5,87	1,9163	-1,39	Mycn
ENSRNOG00000031607	0,000956	0,0000472	5,86	1,91014	2,37	RT1-CE3
Rn30017858	0,00097	0,000048	-5,85	1,89371	-1,76	Hhatl
ENSRNOG00000010263	0,000979	0,0000485	-5,85	1,88238	-2,59	Cldn11
ENSRNOG00000030876	0,000985	0,0000488	-5,84	1,87497	-1,72	Krt72
Rn30006072	0,00101	0,0000501	5,83	1,84879	3,43	Ccr5
Rn30009698	0,00101	0,0000505	-5,82	1,84116	-2,03	Fat4
Rn30017588	0,00102	0,000051	-5,82	1,83013	-1,62	Elovl3
Rn30004671	0,00103	0,0000516	-5,81	1,81864	-1,37	Gnai1
ENSRNOG00000002810	0,00104	0,0000521	5,8	1,80774	2,45	Gfpt2
ENSRNOG00000019745	0,00108	0,0000541	-5,78	1,77065	-2,2	Actn3
Rn30013618	0,00108	0,0000541	5,78	1,77031	1,47	Il1rl1
R000449_01	0,00109	0,0000546	-5,78	1,75956	-1,7	Hspb6
ENSRNOG00000019742	0,00109	0,000055	5,77	1,75307	1,83	Stat3
ENSRNOG00000001528	0,0011	0,0000554	-5,77	1,74629	-1,86	Gap43
ENSRNOG00000007335	0,0011	0,0000557	5,77	1,74068	1,73	Ccl11
ENSRNOG00000017428	0,0011	0,000056	-5,76	1,73519	-1,6	Map1b
R004672_01	0,00112	0,0000571	5,75	1,71519	1,47	RT1-N3
Rn30014358	0,00115	0,0000583	5,74	1,69388	3,75	Ccl19
Rn30000186	0,00115	0,0000587	5,74	1,68625	1,86	RT1-CE4
ENSRNOG00000009514	0,00115	0,0000588	5,73	1,68393	1,58	Mme
Rn30008198	0,00115	0,000059	-5,73	1,68146	-1,52	Mmp27
ENSRNOG00000004899	0,00118	0,0000603	5,72	1,65769	2,06	Kcns3
ENSRNOG00000007907	0,00118	0,0000609	5,71	1,64894	1,95	Tmem178
ENSRNOG00000022741	0,00119	0,000061	5,71	1,64657	1,48	Ilf3
ENSRNOG00000020992	0,00119	0,000061	-5,71	1,64604	-1,61	Selenbp1
ENSRNOG00000005971	0,00119	0,0000615	5,71	1,63805	1,87	Gpr176
Rn30014282	0,00121	0,0000622	5,7	1,62661	1,61	Me2
ENSRNOG00000029500	0,00121	0,0000623	5,7	1,62428	1,31	Tapbp
R002520_01	0,00121	0,0000624	5,7	1,62274	1,28	Junb
ENSRNOG00000029551	0,00121	0,0000625	-5,7	1,62109	-1,52	Krt33b
Rn30011494	0,00121	0,0000626	5,7	1,62019	1,48	Thbs4
R004479_01	0,00123	0,0000638	-5,69	1,6012	-2,5	Abra
Rn30023022	0,00124	0,0000649	5,68	1,5835	1,32	Rarres2
ENSRNOG00000008135	0,00124	0,0000649	5,68	1,58269	1,69	Pla2g4f
Rn30011530	0,00126	0,0000658	5,67	1,56929	3,15	Il17f
Rn30019645	0,00126	0,0000658	-5,67	1,5692	-1,43	Hmcn1
Rn30017016	0,00126	0,0000658	-5,67	1,56807	-1,84	Ppp1r3c
ENSRNOG00000012749	0,00126	0,000066	5,67	1,56558	1,58	C1qb
R002396_01	0,00126	0,000066	-5,67	1,56528	-1,38	Ramp1
Rn30010857	0,00126	0,0000665	-5,66	1,55826	-1,59	Tcea3
R000996_01	0,00127	0,000067	5,66	1,54996	1,38	Myog
R004774_01	0,00129	0,000068	-5,65	1,53566	-1,43	Fap
ENSRNOG00000005809	0,0013	0,0000687	5,64	1,52395	1,51	Arhgdib
R000968_01	0,00131	0,0000694	-5,64	1,5145	-1,65	S100b
ENSRNOG00000007091	0,00133	0,0000705	5,63	1,49828	1,86	Ly6e
ENSRNOG00000031138	0,00133	0,0000705	5,63	1,49787	2,13	Irgm
ENSRNOG00000017720	0,00134	0,0000712	5,62	1,48752	1,61	Mxd1
Rn30007500	0,00134	0,0000713	5,62	1,4871	2,21	Emilin1

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
ENSRNOG00000016794	0,00134	0,0000719	5,62	1,4771	1,48	Phyhd1
Rn30000718	0,00135	0,0000723	-5,61	1,47272	-1,68	Ly6g6d
ENSRNOG00000011907	0,00135	0,0000725	-5,61	1,46905	-1,72	Krt23
ENSRNOG00000016752	0,00136	0,0000733	5,61	1,45869	2,1	Crispld2
Rn30025055	0,00137	0,0000741	-5,6	1,44728	-1,63	Arhgap42
Rn30021624	0,00137	0,0000741	-5,6	1,44708	-1,35	Arhgef19
Rn30004281	0,00137	0,0000741	5,6	1,44657	1,74	Cytip
Rn30018774	0,00137	0,0000742	-5,6	1,4455	-1,43	Capn12
ENSRNOG00000030743	0,00137	0,0000743	5,6	1,44454	1,35	Myog
Rn30015875	0,00137	0,0000743	5,6	1,44345	1,59	Sp110
ENSRNOG00000026653	0,00138	0,0000749	5,59	1,43569	1,71	Niacr1
ENSRNOG00000018982	0,00139	0,0000753	-5,59	1,43074	-1,51	Entpd3
ENSRNOG00000011054	0,0014	0,000076	5,59	1,42146	2,17	Laptm5
Rn30005294	0,0014	0,0000763	5,58	1,4175	1,58	Pde4b
Rn30000849	0,0014	0,0000765	5,58	1,41395	1,33	Arpc1b
R005450_01	0,0014	0,0000767	-5,58	1,41212	-1,56	Agpat5
R000668_01	0,0014	0,0000767	-5,58	1,41147	-2,38	Nnat
ENSRNOG00000000394	0,0014	0,0000767	5,58	1,41099	2,32	Srgn
ENSRNOG00000009982	0,00141	0,0000771	5,58	1,40549	1,41	Np
ENSRNOG00000022764	0,00143	0,0000782	5,57	1,39185	1,94	Evi2a
ENSRNOG00000020330	0,00143	0,0000787	-5,57	1,38489	-1,38	Wdr47
Rn30002095	0,00144	0,0000791	5,56	1,38013	1,38	Hlx
ENSRNOG00000002408	0,00144	0,0000792	5,56	1,37855	1,45	Rbm47
Rn30000012	0,00144	0,0000794	5,56	1,37649	1,87	Cbln1
Rn30016877	0,00145	0,00008	-5,56	1,36877	-1,41	Msx2
ENSRNOG00000008436	0,00147	0,0000814	-5,55	1,35102	-1,69	Krt85
Rn30001385	0,00148	0,000082	-5,54	1,34311	-1,54	Dlx2
R001180_01	0,00149	0,0000822	5,54	1,34065	1,73	Slc4a3
Rn30014836	0,0015	0,0000832	-5,53	1,3276	-1,38	Casq2
Rn30001419	0,0015	0,0000833	-5,53	1,32697	-2,01	Cldn8
ENSRNOG00000010018	0,00151	0,0000836	5,53	1,32292	2,04	Clec4a3
ENSRNOG00000004537	0,00152	0,0000845	-5,52	1,31243	-1,34	Rxrg
Rn30010761	0,00152	0,0000845	-5,52	1,31241	-1,23	Zfp40
Rn30013803	0,00153	0,0000853	-5,52	1,30287	-1,45	Golga7b
Rn30023898	0,00154	0,0000858	-5,52	1,29673	-1,76	Rnase1
Rn30014814	0,00154	0,0000864	-5,51	1,28962	-1,31	Gtf3c1
ENSRNOG00000029682	0,0016	0,0000899	5,49	1,24893	1,29	Clic1
Rn30004209	0,00161	0,0000907	-5,48	1,23992	-1,57	Vit
ENSRNOG00000004317	0,00163	0,0000916	5,48	1,22933	1,55	Vipr2
ENSRNOG00000011071	0,00165	0,0000928	5,47	1,21592	1,38	Nt5e
ENSRNOG00000020833	0,00165	0,0000928	-5,47	1,21553	-1,42	Cspg5
Rn30000975	0,00165	0,0000931	5,47	1,21294	1,78	Foxk1
Rn30003436	0,00166	0,0000936	-5,47	1,20727	-1,26	Slc40a1
ENSRNOG00000018355	0,00166	0,0000938	-5,46	1,20449	-1,47	Msx2
R000003_01	0,00166	0,000094	5,46	1,20288	1,44	Icam1
Rn30024865	0,00167	0,0000951	5,46	1,19106	1,49	Ifi27l2b
Rn30017759	0,00167	0,0000952	-5,46	1,18928	-1,82	Lipl3
ENSRNOG00000000321	0,00167	0,0000953	5,46	1,18915	1,79	Cd24
ENSRNOG00000005807	0,00169	0,0000968	5,45	1,1726	1,93	Ptpn7
R002136_01	0,00171	0,0000979	5,44	1,16163	1,34	P2ry2
Rn30005113	0,00172	0,0000989	5,43	1,15088	1,52	Il1f9

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30002278	0,00172	0,000099	5,43	1,14955	2,23	Ptgs2
ENSRNOG00000011474	0,00176	0,000102	5,42	1,12394	1,52	Ppp1r3b
R003575_01	0,00182	0,000105	5,4	1,09014	1,88	Batf3
Rn30009796	0,00183	0,000106	5,4	1,08075	1,37	Igfbp4
Rn30003409	0,00183	0,000106	5,4	1,0799	1,44	Slc43a2
ENSRNOG00000030625	0,00184	0,000107	5,39	1,06769	1,6	Tf
ENSRNOG00000005715	0,00184	0,000107	-5,39	1,06768	-1,24	Lgr4
R001492_01	0,00184	0,000107	5,39	1,06754	1,48	Gadd45a
ENSRNOG00000009629	0,00184	0,000107	5,39	1,06624	1,52	Car2
Rn30001243	0,00185	0,000108	-5,38	1,061	-1,28	Oas1f
ENSRNOG00000006583	0,00186	0,000108	5,38	1,05695	1,79	Hpgds
ENSRNOG00000020719	0,00186	0,000108	-5,38	1,05581	-1,7	Hrc
Rn30006067	0,00186	0,000109	-5,38	1,05481	-1,37	Laptm4b
Rn30003960	0,00189	0,000111	-5,37	1,03511	-1,49	Sptlc3
Rn30021274	0,00194	0,000114	-5,35	1,00373	-1,76	Rnf222
Rn30026214	0,00199	0,000117	-5,34	0,97885	-1,38	Fndc3c1
Rn30005195	0,002	0,000118	-5,34	0,97153	-1,26	Cdc42ep3
Rn30011248	0,002	0,000118	5,33	0,96957	1,43	Sptlc2
ENSRNOG00000007393	0,002	0,000118	5,33	0,96602	1,41	Ndrg1
Rn30007819	0,00204	0,000121	-5,32	0,94536	-1,47	Capn3
Rn30011542	0,00208	0,000124	-5,31	0,92106	-1,33	Shisa2
Rn30014957	0,0021	0,000125	5,3	0,90907	1,34	Gpr4
Rn30017606	0,00211	0,000125	5,3	0,90696	1,33	Galnt2
ENSRNOG00000033348	0,00213	0,000127	5,29	0,89637	1,63	Duox1
Rn30005434	0,00213	0,000127	-5,29	0,89298	-1,53	Matn2
Rn30002177	0,00213	0,000127	5,29	0,89158	1,35	Rbm47
Rn30016876	0,00213	0,000128	-5,29	0,88884	-1,59	Msx2
Rn30014307	0,00219	0,000131	5,27	0,85928	2,11	Rgs14
R000175_01	0,00221	0,000133	-5,27	0,84943	-1,73	Sult1a1
Rn30008712	0,00221	0,000133	5,27	0,84908	1,75	Khdrbs3
Rn30002492	0,00222	0,000133	5,27	0,84348	1,75	Gfpt2
ENSRNOG00000019283	0,00222	0,000134	5,26	0,84055	1,26	P2ry2
R001026_01	0,00222	0,000134	5,26	0,83801	1,85	Atf3
R000326_01	0,00224	0,000135	5,26	0,82802	2	Zfp36
Rn30015393	0,00227	0,000137	5,25	0,81446	1,41	Phyhd1
Rn30008808	0,00228	0,000138	-5,25	0,80852	-1,44	Pfkm
ENSRNOG00000009331	0,00231	0,00014	5,24	0,79091	1,96	Hck
Rn30010969	0,00233	0,000142	5,23	0,78298	1,5	Cp
Rn30007318	0,00234	0,000142	-5,23	0,77673	-1,5	Stac3
ENSRNOG00000002839	0,00238	0,000145	-5,22	0,75829	-1,35	Slc19a2
ENSRNOG00000025689	0,00239	0,000146	-5,22	0,75276	-1,35	Abhd1
Rn30021826	0,0024	0,000147	-5,21	0,74483	-1,45	Foxe1
ENSRNOG00000002922	0,0024	0,000147	5,21	0,7447	1,55	Adora2b
ENSRNOG00000000827	0,0024	0,000148	5,21	0,73977	1,15	Ier3
Rn30010838	0,00247	0,000152	-5,19	0,70996	-1,86	Myot
Rn30019473	0,00248	0,000153	5,19	0,70357	1,85	Tnfaip8l2
R000424_01	0,00249	0,000153	5,19	0,70153	1,21	Cd82
R004191_01	0,00249	0,000154	-5,19	0,69846	-1,42	Cldn11
ENSRNOG00000005615	0,00249	0,000154	5,18	0,69649	1,45	Gadd45a
Rn30017826	0,0025	0,000155	-5,18	0,69081	-1,31	Pc
Rn30026466	0,00251	0,000156	-5,18	0,68418	-1,57	Ankrd13d

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30023494	0,00252	0,000157	-5,18	0,68035	-1,5	Tmem56
R000727_01	0,00252	0,000157	5,17	0,67625	1,37	Slc16a1
Rn30024422	0,00252	0,000157	5,17	0,67609	1,9	Cpne8
Rn30018719	0,00254	0,000159	-5,17	0,66692	-1,16	Tnnt3
Rn30017950	0,00255	0,000159	5,17	0,66292	1,6	Stat5a
ENSRNOG00000015184	0,00256	0,00016	-5,16	0,65827	-1,6	Clic3
R003337_01	0,00256	0,000161	5,16	0,65379	2,03	A3galt2
ENSRNOG00000019673	0,00257	0,000161	5,16	0,65007	2,01	Zfp36
ENSRNOG00000005679	0,00258	0,000162	-5,16	0,64665	-1,37	Fap
Rn30002381	0,00259	0,000163	5,15	0,64091	1,44	Ugdh
Rn30016826	0,0026	0,000164	-5,15	0,63468	-1,33	Ocln
Rn30019325	0,00263	0,000166	-5,14	0,62041	-1,79	Hsd17b14
Rn30007410	0,00264	0,000167	-5,14	0,61613	-1,3	Plscr4
Rn30001333	0,00267	0,000169	-5,13	0,60356	-1,43	Eln
Rn30025056	0,00268	0,000169	-5,13	0,5992	-1,48	Arhgap42
R003102_01	0,00268	0,00017	-5,13	0,59655	-1,26	Padi3
Rn30007714	0,00269	0,00017	-5,13	0,59471	-1,37	Amotl2
Rn30003555	0,00279	0,000177	-5,11	0,55283	-1,28	Dusp10
R001078_01	0,00279	0,000178	5,11	0,55069	1,3	Reg3g
ENSRNOG00000019217	0,0028	0,000178	-5,1	0,54707	-1,34	Adrb2
Rn30003671	0,0028	0,000179	-5,1	0,54492	-1,77	Kremen2
ENSRNOG00000004280	0,00281	0,000179	5,1	0,54017	1,37	Tcn2
ENSRNOG00000021100	0,00283	0,000181	5,09	0,53054	1,75	Tnfaip8l2
Rn30000026	0,00285	0,000183	5,09	0,52132	1,61	Nuak2
Rn30003465	0,00285	0,000183	5,09	0,52118	1,28	Krt14
R000695_01	0,00288	0,000185	-5,08	0,51076	-1,27	Sh3gl3
Rn30016043	0,00289	0,000186	5,08	0,5058	1,24	Tpm3
ENSRNOG00000030467	0,00293	0,000189	5,07	0,48931	1,48	Ube2l6
ENSRNOG00000033403	0,00293	0,000189	-5,07	0,48463	-2,03	Krt82
Rn30010439	0,00295	0,000191	5,07	0,47874	1,21	Rftn1
ENSRNOG00000021090	0,00295	0,000191	-5,07	0,47797	-1,49	Pygm
R004669_01	0,00297	0,000192	-5,06	0,47037	-1,48	Kcnk3
Rn30010377	0,00298	0,000193	-5,06	0,46485	-1,29	Plac9
Rn30023963	0,003	0,000195	5,05	0,4571	1,46	Tnfrsf21
ENSRNOG00000023919	0,00306	0,000199	-5,04	0,43526	-1,1	Gbas
R002546_01	0,00307	0,0002	5,04	0,43091	1,5	Pfkl
Rn30004445	0,00307	0,000201	-5,04	0,42653	-1,42	Zfp799
R003549_01	0,00307	0,000201	5,04	0,42471	1,77	Csf2
R002873_01	0,00307	0,000201	-5,04	0,42469	-1,18	Suox
R000191_01	0,00309	0,000202	-5,03	0,41944	-1,77	Car3
ENSRNOG00000007329	0,0031	0,000203	-5,03	0,41394	-1,57	Frmd6
Rn30006695	0,00318	0,000209	5,02	0,38388	1,38	Ndrg1
Rn30014853	0,00318	0,00021	-5,01	0,38181	-1,32	Podxl2
Rn30014069	0,00318	0,00021	-5,01	0,38129	-1,42	Prss12
ENSRNOG00000010150	0,00318	0,00021	-5,01	0,38096	-1,18	Strbp
R001501_01	0,00318	0,00021	-5,01	0,38011	-1,4	Ggh
Rn30021647	0,00318	0,00021	-5,01	0,37804	-1,38	Sema3a
ENSRNOG00000012183	0,00318	0,00021	5,01	0,37764	1,45	Glrx1
ENSRNOG00000012807	0,00319	0,000211	5,01	0,37448	1,16	C1qa
Rn30015407	0,00322	0,000213	-5	0,36327	-1,22	Tia1
Rn30002944	0,00325	0,000215	5	0,35498	2,26	Chi3l1

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30001985	0,00325	0,000215	5	0,35376	1,26	Hpse
Rn30011589	0,00325	0,000216	-5	0,35207	-1,42	Tlcd1
ENSRNOG00000002255	0,00325	0,000216	5	0,35044	1,31	Fam162a
R000399_01	0,00325	0,000216	-5	0,35009	-1,36	Capn6
ENSRNOG00000016837	0,00327	0,000218	-4,99	0,34271	-1,65	Ckm
Rn30016404	0,00327	0,000218	-4,99	0,3399	-1,38	Actn2
Rn30010476	0,00329	0,00022	4,99	0,33208	2,26	Emb
Rn30006270	0,00329	0,00022	-4,99	0,33156	-1,35	Nfia
ENSRNOG00000013523	0,0033	0,000221	-4,99	0,32938	-1,36	Krt31
Rn30010819	0,0033	0,000221	4,98	0,32692	1,35	Mocs1
ENSRNOG00000025811	0,00332	0,000222	4,98	0,32046	2,16	Cfp
Rn30002681	0,00334	0,000224	-4,98	0,31327	-2,23	Myh2
Rn30016793	0,00334	0,000224	4,98	0,31173	1,92	Ampd3
ENSRNOG00000031814	0,00334	0,000225	-4,98	0,31102	-1,45	Sort1
Rn30011281	0,00334	0,000225	-4,97	0,30773	-1,21	Txlnb
Rn30026519	0,0034	0,000229	4,97	0,29141	1,64	Sectm1a
ENSRNOG00000008312	0,0034	0,000229	-4,96	0,28964	-2,12	Stra6
Rn30016018	0,00343	0,000232	4,96	0,2792	3,74	Il7r
ENSRNOG00000012557	0,00344	0,000233	4,96	0,27342	1,39	Lgals5,Lgals9
Rn30023383	0,00345	0,000234	4,95	0,26729	1,34	Lrp1
R000417_01	0,00346	0,000235	-4,95	0,2654	-1,18	Fstl1
ENSRNOG00000013805	0,00348	0,000237	4,95	0,25403	2,42	Tnip2
R000270_01	0,00348	0,000238	4,94	0,25325	1,33	Psap
ENSRNOG00000001367	0,00351	0,00024	-4,94	0,24116	-1,34	Gpc2
Rn30004500	0,00351	0,000241	-4,94	0,24083	-1,23	Rabep1
R001365_01	0,00355	0,000243	4,93	0,2303	1,44	Ptprz1
Rn30003078	0,00355	0,000244	-4,93	0,22578	-1,15	Slc6a4
Rn30005621	0,00355	0,000244	-4,93	0,22551	-1,67	Gclc
R000331_01	0,00357	0,000245	4,93	0,22056	1,64	Pde4b
Rn30003064	0,00357	0,000246	-4,93	0,21968	-1,24	Capn8
ENSRNOG00000033744	0,00357	0,000246	4,93	0,21822	1,83	Rasgrp4
Rn30013382	0,00362	0,00025	4,92	0,19988	1,4	Ckmt1
Rn30014598	0,00364	0,000252	-4,91	0,19408	-1,34	Wnt11
Rn30015177	0,00365	0,000253	4,91	0,19036	1,24	Ninj1
Rn30020666	0,00369	0,000256	4,9	0,17827	1,35	Klk13
ENSRNOG00000000763	0,00374	0,00026	4,9	0,1623	1,72	RT1-M3-1
Rn30014971	0,00375	0,000261	-4,89	0,15837	-1,55	Fgfr2
Rn30012029	0,00376	0,000262	-4,89	0,15291	-1,54	Krt33a
Rn30014694	0,00378	0,000264	-4,89	0,14749	-1,89	Mtmr10
Rn30006675	0,00379	0,000265	4,89	0,14334	1,79	Casp4
Rn30021153	0,00383	0,000267	-4,88	0,13248	-1,4	Cep70
ENSRNOG00000026679	0,00384	0,000268	-4,88	0,12913	-1,48	Scn4b
ENSRNOG00000012865	0,00388	0,000272	4,87	0,11563	1,33	Parp3
R002142_01	0,00389	0,000273	-4,87	0,11234	-1,67	Aqp7
Rn30019565	0,00396	0,000278	-4,86	0,09282	-1,48	Hfe2
Rn30001201	0,00396	0,000278	4,86	0,09244	1,35	Orai1
Rn30010526	0,00398	0,00028	-4,85	0,0837	-1,25	Cldn23
Rn30007875	0,00402	0,000284	-4,85	0,07122	-1,31	Vsig8
ENSRNOG00000015618	0,00406	0,000287	-4,84	0,05999	-1,26	Wnt5a
Rn30014341	0,00408	0,000288	4,84	0,05607	1,3	Ghr
Rn30001792	0,00408	0,000289	-4,84	0,05416	-1,8	Sult1d1

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30012035	0,00415	0,000294	-4,83	0,0341	-1,35	Csnk1e
Rn30017967	0,00415	0,000295	4,83	0,0326	1,38	Egln1
Rn30009187	0,00415	0,000295	4,83	0,03069	3,04	Clec4a3
ENSRNOG00000015411	0,00417	0,000297	4,82	0,02681	1,74	Apobec1
R000208_01	0,00418	0,000298	-4,82	0,02292	-1,32	Ldhb
Rn30003489	0,00421	0,0003	-4,82	0,01368	-1,33	Cd55
ENSRNOG00000008180	0,00421	0,000301	4,82	0,01203	2,69	Lyn
ENSRNOG00000001704	0,00424	0,000304	4,81	0,00302	1,31	Runx1
R004320_01	0,00426	0,000305	4,81	-0,00282	1,85	Pdzk1ip1
Rn30015123	0,00435	0,000313	4,79	-0,02783	1,32	Ino80c
Rn30014910	0,00444	0,000319	4,78	-0,04919	1,18	Il10ra
Rn30018169	0,00446	0,000322	4,78	-0,0561	1,12	Sema4a
ENSRNOG00000006235	0,00449	0,000324	-4,78	-0,06384	-1,59	Nell2
Rn30005106	0,0045	0,000325	-4,77	-0,06553	-1,15	Lmcd1
ENSRNOG00000003183	0,0045	0,000325	4,77	-0,0678	1,24	Fmod
Rn30009024	0,0045	0,000326	4,77	-0,06916	1,72	Samd9l
Rn30005357	0,00453	0,000328	4,77	-0,0769	2,64	Gpr176
ENSRNOG00000015547	0,0046	0,000333	4,76	-0,09246	1,31	Jak2
Rn30008695	0,0046	0,000334	4,76	-0,09409	1,4	Ttc39a
ENSRNOG00000000433	0,00465	0,000338	-4,75	-0,10677	-1,32	Prrt1
Rn30004796	0,00468	0,000341	-4,75	-0,11453	-1,71	Fjx1
ENSRNOG00000005332	0,00469	0,000342	-4,75	-0,1182	-1,22	Csdc2
R003383_01	0,00471	0,000343	4,74	-0,1224	1,2	Tgfb1
Rn30022768	0,00473	0,000345	-4,74	-0,1286	-1,34	Radil
Rn30009978	0,00473	0,000345	-4,74	-0,12861	-1,44	Col8a2
ENSRNOG00000015155	0,00473	0,000346	-4,74	-0,12949	-1,37	Tnnc2
Rn30006308	0,00475	0,000347	4,74	-0,13461	1,63	Ano6
Rn30002427	0,00475	0,000348	-4,74	-0,13588	-1,29	Cnst
ENSRNOG00000022116	0,00477	0,00035	4,73	-0,14147	1,53	Gjb6
Rn30004369	0,00478	0,00035	-4,73	-0,14289	-1,32	Mpped2
ENSRNOG00000004275	0,00479	0,000352	-4,73	-0,14681	-1,5	Egfl6
ENSRNOG00000034290	0,00483	0,000355	4,73	-0,15624	1,4	Ccl21b
ENSRNOG00000027017	0,00483	0,000355	4,73	-0,15694	1,74	Rnasel
Rn30014196	0,00486	0,000358	-4,72	-0,16658	-1,25	Tead1
Rn30001254	0,0049	0,000362	4,72	-0,17573	1,26	Slc24a6
ENSRNOG00000018627	0,0049	0,000362	-4,72	-0,17654	-1,27	Plekhb1
ENSRNOG00000013000	0,00491	0,000364	-4,71	-0,18153	-1,15	Ldhb
Rn30023443	0,00491	0,000364	4,71	-0,18233	1,75	Cebpb
ENSRNOG00000020590	0,00491	0,000365	4,71	-0,18414	1,23	Adam15
Rn30002865	0,00492	0,000365	-4,71	-0,18634	-1,76	Trim16
ENSRNOG00000000529	0,00495	0,000369	4,71	-0,19565	1,29	Pim1
ENSRNOG00000000158	0,00499	0,000373	-4,7	-0,20618	-1,51	Cdo1
Rn30021879	0,005	0,000374	-4,7	-0,20942	-1,93	Samd5
R003656_01	0,00503	0,000376	-4,69	-0,2157	-1,89	Gpd1
Rn30011383	0,00504	0,000377	4,69	-0,21896	1,19	Svep1
Rn30010826	0,00512	0,000385	-4,68	-0,23858	-1,79	Myom2
R002568_01	0,00513	0,000385	-4,68	-0,24045	-1,4	Map2k6
Rn30007595	0,00515	0,000387	4,68	-0,24601	1,39	Cfd
Rn30009295	0,00516	0,000388	-4,68	-0,24829	-1,33	Ndn
Rn30002833	0,00517	0,00039	-4,68	-0,25163	-1,16	Gprasp2
Rn30005152	0,00518	0,000391	-4,67	-0,25581	-2,29	Dapl1

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30002510	0,00518	0,000391	-4,67	-0,25629	-1,49	Tob1
R000040_01	0,00522	0,000395	4,67	-0,26549	1,33	S100a4
ENSRNOG00000014656	0,00525	0,000398	-4,66	-0,2733	-1,48	Cox8b
R004292_01	0,00526	0,000399	-4,66	-0,27638	-1,28	Macrod1
Rn30010833	0,00526	0,000399	-4,66	-0,27703	-1,43	Sh3d19
Rn30002836	0,00527	0,0004	-4,66	-0,27848	-1,35	Gprasp2
Rn30026591	0,00529	0,000402	-4,66	-0,28414	-1,51	Fbxl17
Rn30014340	0,00529	0,000403	4,66	-0,28558	1,83	Ghr
Rn30002203	0,00529	0,000403	4,66	-0,2869	1,28	Ralb
Rn30015520	0,00529	0,000404	-4,66	-0,28848	-1,44	Klhl11
Rn30008689	0,0053	0,000405	4,66	-0,29041	1,26	Mme
ENSRNOG00000010957	0,00533	0,000407	-4,65	-0,2971	-1,35	Braf
Rn30017502	0,00536	0,00041	-4,65	-0,30395	-1,1	Fitm1
ENSRNOG00000000991	0,0054	0,000415	4,64	-0,31497	1,3	Arpc1b
Rn30012882	0,00545	0,000419	-4,64	-0,32518	-1,17	Mfsd2
ENSRNOG00000010992	0,00545	0,000419	-4,64	-0,32605	-1,78	Hspb3
ENSRNOG00000029939	0,00546	0,00042	-4,64	-0,32904	-1,31	Gypc
Rn30018326	0,00547	0,000422	4,63	-0,33244	1,38	Nfkbie
ENSRNOG00000009602	0,00547	0,000422	-4,63	-0,33302	-1,64	Flg
ENSRNOG00000007290	0,00551	0,000425	-4,63	-0,33992	-1,55	Atp1a2
Rn30003614	0,00552	0,000426	-4,63	-0,34355	-1,12	Nrcam
Rn30011252	0,00552	0,000427	4,63	-0,34439	1,93	Tgfbi
Rn30017767	0,00555	0,00043	4,62	-0,353	1,04	Nfkb2
Rn30012183	0,00567	0,000441	-4,61	-0,37692	-1,48	Myl1_v2
ENSRNOG00000016975	0,00569	0,000442	-4,61	-0,38121	-1,23	Pxmp4
Rn30014754	0,00574	0,000447	4,6	-0,39053	1,74	Ankrd23
R001329_01	0,00574	0,000447	4,6	-0,3923	1,64	Tgm1
ENSRNOG00000002555	0,00576	0,000449	-4,6	-0,39567	-1,26	Serpinb7
Rn30002012	0,00577	0,00045	-4,6	-0,39893	-1,05	Stbd1
R004296_01	0,00579	0,000452	4,6	-0,40368	1,66	Carhsp1
R000046_01	0,00581	0,000454	4,59	-0,40734	1,67	Lgals3
ENSRNOG00000006120	0,00583	0,000456	-4,59	-0,41271	-1,23	Shh
ENSRNOG00000006767	0,00583	0,000456	4,59	-0,41286	2,96	Cst7
Rn30006130	0,00587	0,00046	-4,59	-0,42106	-1,07	Tgm6
Rn30013825	0,00594	0,000466	4,58	-0,43323	1,13	Prr13
Rn30020009	0,00598	0,00047	-4,58	-0,44262	-1,03	Pcca
Rn30001807	0,00601	0,000472	-4,57	-0,44718	-1,33	Gramd1c
Rn30004333	0,00603	0,000475	-4,57	-0,45329	-1,09	Immp1l
Rn30008784	0,00605	0,000477	-4,57	-0,45741	-1,66	Flg
Rn30013897	0,00605	0,000478	-4,57	-0,45928	-1,17	Tnnc2
ENSRNOG00000009176	0,00606	0,000478	-4,57	-0,46014	-1,2	Mkrn2
ENSRNOG00000008025	0,00606	0,000479	-4,56	-0,4622	-1,18	Bend5
ENSRNOG00000014746	0,00607	0,00048	-4,56	-0,46396	-1,21	Dzip1l
Rn30005425	0,00607	0,00048	-4,56	-0,46458	-1,03	Sulf2
R004673_01	0,00608	0,000482	-4,56	-0,46813	-1,06	Capn8
Rn30009524	0,00608	0,000482	4,56	-0,46851	1,13	Tnip1
ENSRNOG00000013783	0,00612	0,000486	4,56	-0,47625	1,49	Efhd2
Rn30006652	0,00613	0,000487	4,56	-0,47824	1,08	Gpx2
ENSRNOG00000026910	0,00615	0,000489	-4,55	-0,48259	-1,4	Gjb4
Rn30007165	0,00622	0,000495	-4,55	-0,49553	-1,02	Mpdz
R002234_01	0,00622	0,000495	-4,55	-0,49611	-1,71	Pygm

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30011820	0,00623	0,000497	-4,55	-0,49908	-1,36	Mlf1
Rn30003352	0,00623	0,000498	4,54	-0,5018	1,43	Opn3
Rn30018844	0,00631	0,000505	-4,54	-0,51615	-1,72	Nrep
Rn30008696	0,00632	0,000506	4,54	-0,51769	1,28	Ttc39a
ENSRNOG00000020652	0,00632	0,000507	4,54	-0,51922	1,46	Tgfb1
ENSRNOG00000021200	0,00636	0,000511	-4,53	-0,5269	-1,45	Hfe2
Rn30017622	0,00639	0,000514	-4,53	-0,53338	-1,43	Fam158a
ENSRNOG00000018369	0,0064	0,000515	-4,53	-0,53604	-1,06	Prx
ENSRNOG00000001479	0,0064	0,000515	-4,53	-0,5362	-1,46	Gtf2i
Rn30001969	0,00642	0,000517	4,52	-0,53945	1,08	Cwh43
Rn30001253	0,00643	0,000519	4,52	-0,5432	1,27	Slc24a6
ENSRNOG00000017560	0,00646	0,000521	-4,52	-0,5479	-1,15	Mdk
Rn30001529	0,00647	0,000522	-4,52	-0,54969	-1,33	Dfnb31
Rn30019221	0,00648	0,000524	4,52	-0,55338	1,35	Adck4
ENSRNOG00000020657	0,00654	0,00053	4,51	-0,56461	1,08	Shc1
ENSRNOG00000017699	0,00658	0,000534	-4,51	-0,57281	-1,25	Mill1
ENSRNOG00000018262	0,00667	0,000541	4,5	-0,58645	1,32	Ampd3
Rn30010033	0,00667	0,000542	4,5	-0,588	1,32	Nek6
ENSRNOG00000008947	0,00667	0,000543	-4,5	-0,5889	-1,12	Cpz
ENSRNOG00000014142	0,00667	0,000543	4,5	-0,58973	1,42	Ogfrl1
ENSRNOG00000004575	0,0067	0,000546	4,5	-0,59522	1,8	Il1a
Rn30023067	0,00673	0,000549	4,49	-0,60102	1,18	Cfb
ENSRNOG00000005378	0,00682	0,000557	4,48	-0,61554	1,13	Gna15
ENSRNOG00000033835	0,00687	0,000563	-4,48	-0,62561	-1,04	Dnm1
Rn30013423	0,00687	0,000563	-4,48	-0,6261	-1,05	Lig4
R002800_01	0,00692	0,000567	-4,47	-0,63457	-1,29	Pparg
Rn30006591	0,00692	0,000568	-4,47	-0,63566	-1,06	Fbn1
ENSRNOG00000022684	0,00695	0,00057	-4,47	-0,63979	-1,55	Gpc3
Rn30025712	0,00698	0,000575	4,47	-0,64708	1,36	Nmi
Rn30026570	0,00698	0,000575	4,47	-0,64742	1,25	Gpx2
R001246_01	0,00704	0,000581	4,46	-0,65935	1,14	Map3k8
R000100_01	0,00708	0,000585	-4,46	-0,66578	-1,55	Atp1a2
Rn30002705	0,00708	0,000586	-4,46	-0,66661	-1,35	Awat2
Rn30016790	0,0071	0,000588	4,46	-0,67142	1,43	Hpx
ENSRNOG00000019996	0,0071	0,000589	4,46	-0,67174	1,21	Slc16a1
ENSRNOG00000002579	0,00715	0,000593	4,45	-0,67923	1,62	Parm1
Rn30017168	0,00715	0,000593	4,45	-0,6796	2,53	Jak3
Rn30018432	0,00718	0,000597	-4,45	-0,68531	-1,27	Myh14
ENSRNOG00000020206	0,00719	0,0006	4,44	-0,69136	1,08	Ctsd
Rn30019573	0,00719	0,0006	-4,44	-0,69175	-1,16	Pla2g16
Rn30019356	0,00719	0,0006	-4,44	-0,69183	-1,09	Tm7sf2
Rn30015519	0,00719	0,000601	-4,44	-0,69233	-1,05	Spire2
R002765_01	0,00721	0,000602	4,44	-0,69536	1,2	Hk2
R000190_01	0,00723	0,000605	-4,44	-0,69943	-1,46	Tmod1
ENSRNOG00000009005	0,00731	0,000613	4,43	-0,71316	1,12	Slco2a1
Rn30009614	0,00731	0,000613	-4,43	-0,71354	-1,16	Klhl7
Rn30013217	0,00733	0,000615	4,43	-0,71657	1,1	Ap1m1
Rn30003806	0,00733	0,000616	-4,43	-0,71796	-1,6	Dlx3
ENSRNOG00000006388	0,00733	0,000617	4,43	-0,7192	2,02	Pygl
Rn30001756	0,00735	0,000619	-4,43	-0,72296	-1,19	Chodl
R001626_01	0,00736	0,000621	4,43	-0,72547	1,34	Adora2b

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
R003208_01	0,00737	0,000622	-4,43	-0,72741	-1,23	Unc5b
Rn30012701	0,00738	0,000623	4,42	-0,72971	1,54	Tnip2
Rn30020947	0,00745	0,00063	4,42	-0,74053	1,15	Alpk1
ENSRNOG00000012477	0,00747	0,000632	-4,42	-0,74436	-1,37	Eef1a2
Rn30012858	0,00751	0,000635	4,41	-0,74964	1,57	Sbno2
Rn30009034	0,00753	0,000638	-4,41	-0,75373	-1,45	Emid1
ENSRNOG00000009797	0,00759	0,000644	4,41	-0,76273	1,61	Aqp3
Rn30000743	0,00764	0,000648	-4,4	-0,76981	-1,3	Fhl1
Rn30001722	0,00771	0,000655	4,4	-0,77959	1,47	Prodh
ENSRNOG00000005620	0,00771	0,000655	4,4	-0,78077	2,14	Lcp2
ENSRNOG00000008839	0,00772	0,000656	-4,4	-0,7825	-1,87	Pparg
Rn30009838	0,00772	0,000656	-4,4	-0,78263	-1,52	Tbx18
Rn30000670	0,00772	0,000658	4,4	-0,78504	1,3	RT1-N1
ENSRNOG00000013754	0,00772	0,000658	-4,4	-0,78506	-1,17	Krt35
R000432_01	0,00776	0,000661	4,39	-0,7899	1,18	Lum
ENSRNOG00000036604	0,00776	0,000663	4,39	-0,79194	1,99	Ifit2
ENSRNOG00000016099	0,00776	0,000663	-4,39	-0,79257	-1,29	Id4
Rn30023382	0,00782	0,000669	4,39	-0,80128	1,8	Lrp1
ENSRNOG00000029598	0,00783	0,000671	-4,39	-0,80501	-1,34	Robo2
R002140_01	0,00788	0,000676	4,38	-0,81231	1,1	Aqp3
ENSRNOG00000017703	0,0079	0,000679	4,38	-0,81694	1,27	Unc93b1
Rn30013533	0,00791	0,000681	4,38	-0,81928	1,71	Dysf
Rn30002222	0,00794	0,000683	4,38	-0,82277	1,7	Pgk1
ENSRNOG00000016412	0,00795	0,000685	-4,37	-0,82556	-1,04	Fxyd6
ENSRNOG00000026961	0,00798	0,000688	-4,37	-0,83059	-1,44	Xkrx
R002501_01	0,00799	0,00069	-4,37	-0,83326	-1,51	Slc40a1
Rn30013913	0,00803	0,000694	4,37	-0,83875	1,12	Tradd
Rn30009921	0,00803	0,000695	-4,37	-0,84001	-1,53	Dlc1
ENSRNOG00000000651	0,00806	0,000698	4,37	-0,84441	1,17	M6prbp1
Rn30007166	0,0081	0,000701	-4,36	-0,84997	-1,12	Pdhb
R000563_01	0,0081	0,000702	-4,36	-0,85062	-1,56	Cth
Rn30008144	0,00811	0,000703	-4,36	-0,85234	-1,55	Fgf22
Rn30005795	0,00815	0,000708	-4,36	-0,85875	-1,17	Neo1
Rn30019064	0,00816	0,000709	-4,36	-0,86081	-1,28	Atp12a
R004516_01	0,00816	0,00071	-4,36	-0,86163	-1,08	Bambi
Rn30015435	0,00818	0,000711	-4,35	-0,86437	-1,52	Ckm
Rn30014630	0,00818	0,000712	-4,35	-0,86546	-1,2	Kank1
Rn30011937	0,00818	0,000713	4,35	-0,86595	1,38	Sh3glb1
Rn30006619	0,00819	0,000714	-4,35	-0,86796	-1,33	Frmd6
Rn30009788	0,00819	0,000715	-4,35	-0,86898	-1,39	Megf11
ENSRNOG00000000047	0,00819	0,000715	4,35	-0,86974	1,72	Cd82
Rn30007536	0,0082	0,000717	4,35	-0,87172	1,48	Hif1a
ENSRNOG00000000577	0,00827	0,000725	4,34	-0,88416	1,14	Ddit4
ENSRNOG00000012228	0,00827	0,000726	4,34	-0,88506	1,57	Skap2
ENSRNOG00000001417	0,00827	0,000727	4,34	-0,88616	1,1	Plod3
Rn30018163	0,0083	0,00073	-4,34	-0,89078	-1,6	Slc27a6
ENSRNOG00000003743	0,00836	0,000736	4,34	-0,89886	1,06	Dars
Rn30020276	0,00838	0,000739	-4,33	-0,90235	-1,49	Frem2
Rn30021093	0,00838	0,00074	-4,33	-0,9045	-1,14	Fzd10-ps1
Rn30001459	0,00843	0,000746	-4,33	-0,91231	-1,26	Senp7
Rn30010907	0,00846	0,00075	-4,33	-0,91829	-1,32	Myo6

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30005177	0,00846	0,000751	-4,33	-0,91904	-1,44	Ndrg3
Rn30008049	0,00846	0,000753	4,33	-0,92132	1,08	Gjb2
ENSRNOG00000014610	0,00846	0,000753	4,32	-0,92189	1,93	Anpep
ENSRNOG00000018275	0,00851	0,000759	4,32	-0,93045	1,12	Errfi1
Rn30013425	0,00851	0,00076	4,32	-0,93119	1,03	Anpep
Rn30011063	0,00851	0,00076	4,32	-0,93148	1,23	Actg2
R001310_01	0,00853	0,000762	-4,32	-0,93398	-1,11	Thrb
ENSRNOG00000021125	0,00859	0,000769	4,31	-0,94331	1,14	Prdx5
R000593_01	0,00866	0,000776	-4,31	-0,9523	-1,08	Serinc5
ENSRNOG00000013668	0,00869	0,00078	4,31	-0,95721	1,16	Capg
ENSRNOG00000005700	0,0087	0,000782	-4,3	-0,96014	-1,44	Nsg1
Rn30012426	0,00877	0,000789	-4,3	-0,96915	-1,3	Krt31
ENSRNOG00000037563	0,00884	0,000797	4,3	-0,97907	2,03	Cd68
ENSRNOG00000016701	0,00884	0,000797	4,29	-0,9793	1,07	Gng8
ENSRNOG00000031081	0,00884	0,000797	4,29	-0,9796	1,37	Stat2
Rn30012648	0,00886	0,0008	-4,29	-0,98384	-1,47	Krt35
Rn30014947	0,00886	0,000801	-4,29	-0,98462	-1,29	Gnmt
ENSRNOG00000012008	0,00887	0,000802	-4,29	-0,98633	-1,1	S100a3
ENSRNOG00000015859	0,00889	0,000804	4,29	-0,98893	1,22	Chdh
Rn30019190	0,00894	0,00081	-4,29	-0,99541	-1,23	Ltbp3
ENSRNOG00000029079	0,00899	0,000815	-4,28	-1,00179	-1,25	Hspb7
ENSRNOG00000003232	0,00899	0,000815	4,28	-1,00274	1,05	Slc9a3r1
ENSRNOG00000006519	0,00909	0,000827	-4,28	-1,01661	-1,02	Tmem107
Rn30021422	0,0091	0,000828	-4,27	-1,01883	-1,66	Icoslg
ENSRNOG00000018835	0,00911	0,00083	-4,27	-1,02017	-1,34	Notch2
ENSRNOG00000016889	0,00914	0,000833	-4,27	-1,02433	-1,14	Fancc
Rn30001699	0,00917	0,000837	4,27	-1,02866	1,16	Sdf2l1
Rn30019195	0,00919	0,000839	-4,27	-1,03157	-1,19	Clip3
ENSRNOG00000001295	0,0092	0,000842	-4,27	-1,03479	-2,17	S100b
Rn30000606	0,0092	0,000842	4,27	-1,03512	1,61	RT1-CE5
Rn30010263	0,0092	0,000842	-4,27	-1,03516	-1,23	Osr2
Rn30014207	0,00929	0,000852	-4,26	-1,04719	-1,04	Ddhd2
Rn30012640	0,0093	0,000854	4,26	-1,04911	1,41	Sh3bp2
Rn30025187	0,00931	0,000855	-4,26	-1,05095	-1,37	Xkrx
Rn30020531	0,00936	0,00086	-4,25	-1,05647	-1,04	Alox12b
Rn30024414	0,00938	0,000863	-4,25	-1,05972	-1,15	Fam8a1
Rn30009280	0,00954	0,000879	-4,24	-1,07928	-1,85	Trim2
Rn30014510	0,00954	0,00088	4,24	-1,08017	1,1	Chdh
ENSRNOG00000013747	0,00958	0,000885	4,24	-1,08588	1,28	Sh3bp2
Rn30013554	0,00958	0,000886	-4,24	-1,08651	-1,42	Tcf7l1
ENSRNOG00000001859	0,0096	0,000889	4,24	-1,09078	1,24	Sdf2l1
Rn30017804	0,00961	0,00089	4,24	-1,09175	1,14	Chid1
ENSRNOG00000004489	0,00964	0,000894	4,23	-1,09613	1,07	Cd97
ENSRNOG00000038999	0,00966	0,000899	4,23	-1,10137	1,59	RT1-A1
R000447_01	0,00967	0,0009	-4,23	-1,10277	-1,03	Wfdc1
ENSRNOG00000004078	0,00969	0,000903	-4,23	-1,10567	-1,6	Eno3
R001445_01	0,0097	0,000904	-4,23	-1,1074	-1,09	Hsd11b2
ENSRNOG00000012471	0,00971	0,000906	4,23	-1,10921	1,27	Thbs4
ENSRNOG00000006460	0,00973	0,000908	4,23	-1,11223	1,13	Amdhd2
R000948_01	0,00973	0,000909	4,23	-1,11314	1,39	Fmod
ENSRNOG00000012294	0,00974	0,000911	-4,22	-1,11463	-1,56	Heph

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30010933	0,00974	0,000911	-4,22	-1,11507	-1,13	Nfat5
ENSRNOG00000001925	0,00975	0,000912	4,22	-1,11664	1,3	Leprel1
Rn30019238	0,00975	0,000913	-4,22	-1,11709	-1,12	Tdrkh
ENSRNOG00000008367	0,00983	0,000922	-4,22	-1,12779	-1,15	Krt86
ENSRNOG00000032436	0,00983	0,000923	4,22	-1,12863	1,1	Tmod3
ENSRNOG00000007412	0,00983	0,000923	4,22	-1,12869	1,31	Dok1
ENSRNOG00000006302	0,00984	0,000926	-4,22	-1,13189	-1,25	Gclc
Rn30023882	0,00985	0,000927	4,22	-1,13321	1,24	Ang2
Rn30016461	0,00988	0,000933	4,21	-1,13892	1,03	Eno1
Rn30005313	0,00991	0,000937	-4,21	-1,14321	-1,12	Nnmt
Rn30008648	0,00992	0,000938	4,21	-1,14467	1,17	Sfrp2
Rn30015145	0,00993	0,00094	-4,21	-1,14686	-1,36	Hmgcs1
ENSRNOG00000007939	0,00994	0,000942	4,21	-1,14955	1,25	Naprt1
Rn30001727	0,00994	0,000943	-4,21	-1,15016	-1,53	Dgcr8
ENSRNOG00000009348	0,01	0,000954	4,2	-1,16182	1,12	Nos3
ENSRNOG00000018656	0,0101	0,000957	-4,2	-1,16484	-1,3	Ampd1
Rn30002069	0,0101	0,000959	-4,2	-1,16764	-1,57	Fam122b
ENSRNOG00000026060	0,0101	0,000963	-4,2	-1,1711	-1,02	Arsi
Rn30007882	0,0102	0,00097	4,19	-1,17896	1,13	Ncam1
Rn30004150	0,0102	0,000973	-4,19	-1,18203	-2,8	Kera
Rn30007180	0,0102	0,000976	4,19	-1,18516	1,59	Tmem178
Rn30015922	0,0102	0,00098	-4,19	-1,18922	-1,09	Zfp322a
ENSRNOG00000013621	0,0102	0,000982	4,18	-1,19158	2,86	Rnd1
Rn30023417	0,0103	0,000988	-4,18	-1,19685	-2	Krt72
ENSRNOG00000016587	0,0104	0,001	4,17	-1,21127	1,21	Ninj1
ENSRNOG00000004863	0,0104	0,00101	-4,17	-1,21609	-1,49	Mpped2
Rn30003941	0,0105	0,00102	-4,17	-1,22731	-1,22	Azi1
Rn30007052	0,0106	0,00103	-4,16	-1,23617	-2,2	Frzb
ENSRNOG00000008635	0,0107	0,00104	-4,15	-1,2505	-1,04	Mks1
Rn30016794	0,0107	0,00104	4,15	-1,25176	1,25	Ampd3
ENSRNOG00000016210	0,0107	0,00104	-4,15	-1,25361	-1,3	Micalcl
ENSRNOG00000030019	0,0108	0,00105	4,15	-1,26064	1,33	Atp1a1
ENSRNOG00000002413	0,0108	0,00105	-4,15	-1,26184	-1,29	Gpc4
R000081_01	0,0109	0,00106	4,15	-1,26765	1,01	Actg2
R002205_01	0,0109	0,00106	4,15	-1,26804	1,11	Runx1
ENSRNOG00000012478	0,0109	0,00106	-4,14	-1,26909	-1,11	Shox2
Rn30015616	0,0109	0,00106	4,14	-1,27096	1,04	Inpp5d
Rn30007666	0,0109	0,00107	-4,14	-1,27356	-1	Cttnbp2
R000612_01	0,0109	0,00107	4,14	-1,27508	1,07	P4hb
Rn30009443	0,011	0,00107	4,14	-1,28133	1	Eif4e3
ENSRNOG00000007319	0,011	0,00107	4,14	-1,28188	1,45	Trib3
Rn30014496	0,011	0,00108	4,14	-1,28475	1,26	Fam129b
ENSRNOG00000025704	0,0111	0,00108	-4,13	-1,29168	-1,42	Yod1
ENSRNOG00000008961	0,0111	0,00109	-4,13	-1,29664	-1,28	Mapre3
Rn30008344	0,0111	0,00109	-4,13	-1,29729	-1,44	Cidec
Rn30017948	0,0111	0,00109	4,13	-1,29999	1,11	Psmb10
ENSRNOG00000030344	0,0111	0,00109	-4,13	-1,30045	-1,3	Krt34
Rn30016078	0,0112	0,00111	-4,12	-1,31339	-1,41	Gse1
Rn30006161	0,0113	0,00111	-4,12	-1,31634	-1,02	Ovol2
Rn30005187	0,0113	0,00112	-4,12	-1,32323	-1,12	Wnt16
ENSRNOG00000014408	0,0113	0,00112	-4,12	-1,3243	-1,02	Gjb5

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
ENSRNOG00000000858	0,0113	0,00112	-4,12	-1,32498	-1,11	Ng23
Rn30018956	0,0113	0,00112	-4,12	-1,32513	-1,16	Tbxa2r
Rn30002113	0,0113	0,00112	-4,12	-1,32566	-1,29	Mark1
ENSRNOG00000020014	0,0113	0,00112	-4,11	-1,32743	-1,05	Myh14
Rn30020673	0,0115	0,00113	-4,11	-1,33765	-1,06	Fam164a
Rn30010622	0,0115	0,00114	-4,11	-1,33837	-1,1	Pcsk6
Rn30013484	0,0115	0,00114	-4,11	-1,34018	-1,11	Hs3st6
R002946_01	0,0115	0,00114	4,11	-1,34396	1,01	Txn1
Rn30018539	0,0116	0,00116	4,1	-1,35622	1,35	Slc4a3
R003012_01	0,0117	0,00116	-4,1	-1,36125	-1,14	Padi1
Rn30005652	0,0117	0,00116	-4,1	-1,36181	-1,28	Elovl5
R000395_01	0,0117	0,00116	4,1	-1,36207	1,21	Prdx1
Rn30026336	0,0117	0,00117	-4,1	-1,36434	-1,18	Otop2
ENSRNOG00000033617	0,0117	0,00117	-4,09	-1,3675	-1,37	Krt26
ENSRNOG00000026855	0,0118	0,00118	-4,09	-1,37544	-1,28	Abhd12b
Rn30005433	0,0118	0,00118	-4,09	-1,37585	-1,05	Matn2
ENSRNOG00000016374	0,0118	0,00118	-4,09	-1,37636	-1,37	Fgfr2
ENSRNOG00000017484	0,012	0,00121	4,08	-1,39878	1,12	Gja5
Rn30004494	0,012	0,00121	4,08	-1,39967	2,08	Angpt4
R000414_01	0,012	0,00121	4,08	-1,40436	1,11	Prdx5
Rn30011124	0,0121	0,00122	4,07	-1,41003	1,38	Msn
ENSRNOG00000032136	0,0121	0,00122	-4,07	-1,41128	-1,12	Cdc42ep3
ENSRNOG00000007078	0,0122	0,00123	4,07	-1,41783	1,54	Wisp1
Rn30015843	0,0122	0,00123	4,07	-1,42053	1,6	Chmp4bl1
Rn30014303	0,0122	0,00123	-4,07	-1,4228	-1,04	Ptprk
ENSRNOG00000003468	0,0122	0,00124	-4,06	-1,42528	-1,55	Capn8
ENSRNOG00000005861	0,0122	0,00124	4,06	-1,42791	1,49	Hsd11b1
Rn30006170	0,0122	0,00124	-4,06	-1,43038	-1,04	Insig1
Rn30009172	0,0123	0,00125	4,06	-1,43859	1,1	Erap1
Rn30024432	0,0123	0,00126	-4,06	-1,44001	-1,41	Lin9
ENSRNOG00000014838	0,0123	0,00126	4,06	-1,44035	1,35	Glipr2
Rn30010610	0,0123	0,00126	4,06	-1,4416	1,19	Tnfrsf21
Rn30014364	0,0124	0,00126	4,05	-1,44378	2,33	Acap1
ENSRNOG00000026672	0,0124	0,00126	-4,05	-1,44432	-1,28	MGC94199
Rn30011077	0,0124	0,00126	4,05	-1,44443	1,18	B3galnt1
ENSRNOG00000018358	0,0124	0,00127	-4,05	-1,45256	-1,02	Nt5dc2
ENSRNOG00000004554	0,0124	0,00127	4,05	-1,45329	1,48	Dcn
R003564_01	0,0125	0,00128	4,05	-1,45561	1,68	Matk
Rn30015134	0,0125	0,00128	-4,05	-1,45904	-1,13	Rgnef
Rn30018718	0,0125	0,00128	-4,05	-1,46104	-1,12	Tnnt3
ENSRNOG00000022968	0,0126	0,00129	4,04	-1,46511	1,12	Myo5a
ENSRNOG00000025114	0,0126	0,00129	4,04	-1,46918	1,2	Cebpb
Rn30003953	0,0126	0,0013	-4,04	-1,47279	-1,29	Fignl1
R002163_01	0,0126	0,0013	4,04	-1,47532	1,04	Gchfr
ENSRNOG00000006308	0,0127	0,0013	-4,04	-1,47663	-1,06	Mycn
ENSRNOG00000008855	0,0127	0,0013	4,04	-1,47714	1,11	Gjb2
Rn30019172	0,0128	0,00132	-4,03	-1,48676	-1	Etv4
ENSRNOG00000017676	0,0128	0,00132	4,03	-1,49037	1,16	Plvap
Rn30024812	0,0128	0,00132	-4,03	-1,49252	-1,09	Ophn1
ENSRNOG00000005984	0,0129	0,00133	4,03	-1,49616	1,09	Etv6
Rn30017255	0,0129	0,00133	4,03	-1,50006	1,16	Klk11

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30006841	0,0129	0,00133	-4,03	-1,50153	-1,52	Glb1l2
Rn30009375	0,013	0,00134	-4,02	-1,50898	-1,09	Rab30
Rn30001922	0,013	0,00135	-4,02	-1,51251	-1,14	Krtap7-1
Rn30016725	0,013	0,00135	-4,02	-1,51441	-1,54	Tpm1_v6
Rn30009276	0,0132	0,00137	-4,01	-1,52897	-1,3	Lef1
Rn30021612	0,0132	0,00137	-4,01	-1,52997	-1,49	Dpep2
Rn30019037	0,0132	0,00138	4,01	-1,53238	1,25	Shc1
ENSRNOG00000030814	0,0132	0,00138	-4,01	-1,53301	-1,12	Kb23
ENSRNOG00000001383	0,0132	0,00138	4,01	-1,53375	1,75	Slc24a6
ENSRNOG00000024705	0,0132	0,00138	4,01	-1,53573	1,4	Rarres2
R001735_01	0,0132	0,00138	-4,01	-1,53793	-1,33	Lipe
Rn30018959	0,0133	0,0014	4	-1,54916	1,02	Efemp2
R001130_01	0,0133	0,0014	-4	-1,54964	-1,31	Tnfrsf11b
Rn30014285	0,0133	0,0014	-4	-1,54974	-1,55	Suv39h2
ENSRNOG00000029330	0,0134	0,00141	-4	-1,55416	-1,21	Car5b
ENSRNOG00000012482	0,0134	0,00141	-4	-1,55471	-1,17	Ndrg4
Rn30007523	0,0134	0,00141	4	-1,55707	1,23	Bag1
R001833_01	0,0134	0,00141	4	-1,55811	1,01	Pla1a
ENSRNOG00000020644	0,0134	0,00141	-4	-1,55854	-1,1	Nsg2
ENSRNOG00000036672	0,0134	0,00141	4	-1,55982	1,07	Sectm1a
Rn30005020	0,0135	0,00142	3,99	-1,5639	1,26	Abi3
Rn30002155	0,0135	0,00142	-3,99	-1,56538	-1,15	Mfap4
Rn30002876	0,0135	0,00144	3,99	-1,57537	1,07	Slc9a3r1
R000684_01	0,0135	0,00144	3,99	-1,57598	1,15	Map2k1
Rn30023636	0,0135	0,00144	-3,99	-1,57601	-1,52	Trdn
ENSRNOG00000013011	0,0136	0,00145	-3,98	-1,58408	-1,52	Dnajb4
ENSRNOG00000003330	0,0136	0,00145	-3,98	-1,58436	-1,52	Acsf2
Rn30024908	0,0136	0,00145	3,98	-1,58442	1,13	Tmprss4
Rn30021962	0,0136	0,00145	-3,98	-1,585	-1,22	Crabp1
Rn30000911	0,0136	0,00145	-3,98	-1,58721	-1,06	Kctd4
Rn30007043	0,0136	0,00145	3,98	-1,58826	1,08	Insm2
Rn30012562	0,0137	0,00146	3,98	-1,59043	1,44	Capg
ENSRNOG00000014936	0,0137	0,00146	3,98	-1,59178	1,09	Ifitm2
R000504_01	0,0137	0,00146	-3,98	-1,59219	-1,05	Idh1
R001082_01	0,0138	0,00148	-3,97	-1,60755	-1,2	Kcne1
ENSRNOG00000010146	0,0139	0,00149	-3,97	-1,61063	-1,14	Ndn
ENSRNOG00000013572	0,0139	0,00149	-3,97	-1,61077	-1,12	Lxn
ENSRNOG00000009401	0,0139	0,00149	3,97	-1,61468	1,05	Lmo2
Rn30002390	0,0139	0,00149	3,97	-1,61484	1,05	Pla2g4a
ENSRNOG00000009153	0,014	0,00151	-3,96	-1,62668	-1,49	Cidec
Rn30024502	0,014	0,00151	-3,96	-1,62768	-1,07	Nkain4
ENSRNOG00000033352	0,0141	0,00152	-3,96	-1,63101	-1,34	S100a7a
ENSRNOG00000006588	0,0141	0,00152	-3,96	-1,63581	-1,04	Meox2
R001793_01	0,0142	0,00153	-3,95	-1,63878	-1,33	Edn2
Rn30023280	0,0142	0,00154	-3,95	-1,64377	-1,28	Scyl2
ENSRNOG00000031805	0,0142	0,00154	-3,95	-1,64521	-1,05	Krt1-5
Rn30005990	0,0143	0,00155	-3,95	-1,65171	-1,2	Tmem168
Rn30003663	0,0144	0,00156	-3,94	-1,65751	-1,05	Trib2
Rn30005363	0,0146	0,00159	3,94	-1,67601	2,1	Etv6
R000360_01	0,0146	0,00159	3,94	-1,67607	1,11	Ifitm2
Rn30023583	0,0147	0,00161	-3,93	-1,68975	-1,01	Yars2

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30009949	0,0147	0,00161	-3,93	-1,69075	-1,12	Fabp4
Rn30006026	0,0148	0,00161	-3,93	-1,69147	-1,18	Spc25
ENSRNOG00000023538	0,0148	0,00161	-3,93	-1,69371	-1,1	Aldh5a1
ENSRNOG00000000900	0,0148	0,00162	-3,92	-1,69839	-1,21	Tpst1
Rn30008644	0,0148	0,00162	-3,92	-1,7001	-1,5	Pdzd8
ENSRNOG00000005434	0,0149	0,00163	-3,92	-1,70241	-1,02	Sptbn1
ENSRNOG00000022581	0,015	0,00164	3,92	-1,70903	1,21	Atp10a
ENSRNOG00000010516	0,015	0,00164	3,92	-1,71162	1,19	Plau
R000219_01	0,015	0,00165	3,92	-1,71321	1,12	B2m
Rn30018773	0,015	0,00165	-3,91	-1,71639	-1,04	Inpp5f
Rn30014896	0,0152	0,00167	-3,91	-1,72644	-1,45	Dmrt2
Rn30011215	0,0152	0,00167	3,91	-1,7286	2,82	Sfpi1
Rn30007148	0,0153	0,00168	-3,91	-1,73468	-1,51	Mst4
Rn30009664	0,0153	0,00168	3,9	-1,73671	1,02	Col12a1
Rn30016565	0,0153	0,00169	-3,9	-1,73775	-1,06	Nek4
Rn30015020	0,0153	0,00169	-3,9	-1,73911	-1,12	Pdlim5
ENSRNOG00000014372	0,0153	0,00169	-3,9	-1,74028	-1,15	Gjb3
Rn30001433	0,0153	0,00169	-3,9	-1,74078	-1,76	Hoxd13
ENSRNOG00000015416	0,0153	0,0017	3,9	-1,74282	1,13	Obfc2a
ENSRNOG00000019737	0,0154	0,00171	3,9	-1,74881	1,07	Sema4a
ENSRNOG00000025895	0,0154	0,00171	-3,9	-1,74939	-1,2	Sdpr
ENSRNOG00000002188	0,0154	0,00171	3,9	-1,75246	1,17	Hpse
ENSRNOG00000007604	0,0155	0,00172	3,89	-1,75958	1,56	Igsf8
Rn30000103	0,0155	0,00172	-3,89	-1,76012	-1,04	Nebl
ENSRNOG00000013426	0,0155	0,00173	-3,89	-1,76058	-1,08	Mrgprf
Rn30007605	0,0155	0,00173	-3,89	-1,76485	-1,37	Krt86
Rn30022556	0,0156	0,00174	-3,89	-1,76627	-1,04	Scel
Rn30010542	0,0156	0,00174	3,89	-1,76788	1,12	Nkain1
Rn30012154	0,0156	0,00174	-3,89	-1,76824	-1,75	Krt34
R005560_01	0,0157	0,00176	3,88	-1,77964	1,31	Rffl
ENSRNOG00000013003	0,0158	0,00177	-3,88	-1,78845	-1,02	Srms
ENSRNOG00000027096	0,0158	0,00178	3,88	-1,7894	1,09	Ctsw
ENSRNOG00000024011	0,0158	0,00178	-3,88	-1,78955	-1,05	Ank3
ENSRNOG00000020332	0,0158	0,00178	-3,88	-1,79017	-1,31	Tnnt3
R003725_01	0,0158	0,00178	3,88	-1,79177	1,11	Dnajc3
Rn30000430	0,0159	0,00179	3,87	-1,79737	1,21	Fgd2
Rn30005266	0,016	0,0018	-3,87	-1,80127	-1,11	Tcf7
ENSRNOG00000013415	0,016	0,0018	3,87	-1,8052	1,19	Ptpn18
ENSRNOG00000033498	0,016	0,00181	3,87	-1,80656	1,13	Cib1
Rn30001168	0,016	0,00181	3,87	-1,80839	1	P2rx4
ENSRNOG00000012302	0,016	0,00181	-3,87	-1,80864	-1,35	Gucy1a3
Rn30010356	0,016	0,00181	3,87	-1,81073	1,12	Zc3h13
Rn30016350	0,016	0,00181	3,87	-1,81104	1,05	Sfrp1
Rn30007263	0,016	0,00182	3,86	-1,81331	1,24	Adipor2
Rn30007121	0,0161	0,00182	3,86	-1,8151	1,04	Dennd3
R004280_01	0,0161	0,00183	3,86	-1,81887	1,01	Degs1
ENSRNOG00000010453	0,0161	0,00183	-3,86	-1,81937	-1,27	Klhl7
Rn30000325	0,0162	0,00184	-3,86	-1,82527	-1,32	Egfl8
ENSRNOG00000002095	0,0162	0,00184	-3,86	-1,82645	-1,33	Arhgap24
ENSRNOG00000010510	0,0163	0,00185	3,85	-1,83282	1,82	Col12a1
R002037_01	0,0164	0,00187	-3,85	-1,84156	-1,08	Kcnh2

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
ENSRNOG00000009683	0,0164	0,00187	3,85	-1,84246	1	Sdcbp
R000130_01	0,0164	0,00187	3,85	-1,84432	1,06	Cstb
ENSRNOG00000006735	0,0164	0,00188	3,85	-1,8467	1,32	Cdkn2b
Rn30003638	0,0164	0,00188	-3,85	-1,84798	-1,03	Toag1
R005368_01	0,0164	0,00189	-3,85	-1,85038	-1,44	Hrc
ENSRNOG00000008410	0,0165	0,00189	-3,84	-1,85206	-1,59	Cep63
Rn30018776	0,0165	0,0019	-3,84	-1,85605	-1,12	Capn12
Rn30016501	0,0166	0,00191	-3,84	-1,86373	-1,22	Ccdc3
Rn30004690	0,0166	0,00191	-3,84	-1,86422	-1,16	Gnptab
Rn30000873	0,0166	0,00191	-3,84	-1,86438	-1,02	Fam101a
Rn30006456	0,0168	0,00194	3,83	-1,87841	1,32	Endou
ENSRNOG00000001348	0,0169	0,00195	3,83	-1,88413	1,05	Erp29
ENSRNOG00000016731	0,017	0,00197	-3,82	-1,89467	-1,14	Tpm2
Rn30012887	0,017	0,00198	3,82	-1,89791	1,21	Map4k4
Rn30000947	0,0171	0,00198	-3,82	-1,90111	-1,04	Lass4
Rn30004935	0,0172	0,002	3,82	-1,91008	1,19	Csda
ENSRNOG00000017786	0,0173	0,00201	-3,81	-1,91609	-1,04	Acta1
ENSRNOG00000010303	0,0173	0,00202	-3,81	-1,91869	-1,04	Trim32
Rn30012489	0,0174	0,00202	-3,81	-1,9216	-1,26	Fam135a
Rn30021012	0,0174	0,00203	-3,81	-1,92298	-1,53	Pmp2
Rn30021042	0,0174	0,00203	-3,81	-1,92315	-1,36	Cdkn2aip
ENSRNOG00000012879	0,0174	0,00203	-3,81	-1,92324	-1,12	Fabp3
Rn30009753	0,0174	0,00203	-3,81	-1,92333	-1,27	Ctnnal1
ENSRNOG00000005464	0,0174	0,00204	-3,81	-1,92825	-1,25	Hspc159
Rn30010901	0,0174	0,00204	-3,81	-1,93	-1,44	Krt28
ENSRNOG00000001500	0,0175	0,00206	3,8	-1,93704	1,01	Rab4b
Rn30001127	0,0175	0,00206	3,8	-1,93731	1,04	Snx8
ENSRNOG00000017895	0,0176	0,00207	3,8	-1,94329	1,06	Eno1
Rn30024193	0,0176	0,00207	-3,8	-1,94483	-1,28	Sdpr
Rn30026269	0,0176	0,00207	3,8	-1,94523	1,13	Arpc5
ENSRNOG00000019698	0,0178	0,00209	3,79	-1,95566	1,04	Ssbp4
Rn30015360	0,0178	0,00209	-3,79	-1,95579	-1,17	Fgfr4
Rn30007427	0,0178	0,0021	3,79	-1,95668	1,42	Plod2
Rn30004002	0,0178	0,0021	3,79	-1,95789	1,11	Cd97
R004101_01	0,0178	0,0021	3,79	-1,95923	1,07	Tapbp
ENSRNOG00000030142	0,0179	0,00212	3,78	-1,96936	1,13	Hist1h4b
ENSRNOG00000001057	0,0179	0,00213	-3,78	-1,9716	-1,08	Ctxn1
ENSRNOG00000006589	0,0179	0,00213	3,78	-1,97271	1,05	Mif
ENSRNOG00000028845	0,018	0,00214	-3,78	-1,97747	-1,12	Ebf1
Rn30004446	0,018	0,00215	-3,78	-1,98051	-4,48	Birc6
R003711_01	0,018	0,00215	-3,78	-1,98173	-1,23	Itpkb
R002705_01	0,018	0,00215	3,78	-1,98303	1,4	Pygl
R001364_01	0,018	0,00215	-3,78	-1,98313	-1,25	Arc
ENSRNOG00000019885	0,0181	0,00216	-3,78	-1,98781	-1,04	Magi3
Rn30011115	0,0181	0,00216	-3,78	-1,98786	-1,68	Egflam
R000858_01	0,0181	0,00217	3,77	-1,989	1,04	Ccbl1
R003594_01	0,0182	0,00217	-3,77	-1,993	-1,05	Egr3
Rn30015958	0,0182	0,00217	3,77	-1,99348	1,24	Zyx
ENSRNOG00000018740	0,0182	0,00218	3,77	-1,99425	1,66	Ugt1a5
R004272_01	0,0182	0,00218	-3,77	-1,99671	-1,26	Capn8
Rn30012389	0,0185	0,00223	-3,76	-2,02056	-1,16	Cdh11

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
ENSRNOG00000020848	0,0186	0,00224	3,76	-2,02212	1,02	Adck4
Rn30018851	0,0186	0,00224	-3,76	-2,02326	-1,11	Wnk4
ENSRNOG00000020699	0,0188	0,00228	3,75	-2,03888	2,32	Cd37
Rn30012346	0,0188	0,00228	3,75	-2,03939	1,3	Atp6v0a4
Rn30005470	0,0188	0,00228	3,75	-2,04166	1,52	Cd44
Rn30018158	0,0189	0,00229	3,75	-2,04381	1,05	Dph3
Rn30008771	0,0189	0,00229	3,75	-2,04432	1,03	Snai1
Rn30003833	0,0189	0,00229	-3,75	-2,0465	-1,17	Timp3
ENSRNOG00000003242	0,0189	0,00229	-3,74	-2,04747	-1,27	Gulp1
Rn30015221	0,0189	0,0023	3,74	-2,04786	1,37	Dsg3
ENSRNOG00000003736	0,0189	0,0023	-3,74	-2,0516	-1,03	Col5a2
ENSRNOG00000010286	0,019	0,00232	-3,74	-2,05761	-1,02	Cast
Rn30006686	0,019	0,00232	3,74	-2,0584	1,31	Iah1
Rn30006107	0,019	0,00232	-3,74	-2,06032	-1,03	Setmar
Rn30007370	0,019	0,00233	3,74	-2,0628	1,66	Shmt2
Rn30001764	0,019	0,00233	3,74	-2,06312	1,23	Leprel1
Rn30006931	0,0191	0,00234	3,74	-2,06577	1,33	Cd63
ENSRNOG00000010635	0,0191	0,00234	3,74	-2,0666	1,03	Igfbp4
ENSRNOG00000011826	0,0192	0,00236	-3,73	-2,07527	-1,66	Lzts1
ENSRNOG00000008019	0,0192	0,00236	-3,73	-2,07627	-1,19	Oxr1
ENSRNOG00000013141	0,0192	0,00237	3,73	-2,07992	1,26	Eno2
Rn30016500	0,0192	0,00237	-3,73	-2,08008	-1,4	St3gal2
R000650_01	0,0193	0,00238	3,73	-2,08202	1,35	Slc9a1
Rn30023126	0,0193	0,00238	-3,73	-2,08585	-1,23	Stk39
Rn30014289	0,0193	0,00239	3,72	-2,08786	1,2	Cndp2
ENSRNOG00000014630	0,0195	0,00241	-3,72	-2,09848	-1,26	Iws1
R003792_01	0,0196	0,00242	3,72	-2,10254	1,05	Ramp3
Rn30000454	0,0197	0,00245	3,71	-2,11215	1,16	Sar1a
ENSRNOG00000015948	0,0198	0,00245	3,71	-2,11409	1,17	Slc1a5
Rn30011888	0,0198	0,00246	3,71	-2,11622	1,04	Spon1
ENSRNOG00000016066	0,02	0,00248	-3,7	-2,12622	-1,62	Bambi
Rn30025835	0,02	0,00249	3,7	-2,12845	1,12	Rps6ka1
ENSRNOG00000006946	0,02	0,00249	3,7	-2,12915	2,09	Arhgap9
Rn30003424	0,02	0,00249	-3,7	-2,12967	-1,1	Dnaja3
Rn30017401	0,02	0,0025	-3,7	-2,13172	-1,17	Ankrd13d
ENSRNOG00000020562	0,0202	0,00252	3,7	-2,14192	1,27	Slc22a18
Rn30017304	0,0202	0,00252	-3,7	-2,14294	-2,56	Accn2
Rn30013458	0,0204	0,00255	-3,69	-2,15331	-1	Cbfb
Rn30012795	0,0204	0,00256	-3,69	-2,15602	-1,06	Igsf10
R000791_01	0,0205	0,00257	3,69	-2,16228	1,53	Anxa3
Rn30024793	0,0205	0,00257	-3,69	-2,16264	-1,33	Aadacl4
ENSRNOG00000002210	0,0205	0,00258	3,68	-2,16572	1,01	Hsd17b11
Rn30011941	0,0205	0,00258	3,68	-2,16597	1,06	Nudt16
ENSRNOG00000013917	0,0206	0,00259	-3,68	-2,1704	-1,09	Igsf10
Rn30021644	0,0206	0,0026	3,68	-2,17228	1,75	Parp14
Rn30011822	0,0207	0,00261	-3,68	-2,17821	-1,01	Mlf1
Rn30023432	0,0209	0,00265	-3,67	-2,19255	-1,2	Krt72
Rn30017386	0,0209	0,00265	3,67	-2,193	1,09	Sfrp4
Rn30007406	0,0209	0,00267	3,67	-2,1976	1,28	Irf1
Rn30005656	0,0212	0,0027	-3,66	-2,21031	-1,11	Klhl9
ENSRNOG00000003476	0,0212	0,0027	-3,66	-2,21048	-1,57	Slc6a4

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
ENSRNOG00000012329	0,0212	0,00271	3,66	-2,21475	1,35	Tmem66
Rn30011665	0,0213	0,00272	-3,66	-2,21636	-1,14	Mfsd6
R001338_01	0,0213	0,00272	-3,66	-2,2179	-1,28	Ptprv
Rn30013903	0,0213	0,00273	-3,66	-2,22177	-1,04	Gem
ENSRNOG00000002977	0,0213	0,00273	-3,66	-2,22267	-1,19	Ttc19
ENSRNOG00000005478	0,0213	0,00273	-3,66	-2,22285	-1,28	Fkbp9
Rn30017461	0,0213	0,00273	3,65	-2,22311	1,07	Mobkl2a
ENSRNOG00000036871	0,0213	0,00274	-3,65	-2,22431	-1,17	Kb21
Rn30015915	0,0214	0,00275	3,65	-2,22892	1,02	Trex2
ENSRNOG00000010079	0,0215	0,00277	-3,65	-2,23527	-1,13	Car3
ENSRNOG00000000894	0,0216	0,00278	-3,65	-2,23996	-1,32	Fry
R004340_01	0,0217	0,0028	3,64	-2,24677	1,06	Ehd4
Rn30008145	0,0218	0,00281	-3,64	-2,25199	-1,27	Mapre3
Rn30002090	0,0218	0,00282	-3,64	-2,25495	-1,16	Kcnj12
Rn30006752	0,0219	0,00283	-3,64	-2,25821	-1,13	Aloxe3
Rn30024649	0,0219	0,00284	3,64	-2,26088	1,15	Krt17
ENSRNOG00000006921	0,0219	0,00284	-3,64	-2,26146	-1,27	Rbl1
ENSRNOG00000020270	0,0223	0,00291	3,62	-2,28551	1,05	Anxa8
ENSRNOG00000029336	0,0224	0,00292	-3,62	-2,28791	-1,13	Zfp180
Rn30025346	0,0225	0,00294	-3,62	-2,29649	-1,27	Krtap3-3l1,Krtap3-3
Rn30006451	0,0226	0,00295	-3,62	-2,2993	-1,04	Bbs5
ENSRNOG00000036812	0,0226	0,00296	-3,61	-2,30162	-1,01	Ndrg3
ENSRNOG00000011680	0,0229	0,00301	3,61	-2,31785	1,18	Il16
ENSRNOG00000024468	0,0229	0,00301	-3,61	-2,31846	-1,03	Traf3ip1
R005089_01	0,0229	0,00301	3,61	-2,31878	1,09	Irf5
Rn30014892	0,0229	0,00301	3,61	-2,31912	1,27	Lysmd3
R000214_01	0,0229	0,00301	3,61	-2,32035	1,29	Tcn2
Rn30012751	0,023	0,00303	-3,6	-2,32557	-1,09	Calm2
Rn30001207	0,023	0,00303	3,6	-2,32764	1,25	Psmd9
ENSRNOG00000002828	0,0232	0,00306	-3,6	-2,33662	-1,07	Tob1
Rn30003094	0,0233	0,00308	-3,59	-2,34195	-1,08	Prkca
ENSRNOG00000010235	0,0234	0,0031	3,59	-2,34904	1,35	Pkig
Rn30005672	0,0234	0,00311	3,59	-2,35117	1,05	Galk1
Rn30005824	0,0235	0,00312	-3,59	-2,35652	-1,02	Atl2
R001233_01	0,0237	0,00315	-3,58	-2,36599	-1,16	Tnni2
ENSRNOG00000015849	0,0237	0,00316	-3,58	-2,36662	-1,05	Sepp1
Rn30017279	0,0242	0,00324	3,57	-2,39174	1,1	Eif3c
Rn30014628	0,0243	0,00325	3,57	-2,39517	1,27	Atp1a1
ENSRNOG00000017808	0,0243	0,00325	-3,57	-2,39643	-1,18	Klf15
R002524_01	0,0243	0,00326	-3,56	-2,40023	-1,08	Bbs2
Rn30017684	0,0245	0,00328	-3,56	-2,40567	-1,9	Adrb2
Rn30014807	0,0248	0,00333	-3,55	-2,42107	-1,11	Micalcl
Rn30024766	0,0248	0,00333	-3,55	-2,42107	-1,05	Slc6a19
Rn30000977	0,0249	0,00336	3,55	-2,43073	1,05	Foxk1
Rn30023416	0,0251	0,00339	-3,54	-2,43819	-1,31	Krt73
Rn30022555	0,0255	0,00346	-3,53	-2,45757	-1,09	Scel
Rn30022258	0,0256	0,00347	-3,53	-2,46232	-1,1	Tbc1d30
Rn30022473	0,0256	0,00348	3,53	-2,46305	1,01	Cbln1
ENSRNOG00000002657	0,0257	0,00348	3,53	-2,4657	1,28	Pla2g4a
R002532_01	0,0257	0,0035	-3,53	-2,47003	-1,03	Gjb5
Rn30000511	0,0258	0,00351	3,53	-2,47291	1,02	Bicc1

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30006244	0,0259	0,00353	3,52	-2,4799	1,32	Arhgap9
Rn30002721	0,0259	0,00353	3,52	-2,47998	1,06	Tbc1d9b
ENSRNOG00000012151	0,0259	0,00353	-3,52	-2,47998	-1,05	Itpripl1
ENSRNOG00000015845	0,026	0,00356	3,52	-2,48811	1,07	Fam129b
ENSRNOG00000030871	0,0265	0,00364	-3,51	-2,50833	-1,04	Calm2
ENSRNOG00000010952	0,0267	0,00367	-3,5	-2,51836	-1,04	Ift122
ENSRNOG00000024533	0,0267	0,00367	-3,5	-2,51864	-1,23	Aer61
ENSRNOG00000015237	0,0267	0,00367	3,5	-2,5188	1,32	Gle1
Rn30016328	0,0269	0,00371	-3,5	-2,52778	-1,12	Mccc2
Rn30007650	0,0269	0,00372	3,5	-2,53012	1,46	Lpo
Rn30022157	0,027	0,00373	-3,5	-2,53378	-1,01	Pigg
Rn30017980	0,027	0,00373	3,5	-2,53495	1,18	MGC93975
Rn30007217	0,0272	0,00377	3,49	-2,54453	1,04	Bcl2l1
R003120_01	0,0274	0,0038	3,49	-2,55269	1,32	Slc7a5
Rn30005992	0,0275	0,00383	-3,48	-2,559	-1	Cav1
ENSRNOG00000016890	0,0276	0,00385	-3,48	-2,56407	-1,31	Tppp3
Rn30002706	0,0277	0,00385	-3,48	-2,56632	-1,09	Atp2b4
ENSRNOG00000007390	0,0278	0,00387	3,48	-2,56961	1,2	Nfkbia
ENSRNOG00000018847	0,0278	0,00388	3,48	-2,57207	1,02	Stx5
R005285_01	0,0278	0,00388	-3,48	-2,57305	-1,03	Mtmr2
Rn30019001	0,0279	0,0039	-3,47	-2,5775	-1,28	Mcpt2
Rn30007814	0,0281	0,00392	3,47	-2,5835	1,32	Steap4
ENSRNOG00000018715	0,0281	0,00392	3,47	-2,58395	1,08	Clec10a
Rn30011701	0,0281	0,00392	-3,47	-2,58429	-1,05	Nfya
R004671_01	0,0281	0,00394	-3,47	-2,58733	-1,07	Phyh
Rn30021568	0,0282	0,00394	-3,47	-2,58932	-1,37	Fndc1
Rn30001590	0,0282	0,00395	3,47	-2,5909	1,02	Lrrc33
ENSRNOG00000032637	0,0284	0,00399	-3,46	-2,5998	-1,01	Krtap1-5
Rn30021632	0,0285	0,004	3,46	-2,60354	1,17	Ostc
Rn30017761	0,0286	0,00402	-3,46	-2,60825	-1,09	Srpk3
ENSRNOG00000000844	0,0288	0,00405	-3,45	-2,61603	-1,37	Ly6g6d
Rn30015714	0,0288	0,00405	-3,45	-2,61696	-1,01	Synj2
ENSRNOG00000015880	0,0289	0,00408	-3,45	-2,62199	-1,02	Dpep1
Rn30020557	0,0289	0,00408	3,45	-2,62344	1,21	mrpl24
ENSRNOG00000028865	0,029	0,0041	-3,45	-2,62732	-1,12	Kprp
R002853_01	0,0291	0,00411	-3,45	-2,63153	-1,03	Klf15
ENSRNOG00000000186	0,0294	0,00416	-3,44	-2,64346	-1,86	Tst
Rn30002156	0,0297	0,0042	3,44	-2,65201	1,22	Trim41
R001278_01	0,0297	0,00421	-3,43	-2,65355	-1,12	F3
Rn30000702	0,0299	0,00424	3,43	-2,6607	1,07	Flot1
Rn30005202	0,0299	0,00424	-3,43	-2,66132	-1,24	Cav3
Rn30016065	0,0302	0,00431	-3,42	-2,6768	-1,04	Tcf12
ENSRNOG00000022364	0,0302	0,00431	-3,42	-2,67792	-1,76	Dsg4
R002934_01	0,0303	0,00434	-3,42	-2,68469	-1,25	S100a3
Rn30011573	0,0308	0,00441	-3,41	-2,69999	-1,16	Arhgap29
ENSRNOG00000014635	0,031	0,00444	3,41	-2,70833	1,06	Clta
ENSRNOG00000015591	0,0311	0,00446	3,4	-2,71157	1,1	Cndp2
Rn30009289	0,0311	0,00446	-3,4	-2,71182	-1,21	Acot2
Rn30010995	0,0311	0,00446	-3,4	-2,71204	-1,12	Smarca2
R004952_01	0,0311	0,00447	-3,4	-2,71507	-1,39	Ift80
R002007_01	0,0313	0,00451	-3,4	-2,72265	-1	Gap43

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
Rn30006636	0,0315	0,00454	-3,4	-2,7293	-1	Zbtb33
Rn30010849	0,0318	0,00459	-3,39	-2,74147	-1,16	Pam
Rn30009038	0,0318	0,0046	3,39	-2,74324	1,15	Ftsj3
Rn30018137	0,0318	0,00461	3,39	-2,74487	1,12	Ssbp4
Rn30019223	0,032	0,00464	3,38	-2,75218	1,04	Hcst
Rn30024911	0,0322	0,00469	3,38	-2,76116	1,24	Niacr1
Rn30001678	0,0323	0,00469	3,38	-2,76206	1,1	Fam128b
ENSRNOG00000018646	0,0325	0,00473	3,37	-2,77054	1,29	Hbegf
Rn30003778	0,0325	0,00473	3,37	-2,77114	1,26	Irak3
Rn30000995	0,0325	0,00475	-3,37	-2,77413	-1,15	Tesc
Rn30000381	0,0328	0,00481	3,37	-2,78761	1,02	Bak1
ENSRNOG00000021201	0,0329	0,00482	3,36	-2,78881	1,04	Txnip
ENSRNOG00000015857	0,0329	0,00483	3,36	-2,79205	1,01	Ctsa
Rn30007403	0,0334	0,00491	-3,36	-2,80692	-1,05	Brpf1
Rn30012777	0,0334	0,00492	-3,35	-2,80928	-2,32	Cby1
Rn30015873	0,0335	0,00495	3,35	-2,81446	1,34	Sp110
ENSRNOG00000013532	0,0336	0,00496	-3,35	-2,81668	-1,35	Pgam2
Rn30010768	0,0337	0,00499	3,35	-2,82259	1,5	Fes
Rn30002250	0,0338	0,00501	-3,35	-2,82723	-1,09	Zfp62
Rn30014012	0,0341	0,00506	-3,34	-2,83641	-1,02	Dip2c
Rn30000112	0,0344	0,00511	-3,34	-2,84613	-1,02	Megf6
Rn30004736	0,0345	0,00513	-3,33	-2,8501	-1,38	Prkd3
Rn30014856	0,0345	0,00513	3,33	-2,85146	1,04	Myo9b
Rn30017161	0,0345	0,00514	3,33	-2,85246	1,47	Klk7
Rn30009678	0,0347	0,00516	3,33	-2,85763	1,04	Tlr4
Rn30005770	0,0347	0,00517	3,33	-2,85792	1,4	Ero1l
Rn30000809	0,0347	0,00518	3,33	-2,8612	1,07	Rpo1-3
Rn30013470	0,0355	0,00535	-3,31	-2,89271	-1,14	Zfp385d
ENSRNOG00000006462	0,0357	0,00538	3,31	-2,89841	1,04	Ero1l
Rn30016572	0,0357	0,00539	3,31	-2,90018	1,25	Hdhd2
ENSRNOG00000003338	0,036	0,00545	-3,3	-2,91151	-1,05	Pmp22
R002833_01	0,0364	0,00552	-3,3	-2,92329	-1,18	Tgfb2
R000625_01	0,0364	0,00552	3,3	-2,9236	1,23	Sdcbp
ENSRNOG00000017445	0,0366	0,00556	-3,29	-2,93149	-1,02	Tubb2b
ENSRNOG00000018184	0,0367	0,00558	-3,29	-2,93392	-1,22	Tpm1_v6
ENSRNOG00000020385	0,0367	0,00559	-3,29	-2,93648	-1,16	Fads3
ENSRNOG00000007966	0,0369	0,00561	3,29	-2,94038	1,16	B4galt1
Rn30012025	0,037	0,00563	-3,29	-2,94397	-1,16	Krtap17-1
ENSRNOG00000000466	0,0371	0,00566	-3,28	-2,94858	-1,14	Hsd17b8
Rn30004568	0,0372	0,00569	3,28	-2,95355	1	Bzw2
Rn30014642	0,0373	0,00571	3,28	-2,95762	1,34	Mafb
Rn30003837	0,0379	0,00583	3,27	-2,97824	1,33	Tor3a
Rn30008858	0,0384	0,00594	-3,26	-2,9957	-1,25	Api5
R000524_01	0,0387	0,00599	-3,25	-3,00486	-1,24	Hpd
Rn30013716	0,0387	0,00599	3,25	-3,00514	1,32	Fam63b
Rn30020105	0,039	0,00604	-3,25	-3,01316	-1,01	Gpr120
ENSRNOG00000006328	0,039	0,00606	-3,25	-3,0153	-1,32	Wwp1
Rn30011503	0,0392	0,00608	-3,25	-3,01979	-1,12	Eef1a2
Rn30026000	0,0392	0,00609	-3,25	-3,02026	-1,34	Nit2
ENSRNOG00000008106	0,0393	0,00613	3,24	-3,02787	1,47	Shmt2
Rn30026856	0,0395	0,00616	3,24	-3,03251	1,1	Inf2

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
ENSRNOG00000014090	0,0396	0,00619	3,24	-3,03713	1,4	Retsat
Rn30019802	0,0396	0,0062	3,24	-3,03915	1	Hddc2
R005073_01	0,0397	0,00622	3,24	-3,04141	1,21	Gadd45g
Rn30010114	0,0397	0,00623	3,23	-3,04276	1,7	Anxa11
ENSRNOG00000002460	0,0397	0,00623	3,23	-3,04316	1,42	Serpinb2
ENSRNOG00000011195	0,0399	0,00628	-3,23	-3,0513	-1,01	Prkra
ENSRNOG00000014999	0,0403	0,00635	3,22	-3,06209	1,02	Tnpo1
Rn30000141	0,0403	0,00635	3,22	-3,06294	1,29	Vwa5a
Rn30013614	0,0403	0,00636	-3,22	-3,06344	-1,04	Ccin
R004496_01	0,0407	0,00645	-3,22	-3,07758	-1,13	Asrgl1
Rn30025274	0,0407	0,00646	-3,22	-3,079	-1,06	Krtap1-5
Rn30017928	0,0411	0,00653	3,21	-3,09069	1	Irf9
Rn30020337	0,0414	0,00659	3,21	-3,09854	1,1	Tnfrsf18
Rn30001471	0,0415	0,00661	-3,2	-3,10272	-1,4	Wrb
ENSRNOG00000012137	0,0418	0,00668	-3,2	-3,11273	-1,13	Ccdc84
R005159_01	0,042	0,00672	-3,2	-3,11783	-1,15	Pus3
Rn30006900	0,0422	0,00676	-3,19	-3,12468	-1,1	Xirp2
R002680_01	0,0428	0,00689	-3,18	-3,14354	-1,03	Ppp1r14a
Rn30021240	0,0428	0,0069	-3,18	-3,14435	-1,04	Serhl2
ENSRNOG00000006472	0,0429	0,00691	-3,18	-3,14558	-1,04	Hspa2
ENSRNOG00000025087	0,0429	0,00692	-3,18	-3,14788	-1,12	Krt73
Rn30015218	0,0429	0,00694	3,18	-3,14979	1,06	Tln1
Rn30018011	0,0429	0,00694	-3,18	-3,1499	-1,05	Tbx15
R004698_01	0,0434	0,00702	-3,17	-3,16179	-1,18	Cav2
Rn30019588	0,0434	0,00704	3,17	-3,1645	1,05	Vps16
Rn30014863	0,0439	0,00713	3,17	-3,17701	1,17	Mphosph10
ENSRNOG00000006364	0,0442	0,0072	-3,16	-3,18602	-1,4	Dld
ENSRNOG00000002572	0,0442	0,0072	3,16	-3,18657	1,22	Cacybp
ENSRNOG00000015051	0,0443	0,00722	-3,16	-3,18975	-1,06	Golga7b
R002637_01	0,0443	0,00723	-3,16	-3,1904	-1,02	Pecr
ENSRNOG00000014573	0,0448	0,00734	3,15	-3,20513	1,04	Ckmt1
Rn30019717	0,0448	0,00734	-3,15	-3,20569	-1,04	Car6
ENSRNOG00000019164	0,045	0,00738	3,15	-3,21025	1,01	Uba1
ENSRNOG00000016012	0,0455	0,00749	-3,14	-3,22525	-1,02	Spats2l
Rn30015411	0,0456	0,00752	-3,14	-3,22949	-1	Fgfr3
ENSRNOG00000007364	0,0459	0,00762	-3,13	-3,2423	-1,41	Rab15
ENSRNOG00000022943	0,0463	0,00771	-3,13	-3,25365	-1,44	Dgka
ENSRNOG00000016496	0,0463	0,00772	3,12	-3,25538	1,21	Ctsc
R002107_01	0,0464	0,00775	-3,12	-3,25862	-1,38	Ppp3cb
Rn30021772	0,0465	0,0078	-3,12	-3,26522	-1,25	Atg9b
ENSRNOG00000020136	0,0466	0,00781	3,12	-3,26665	1,02	Tgm1
ENSRNOG00000004360	0,0466	0,00782	-3,12	-3,26761	-1,23	Sip1
R002915_01	0,0473	0,00795	-3,11	-3,28464	-1,21	Gpr37
ENSRNOG00000002358	0,0473	0,00797	3,11	-3,28601	1,12	Scpep1
ENSRNOG00000010475	0,0473	0,00799	3,11	-3,2887	1,4	Casp3
Rn30024402	0,0473	0,00799	3,11	-3,2894	1,05	Tcof1
Rn30017835	0,0474	0,00802	-3,11	-3,2923	-1,02	Zfp110
Rn30000632	0,0475	0,00803	3,1	-3,29386	1,07	RT1-M3-1
ENSRNOG00000017932	0,0477	0,00809	-3,1	-3,30127	-2	St3gal2
Rn30012238	0,0479	0,00813	3,1	-3,30609	1,04	Rnf217
Rn30006650	0,0479	0,00813	-3,1	-3,30651	-1,09	Casp14

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
ENSRNOG00000019549	0,0479	0,00814	-3,1	-3,30737	-1,28	Akap12
Rn30015626	0,0486	0,00836	-3,08	-3,33365	-1,02	Pla2g2e
Rn30002138	0,0493	0,00855	-3,07	-3,35555	-1,12	Itm2a
ENSRNOG00000020660	0,0494	0,00856	3,07	-3,35685	1,37	Cfl1
Rn30016143	0,0502	0,00875	-3,06	-3,37872	-1,11	Obp3
Rn30011662	0,0504	0,0088	-3,06	-3,3839	-1,12	Postn
Rn30007216	0,0509	0,00894	3,05	-3,39917	1,06	Edem1
ENSRNOG00000006353	0,0512	0,00901	-3,05	-3,40765	-1,16	Gyltl1b
Rn30013917	0,0516	0,0091	-3,04	-3,41744	-1,07	Clic3
ENSRNOG00000008943	0,0518	0,00914	-3,04	-3,42173	-1,37	Penk
ENSRNOG00000006697	0,0518	0,00915	-3,04	-3,4227	-1,25	Tmem55a
Rn30019462	0,0523	0,00929	-3,03	-3,43722	-1,22	Tmod4
ENSRNOG00000014369	0,0524	0,00932	3,03	-3,44052	1,06	Slc27a4
Rn30017712	0,0527	0,00938	3,03	-3,44636	1,08	Bcar1
ENSRNOG00000004882	0,0528	0,00941	-3,02	-3,44988	-1,05	Capn6
Rn30020054	0,0532	0,00951	-3,02	-3,45981	-1,05	Rcbtb1
ENSRNOG00000014453	0,0533	0,00953	-3,02	-3,46235	-1,26	Anxa5
ENSRNOG00000009325	0,0534	0,00956	3,02	-3,46553	1,17	Fuca1
Rn30005964	0,0537	0,00964	-3,01	-3,4737	-1,05	Usp2
Rn30024749	0,0543	0,00976	3	-3,48592	1,62	Ppap2a
ENSRNOG00000020150	0,0548	0,00989	3	-3,49898	1,07	Il18bp
ENSRNOG00000012156	0,0548	0,0099	3	-3,49969	1,23	Ostf1
Rn30002114	0,0549	0,00992	3	-3,50191	1,21	Trim25
ENSRNOG00000021298	0,0549	0,00993	-3	-3,50209	-1,09	Dstyk
Rn30020061	0,0549	0,00993	3	-3,50225	1,09	Slfn5
ENSRNOG00000016539	0,0554	0,01	2,99	-3,5131	1,1	Rab24
ENSRNOG00000012062	0,0555	0,0101	2,99	-3,5156	1,3	Npc2
Rn30009292	0,0557	0,0101	-2,99	-3,52085	-1,02	Ttll1
ENSRNOG00000015149	0,0561	0,0102	2,98	-3,52936	1,05	Nrg4
Rn30021369	0,0561	0,0102	-2,98	-3,52962	-1,01	Trip12
Rn30015708	0,0561	0,0102	-2,98	-3,53189	-1,01	Syngr1
ENSRNOG00000016826	0,0564	0,0103	-2,98	-3,53955	-1,04	Pla2g2d
ENSRNOG00000001158	0,0571	0,0105	2,97	-3,55584	1,6	Abcg1
Rn30007551	0,0573	0,0106	-2,96	-3,56307	-1,61	Mpo
Rn30011617	0,0573	0,0106	2,96	-3,56317	1,01	Lpxn
Rn30011430	0,058	0,0107	-2,96	-3,57957	-2,06	Rhobtb3
R002146_01	0,0583	0,0108	2,95	-3,58659	1,4	Renbp
ENSRNOG00000003928	0,0586	0,0109	2,95	-3,59446	1,2	Tmco1
ENSRNOG00000001201	0,0589	0,011	2,94	-3,60142	1,14	Cstb
ENSRNOG00000015568	0,0589	0,011	2,94	-3,60489	1,18	Ppapdc1b
Rn30013222	0,0591	0,0111	-2,94	-3,61059	-1,1	Chac1
ENSRNOG00000010390	0,0593	0,0111	2,94	-3,61487	1,34	Hmbs
ENSRNOG00000010589	0,0593	0,0111	-2,94	-3,61526	-1,12	Znf622
ENSRNOG00000014170	0,0593	0,0111	-2,94	-3,61565	-1,12	Dbn1
Rn30015104	0,0594	0,0112	-2,93	-3,6199	-1,2	Pitrm1
R002635_01	0,0595	0,0112	2,93	-3,62143	1,09	Cox17
ENSRNOG00000012415	0,0596	0,0112	-2,93	-3,62447	-1,07	Brp44l
Rn30005203	0,0604	0,0114	-2,92	-3,6416	-1,3	Il1f10
Rn30016490	0,0604	0,0115	2,92	-3,64298	1,16	Gapvd1
Rn30003423	0,0604	0,0115	-2,92	-3,64387	-1,04	Scoc
Rn30021071	0,0604	0,0115	2,92	-3,64395	1,01	Evi2a

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
ENSRNOG00000007492	0,0611	0,0117	2,91	-3,6591	1,51	Rpn2
Rn30011426	0,0611	0,0117	-2,91	-3,65961	-1,18	S100a1
ENSRNOG00000013733	0,0612	0,0117	2,91	-3,66188	1,11	Ppp4r1
ENSRNOG00000030808	0,0612	0,0117	-2,91	-3,66237	-1,53	Oas1f
Rn30024919	0,0612	0,0117	-2,91	-3,66311	-1,18	Plekhf2
Rn30011615	0,0616	0,0118	-2,91	-3,67233	-1,12	Trdn
ENSRNOG00000001548	0,0623	0,012	2,9	-3,6891	1,06	Nfe2l2
Rn30003208	0,0629	0,0122	-2,89	-3,70769	-1,35	Grem2
ENSRNOG00000020276	0,0634	0,0124	-2,88	-3,71699	-1,49	Tnni2
ENSRNOG00000027260	0,0638	0,0125	2,88	-3,72357	1,14	Adprh
ENSRNOG00000001964	0,0647	0,0127	2,87	-3,74316	1,41	Cd47
Rn30007432	0,0656	0,0129	-2,86	-3,75789	-1,18	Appl2
Rn30005539	0,0657	0,0129	-2,86	-3,76076	-1,24	Etaa1
Rn30011157	0,067	0,0133	2,85	-3,78662	1,15	Col17a1
ENSRNOG00000006950	0,067	0,0133	-2,85	-3,78714	-1,23	Padi3
ENSRNOG00000011196	0,0706	0,0142	-2,81	-3,85292	-1,18	Krt25
Rn30014690	0,0709	0,0143	2,81	-3,8598	1,13	Mpzl2
ENSRNOG00000018105	0,0738	0,0151	-2,78	-3,91096	-1,08	Thtpa
Rn30008638	0,0744	0,0152	-2,78	-3,92004	-1,35	Mrpl12
Rn30005906	0,0745	0,0153	-2,77	-3,92291	-1,21	Tmem70
Rn30016600	0,0756	0,0156	-2,76	-3,94332	-1,18	Mrpl48
Rn30021402	0,0769	0,016	-2,75	-3,96442	-1,65	Silv
ENSRNOG00000008039	0,0772	0,016	-2,75	-3,96832	-1,12	Cul5
Rn30015450	0,0788	0,0165	2,73	-3,99763	1,48	Dsg1b
Rn30002976	0,079	0,0166	-2,73	-4,00025	-1,01	Col3a1
Rn30013379	0,0793	0,0166	2,73	-4,00568	1,33	Fkbp11
ENSRNOG00000010331	0,0797	0,0168	2,73	-4,01229	1,04	Ctsb
Rn30015874	0,0797	0,0168	2,73	-4,01272	1,05	Sp110
ENSRNOG00000017826	0,0805	0,017	-2,72	-4,02643	-1,24	Mtrr
Rn30016214	0,0812	0,0172	-2,71	-4,0377	-1,02	Usp6nl
R003212_01	0,0825	0,0176	2,7	-4,05733	1,16	Wnt4
ENSRNOG00000003302	0,0826	0,0176	2,7	-4,06023	1,05	Flcn
ENSRNOG00000003359	0,0827	0,0176	-2,7	-4,06101	-1,31	Ogt
Rn30009645	0,0828	0,0177	-2,7	-4,06424	-1,25	Zdhhc21
ENSRNOG00000008782	0,0829	0,0177	-2,7	-4,06605	-1,29	Sfrs18
Rn30018007	0,0835	0,0179	-2,69	-4,07762	-2,15	Pde2a
ENSRNOG00000010381	0,0837	0,018	2,69	-4,08103	1,07	Mknk1
ENSRNOG00000014777	0,084	0,0181	2,69	-4,08704	1,17	Prpf4
ENSRNOG00000006340	0,0845	0,0183	-2,68	-4,09829	-1,34	Memo1
Rn30009519	0,0847	0,0184	2,68	-4,10053	1,1	Mrps23
Rn30008230	0,0853	0,0185	2,67	-4,10983	1,46	Rnf126
R001375_01	0,0858	0,0187	-2,67	-4,11861	-1,15	Crisp3
R003573_01	0,0869	0,019	-2,66	-4,135	-1,02	Hspa2
R004187_01	0,0876	0,0192	2,66	-4,14522	1,06	Fgl2
Rn30000942	0,0884	0,0195	2,65	-4,15609	1	Rac1
Rn30011544	0,089	0,0197	2,64	-4,16715	1,08	Zfp91
Rn30016563	0,0891	0,0198	-2,64	-4,17075	-1,63	Nfatc2ip
Rn30012310	0,0891	0,0198	2,64	-4,17167	1,14	Tmub1
ENSRNOG00000016770	0,0907	0,0203	2,63	-4,19704	2,29	Calm3
ENSRNOG00000015660	0,093	0,0211	-2,61	-4,23526	-1,07	Pex3
Rn30011226	0,0933	0,0212	-2,61	-4,23821	-1,19	Zfyve21

(continued)

Table S1. (continued)

ID	adj.P.Val	P.Value	t	B	logFC	gene_symbol
ENSRNOG00000036790	0,0937	0,0214	-2,6	-4,24585	-1,22	Olfml1
R001070_01	0,0939	0,0215	2,6	-4,25006	1,04	Ocm
ENSRNOG00000017472	0,0944	0,0216	-2,6	-4,2568	-1,35	Tcf12
ENSRNOG00000010176	0,095	0,0218	2,59	-4,26699	1,06	Map2k1
ENSRNOG00000009768	0,0953	0,0219	-2,59	-4,27081	-1,05	Npy
Rn30011985	0,102	0,0242	2,54	-4,3635	1,16	Cyba
R000138_01	0,104	0,0246	2,53	-4,38141	1,07	Psma5
Rn30010006	0,105	0,0253	2,51	-4,40684	1,14	Alg9
ENSRNOG00000017469	0,105	0,0253	2,51	-4,40765	1,21	Anxa1
ENSRNOG00000010805	0,105	0,0253	-2,51	-4,40846	-1,05	Fabp4
Rn30000500	0,106	0,0257	2,51	-4,42183	1,08	Lama4
ENSRNOG00000040315	0,107	0,0258	2,5	-4,42652	1,09	Ly96
ENSRNOG00000020726	0,108	0,0262	2,5	-4,43997	1,9	Sipa1
Rn30012239	0,11	0,0268	2,48	-4,46247	1,1	Rnf217
Rn30008590	0,11	0,0269	2,48	-4,46459	1,1	Tf
Rn30011811	0,115	0,0287	2,45	-4,52826	1,03	Lrrc17
ENSRNOG00000024568	0,115	0,0288	-2,45	-4,53035	-1,51	Ndufs7
ENSRNOG00000010512	0,115	0,0288	2,45	-4,5305	1,33	Yipf1
ENSRNOG00000037992	0,115	0,0288	2,45	-4,53189	1,32	Leprot
ENSRNOG00000000421	0,116	0,0291	2,44	-4,5413	1,52	Skiv2l
ENSRNOG00000018651	0,118	0,0299	-2,43	-4,56803	-1,9	Agtpbp1
Rn30012108	0,119	0,0303	2,42	-4,57759	1,03	Map3k1
ENSRNOG00000012080	0,122	0,0313	2,4	-4,61011	1,11	Itga1
Rn30003184	0,122	0,0314	2,4	-4,61387	1,7	Figf
Rn30010492	0,124	0,0319	2,39	-4,62907	1,07	Ndufs4
Rn30001457	0,124	0,0319	-2,39	-4,62916	-1,17	Zbtb11
ENSRNOG00000000815	0,124	0,032	2,39	-4,63152	1,19	Smpdl3a
ENSRNOG00000013683	0,126	0,0331	-2,37	-4,66216	-3,29	S1pr1
ENSRNOG00000031965	0,128	0,0339	2,36	-4,68452	1,27	Impdh2
Rn30006360	0,13	0,0344	2,35	-4,70021	1,08	Timm17a
ENSRNOG00000016655	0,132	0,0354	2,34	-4,72716	1,04	Pex6
ENSRNOG00000014647	0,134	0,0361	-2,33	-4,74429	-1,09	Cbfb
ENSRNOG00000009334	0,134	0,0362	2,32	-4,74692	1,03	Traf4af1
ENSRNOG00000000967	0,134	0,0362	2,32	-4,74713	1,06	Aacs
ENSRNOG00000019183	0,136	0,0372	-2,31	-4,77188	-1,07	Alox15
Rn30001676	0,137	0,0372	-2,31	-4,77386	-1,12	Ppfibp1
ENSRNOG00000027654	0,137	0,0374	-2,31	-4,77697	-1,4	Appbp2
ENSRNOG00000014338	0,138	0,0379	2,3	-4,79092	1,66	Slc25a25
R004168_01	0,149	0,0425	-2,24	-4,89783	-1,03	Snx16
ENSRNOG00000004060	0,151	0,0433	2,23	-4,91505	1,13	Calm1
ENSRNOG00000016896	0,159	0,0472	2,18	-4,99407	1,07	Rpl3
Rn30024767	0,161	0,048	-2,17	-5,01035	-1,07	Slc6a19

Table S2. Genes that closely correlated with skin injury obtained from DisGENET database.

Disease	Disease_id	Gene	Gene_id	UniProt	Gene_Full_Name	Protein_Class	N_diseases_g	DSI_g	DPI_g	pLI	Score_gda	EL_gda	EI_gda	N_PMIDs	N_SNPs_gda	First_Ref	Last_Ref
Skin lesion	C0037284	PTEN	5728	P60484	phosphatase and tensin homolog	Enzyme	1349	0,305	0,923	0,25651	0,14		1	4	1	2001	2014
Skin lesion	C0037284	TNF	7124	P01375	tumor necrosis factor	Signaling	2724	0,231	0,962	0,8033	0,1		0,977	44	0	1997	2019
Skin lesion	C0037284	TP53	7157	P04637	tumor protein p53	Transcription factor	2494	0,236	0,962	0,53235	0,1		1	12	3	1993	2018
Skin lesion	C0037284	TSLP	85480	Q969D9	thymic stromal lymphopoietin		220	0,486	0,808	0,0040357	0,1		1	10	0	2010	2019
Skin lesion	C0037284	IL6	3569	P05231	interleukin 6		2367	0,248	0,962	0,31536	0,1		1	14	0	1998	2019
Skin lesion	C0037284	IL4	3565	P05112	interleukin 4		996	0,332	0,962	0,0047372	0,1		1	23	0	1994	2020
Skin lesion	C0037284	IL17A	3605	Q16552	interleukin 17A		1074	0,324	0,923	0,043049	0,1		1	38	0	2008	2020
Skin lesion	C0037284	IL22	50616	Q9GZX6	interleukin 22		551	0,393	0,885	0,0001884	0,1		1	12	0	2007	2018
Skin lesion	C0037284	BRAF	673	P15056	B-Raf proto-oncogene, serine/threonine kinase	Kinase	1228	0,319	0,846	0,99995	0,1		0,909	11	2	2009	2017
Skin lesion	C0037284	IFNG	3458	P01579	interferon gamma		1519	0,288	0,962	0,47156	0,1		1	17	0	1994	2019
Skin lesion	C0037284	IL23A	51561	Q9NPF7	interleukin 23 subunit alpha	Signaling	427	0,415	0,846	0,35806	0,1		1	10	0	2008	2019
Skin lesion	C0037284	IL10	3586	P22301	interleukin 10		1679	0,281	0,923	0,0058874	0,1		1	17	1	1996	2019
Skin lesion	C0037284	CCL17	6361	Q92583	C-C motif chemokine ligand 17	Signaling	162	0,518	0,808	0,0001393	0,09		1	9	0	2012	2018
Skin lesion	C0037284	IL5	3567	P05113	interleukin 5		359	0,437	0,846	0,0056529	0,09		1	9	0	1994	2020
Skin lesion	C0037284	IL1B	3553	P01584	interleukin 1 beta		1801	0,276	0,962	0,13005	0,09		1	9	0	1995	2019
Skin lesion	C0037284	IL13	3596	P35225	interleukin 13		587	0,386	0,846	0,014426	0,09		1	9	0	1996	2019
Skin lesion	C0037284	IFNA1	3439	P01562	interferon alpha 1		662	0,371	0,923		0,08		0,875	8	0	2008	2019
Skin lesion	C0037284	IFNA13	3447	P01562	interferon alpha 13		646	0,374	0,923		0,08		0,875	8	0	2008	2019
Skin lesion	C0037284	IL33	90865	O95760	interleukin 33		487	0,409	0,885	8,293E-10	0,08		1	8	0	2011	2018
Skin lesion	C0037284	TGFB1	7040	P01137	transforming growth factor beta 1	Signaling	1558	0,287	0,962	0,03685	0,07		0,857	7	0	2004	2016
Skin lesion	C0037284	CCL2	6347	P13500	C-C motif chemokine ligand 2	Signaling	1157	0,321	0,962	0,60786	0,06		1	6	0	2001	2019
Skin lesion	C0037284	STAT3	6774	P40763	signal transducer and activator of transcription 3	Nucleic acid binding	1193	0,32	0,923	1	0,06		0,667	6	0	2014	2019
Skin lesion	C0037284	S100A7	6278	P31151	S100 calcium binding protein A7	Calcium-binding protein	119	0,546	0,769	0,45274	0,06		0,833	6	0	2002	2020
Skin lesion	C0037284	CASP1	834	P29466	caspase 1	Enzyme	444	0,413	0,885	3,518E-05	0,06		1	6	0	2006	2018
Skin lesion	C0037284	IL15	3600	P40933	interleukin 15		426	0,422	0,846	0,70859	0,06		0,833	6	0	1999	2017
Skin lesion	C0037284	CAMP	820	P49913	cathelicidin antimicrobial peptide		262	0,466	0,846	0,0043897	0,06		0,833	6	0	2009	2020
Skin lesion	C0037284	IL31	386653	Q6EBC2	interleukin 31		88	0,575	0,731	0,011445	0,06		1	6	0	2004	2019
Skin lesion	C0037284	ICAM1	3383	P05362	intercellular adhesion molecule 1		737	0,364	0,962	0,035295	0,05		1	5	1	2010	2018
Skin lesion	C0037284	AS3MT	57412	Q9HBK9	arsenite methyltransferase	Enzyme	56	0,638	0,538	7,977E-11	0,05		1	5	1	2009	2019
Skin lesion	C0037284	TSC2	7249	P49815	TSC complex subunit 2	Enzyme modulator	410	0,439	0,808	1	0,05		1	5	0	2008	2018
Skin lesion	C0037284	NCAM1	4684	P13591	neural cell adhesion molecule 1		445	0,415	0,885	0,99999	0,05		1	5	0	2002	2017
Skin lesion	C0037284	TRBV20OR9-2	6962		T cell receptor beta variable 20/OR9-2 (non-functional)		456	0,403	0,923		0,05		1	5	0	1995	2018
Skin lesion	C0037284	FLG	2312	P20930	filaggrin	Cellular structure	173	0,525	0,846	0,0002879	0,05		1	5	0	2012	2020
Skin lesion	C0037284	FOXP3	50943	Q9BZS1	forkhead box P3		688	0,368	0,846	0,99424	0,05		1	5	0	2007	2017
Skin lesion	C0037284	TSC1	7248	Q92574	TSC complex subunit 1		391	0,44	0,808	1	0,04		1	4	0	2009	2018
Skin lesion	C0037284	IL1A	3552	P01583	interleukin 1 alpha		1002	0,333	0,962	0,0001602	0,04		1	4	0	2009	2018
Skin lesion	C0037284	ERCC2	2068	P18074	ERCC excision repair 2, TFIIH core complex helicase subunit	Enzyme	499	0,42	0,846	7,065E-20	0,04		1	4	0	2003	2017
Skin lesion	C0037284	KIT	3815	P10721	KIT proto-oncogene, receptor tyrosine kinase	Kinase	715	0,366	0,808	0,98087	0,04		1	4	3	1999	2018
Skin lesion	C0037284	IL2	3558	P60568	interleukin 2		950	0,336	0,885	0,47968	0,04		1	4	0	1989	2015
Skin lesion	C0037284	CCR4	1233	P51679	C-C motif chemokine receptor 4	G-protein coupled receptor	168	0,51	0,731	0,06863	0,04		1	4	0	2002	2019
Skin lesion	C0037284	GATA3	2625	P23771	GATA binding protein 3		429	0,415	0,846	0,89887	0,04		1	4	0	2004	2018
Skin lesion	C0037284	IL18	3606	Q14116	interleukin 18		750	0,365	0,923	0,030717	0,04		1	4	0	2002	2019
Skin lesion	C0037284	PCNA	5111	P12004	proliferating cell nuclear antigen	Nucleic acid binding	581	0,382	0,846	0,97606	0,04		1	4	0	1999	2018
Skin lesion	C0037284	STAT1	6772	P42224	signal transducer and activator of transcription 1	Nucleic acid binding	531	0,399	0,885	0,99999	0,04		1	4	0	2017	2018
Skin lesion	C0037284	CD274	29126	Q9NZQ7	CD274 molecule	Receptor	1011	0,324	0,923	0,01916	0,04		1	4	0	2016	2018
Skin lesion	C0037284	MSH2	4436	P43246	mutS homolog 2	Nucleic acid binding	490	0,406	0,808	0,89539	0,04		1	4	0	1996	2016
Skin lesion	C0037284	BCL2	596	P10415	BCL2 apoptosis regulator	Signaling	1456	0,291	0,885	0,55903	0,04		1	4	0	2003	2015
Skin lesion	C0037284	HMGB1	3146	P09429	high mobility group box 1	Nucleic acid binding	724	0,368	0,923	0,82035	0,04		1	4	0	2005	2018
Skin lesion	C0037284	MAPK1	5594	P28482	mitogen-activated protein kinase 1	Kinase	1059	0,33	0,923	0,99698	0,04		1	4	0	2007	2019
Skin lesion	C0037284	HIF1A	3091	Q16665	hypoxia inducible factor 1 subunit alpha	Transcription factor	1044	0,327	0,923	0,9777	0,04		1	4	0	2008	2018

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Table S2. (continued)

Disease	Disease_id	Gene	Gene_id	UniProt	Gene_Full_Name	Protein_Class	N_diseases_g	DSI_g	DPI_g	pLI	Score_gda	EL_gda	EI_gda	N_PMIDs	N_SNPs_gda	First_Ref	Last_Ref
Skin lesion	C0037284	EGF	1950	P01133	epidermal growth factor		774	0,357	0,923	8,529E-17	0,04		1	4	0	2016	2019
Skin lesion	C0037284	EGFR	1956	P00533	epidermal growth factor receptor	Kinase	1394	0,295	0,885	0,36837	0,04		1	4	0	2011	2018
Skin lesion	C0037284	GSTM1	2944	P09488	glutathione S-transferase mu 1		627	0,38	0,923	0,0020641	0,03		1	3	0	2006	2007
Skin lesion	C0037284	ANXA1	301	P04083	annexin A1		336	0,442	0,885	1,201E-07	0,03		1	3	0	2018	2019
Skin lesion	C0037284	CCL22	6367	O00626	C-C motif chemokine ligand 22	Signaling	182	0,5	0,846	0,0084014	0,03		1	3	0	2001	2018
Skin lesion	C0037284	MTOR	2475	P42345	mechanistic target of rapamycin kinase	Kinase	960	0,343	0,885	1	0,03		1	3	0	2017	2017
Skin lesion	C0037284	AHR	196	P35869	aryl hydrocarbon receptor	Transcription factor	532	0,41	0,923	0,99999	0,03		1	3	0	2017	2019
Skin lesion	C0037284	TRIM21	6737	P19474	tripartite motif containing 21		229	0,485	0,808	3,355E-09	0,03		1	3	0	2008	2017
Skin lesion	C0037284	GSTP1	2950	P09211	glutathione S-transferase pi 1		610	0,383	0,923	0,014155	0,03		1	3	1	2006	2011
Skin lesion	C0037284	DSG1	1828	Q02413	desmoglein 1	Cell adhesion	81	0,606	0,538	0,92688	0,03		1	3	0	2007	2020
Skin lesion	C0037284	EPHB2	2048	P29323	EPH receptor B2	Kinase	649	0,374	0,846	0,99997	0,03		1	3	0	2007	2019
Skin lesion	C0037284	CCL5	6352	P13501	C-C motif chemokine ligand 5	Signaling	514	0,403	0,885	0,0017516	0,03		1	3	0	2005	2017
Skin lesion	C0037284	DEFB4A	1673	O15263	defensin beta 4A		177	0,507	0,769	0,0011637	0,03		1	3	0	2017	2019
Skin lesion	C0037284	TLR4	7099	O00206	toll like receptor 4		1174	0,321	0,962	4,613E-09	0,03		1	3	0	2007	2018
Skin lesion	C0037284	HLA-C	3107	P10321	major histocompatibility complex, class I, C		435	0,415	0,846	1,57E-06	0,03		1	3	0	2007	2019
Skin lesion	C0037284	MIR155	406947		microRNA 155		584	0,384	0,885		0,03		1	3	0	2013	2019
Skin lesion	C0037284	BMI1	648	P35226	BMI1 proto-oncogene, polycomb ring finger		309	0,448	0,808	0,94286	0,03		1	3	0	2007	2009
Skin lesion	C0037284	GCG	2641	P01275	glucagon		441	0,431	0,885	0,034814	0,03		1	3	0	2017	2019
Skin lesion	C0037284	IL2RA	3559	P01589	interleukin 2 receptor subunit alpha	Receptor	540	0,389	0,885	0,054709	0,03		1	3	0	1999	2019
Skin lesion	C0037284	IL17F	112744	Q96PD4	interleukin 17F		236	0,48	0,808	0,039165	0,03		0,667	3	0	2009	2014
Skin lesion	C0037284	CXCL8	3576	P10145	C-X-C motif chemokine ligand 8	Signaling	1254	0,31	0,962	0,0002738	0,03		1	3	0	1998	2017
Skin lesion	C0037284	MIR146A	406938		microRNA 146a		505	0,398	0,885		0,03		1	3	0	2012	2019
Skin lesion	C0037284	PAK1	5058	Q13153	p21 (RAC1) activated kinase 1	Kinase	221	0,494	0,808	0,0013306	0,03		1	3	0	2017	2018
Skin lesion	C0037284	MIR21	406991		microRNA 21		726	0,363	0,846		0,03		1	3	0	2012	2017
Skin lesion	C0037284	IL24	11009	Q13007	interleukin 24		202	0,498	0,769	5,883E-07	0,03		0,667	3	0	2006	2014
Skin lesion	C0037284	PIK3CA	5290	P42336	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha	Kinase	1511	0,292	0,923	1	0,03		1	3	0	2014	2019
Skin lesion	C0037284	TNFRSF8	943	P28908	TNF receptor superfamily member 8		301	0,444	0,808	0,86407	0,03		1	3	0	2014	2018
Skin lesion	C0037284	CD28	940	P10747	CD28 molecule		364	0,436	0,885	0,35779	0,03		1	3	0	1994	2014
Skin lesion	C0037284	MLH1	4292	P40692	mutL homolog 1	Nucleic acid binding	526	0,399	0,808	0,0000341	0,03		1	3	0	1999	2006
Skin lesion	C0037284	MRC1	4360	P22897	mannose receptor C-type 1		431	0,413	0,846	0,94335	0,03		1	3	0	2015	2019
Skin lesion	C0037284	CDKN2A	1029	P42771;Q8N726	cyclin dependent kinase inhibitor 2A		1314	0,3	0,885	0,39474	0,03		1	3	0	2007	2013
Skin lesion	C0037284	DEFB4B	100289462	O15263	defensin beta 4B		166	0,51	0,769	0,067977	0,03		1	3	0	2017	2019
Skin lesion	C0037284	SLCO6A1	133482	Q86UG4	solute carrier organic anion transporter family member 6A1	Transporter	449	0,412	0,885	2,881E-11	0,03		0,667	3	0	2007	2013
Skin lesion	C0037284	COMMD3-BMI1	100532731	P35226	COMMD3-BMI1 readthrough		202	0,488	0,769	0,0014998	0,03		1	3	0	2007	2009
Skin lesion	C0037284	MIF	4282	P14174	macrophage migration inhibitory factor		455	0,412	0,885	0,012262	0,03		1	3	0	1997	2018
Skin lesion	C0037284	ISG20	3669	Q96AZ6	interferon stimulated exonuclease gene 20		414	0,414	0,846	0,002899	0,03		1	3	0	1999	2019
Skin lesion	C0037284	GSTK1	373156	Q9Y2Q3	glutathione S-transferase kappa 1		445	0,412	0,885	1,937E-06	0,03		0,667	3	0	2007	2013
Skin lesion	C0037284	PDGFRA	5156	P16234	platelet derived growth factor receptor alpha	Kinase	452	0,415	0,808	1	0,02		1	2	0	2013	2017
Skin lesion	C0037284	CXCR3	2833	P49682	C-X-C motif chemokine receptor 3	G-protein coupled receptor	367	0,436	0,808	0,181	0,02		1	2	0	2017	2017
Skin lesion	C0037284	PIK3CB	5291	P42338	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit beta	Kinase	1083	0,322	0,885	0,99964	0,02		1	2	0	2014	2019
Skin lesion	C0037284	PIK3CD	5293	O00329	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta	Kinase	1119	0,319	0,885	0,99999	0,02		1	2	0	2014	2019
Skin lesion	C0037284	NFE2L2	4780	Q16236	nuclear factor, erythroid 2 like 2	Enzyme	823	0,357	0,885	0,0035719	0,02		0,5	2	0	2014	2016
Skin lesion	C0037284	SMUG1	23583	Q53HV7	single-strand-selective monofunctional uracil-DNA glycosylase 1		1034	0,322	0,923	0,0004515	0,02		1	2	0	2018	2019
Skin lesion	C0037284	PLA2G1B	5319	P04054	phospholipase A2 group IB	Enzyme	268	0,468	0,846	1,006E-10	0,02		1	2	0	2017	2018
Skin lesion	C0037284	MYD88	4615	Q99836	MYD88 innate immune signal transduction adaptor	Enzyme modulator	480	0,414	0,923	0,12443	0,02		1	2	0	2017	2018
Skin lesion	C0037284	MYB	4602	P10242	MYB proto-oncogene, transcription factor		206	0,49	0,692	0,81924	0,02		1	2	0	2001	2019
Skin lesion	C0037284	GABPA	2551	Q06546	GA binding protein transcription factor subunit alpha	Transcription factor	632	0,379	0,885	0,99812	0,02		0,5	2	0	2014	2016

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Table S2. (continued)

Disease	Disease_id	Gene	Gene_id	UniProt	Gene_Full_Name	Protein_Class	N_diseases_g	DSI_g	DPI_g	pLI	Score_gda	EL_gda	EI_gda	N_PMIDs	N_SNPs_gda	First_Ref	Last_Ref
Skin lesion	C0037284	HPGDS	27306	O60760	hematopoietic prostaglandin D synthase		570	0,388	0,923	1,806E-06	0,02		1	2	0	2006	2007
Skin lesion	C0037284	NSDHL	50814	Q15738	NAD(P) dependent steroid dehydrogenase-like	Enzyme	80	0,621	0,538	0,96393	0,02		1	2	0	2016	2019
Skin lesion	C0037284	PDGFRB	5159	P09619	platelet derived growth factor receptor beta	Kinase	492	0,416	0,846	0,9041	0,02		1	2	0	2002	2012
Skin lesion	C0037284	IL21R	50615	Q9HBE5	interleukin 21 receptor	Receptor	110	0,55	0,731	0,99835	0,02		1	2	0	2007	2015
Skin lesion	C0037284	IL27	246778	Q8NEV9	interleukin 27		286	0,457	0,808	0,78232	0,02		1	2	0	2013	2017
Skin lesion	C0037284	IL20	50604	Q9NYY1	interleukin 20		111	0,556	0,769	1,345E-06	0,02		1	2	0	2005	2009
Skin lesion	C0037284	CD207	50489	Q9UJ71	CD207 molecule	Receptor	50	0,631	0,692	2,818E-06	0,02		1	2	0	2017	2018
Skin lesion	C0037284	SDF4	51150	Q9BRK5	stromal cell derived factor 4	Calcium-binding protein	74	0,595	0,654	0,0091042	0,02		1	2	0	2008	2017
Skin lesion	C0037284	GJB2	2706	P29033	gap junction protein beta 2	Cell-cell junction	392	0,441	0,846	6,562E-16	0,02		1	2	0	2012	2017
Skin lesion	C0037284	SOAT1	6646	P35610	sterol O-acyltransferase 1	Enzyme	389	0,424	0,846	7,362E-10	0,02		1	2	0	2015	2017
Skin lesion	C0037284	IL17B	27190	Q9UHF5	interleukin 17B		116	0,553	0,769	0,033631	0,02		1	2	0	2005	2009
Skin lesion	C0037284	FGF7	2252	P21781	fibroblast growth factor 7	Signaling	167	0,519	0,846	0,77089	0,02		1	2	0	1998	2019
Skin lesion	C0037284	IL17D	53342	Q8TAD2	interleukin 17D		259	0,464	0,808	0,19796	0,02		1	2	0	2013	2017
Skin lesion	C0037284	MTHFR	4524	P42898	methylenetetrahydrofolate reductase		985	0,337	0,885	3,207E-10	0,02		0,5	2	1	2007	2018
Skin lesion	C0037284	GSTT1	2952	P30711	glutathione S-transferase theta 1		541	0,393	0,923	0,0001483	0,02		1	2	0	2007	2007
Skin lesion	C0037284	FOXA1	3169	P55317	forkhead box A1	Transcription factor	138	0,522	0,731	0,22227	0,02		1	2	0	2016	2017
Skin lesion	C0037284	HSPA4	3308	P34932	heat shock protein family A (Hsp70) member 4		550	0,394	0,923	0,99954	0,02		1	2	0	1993	2010
Skin lesion	C0037284	MIR150	406942		microRNA 150		282	0,455	0,808		0,02		1	2	0	2017	2017
Skin lesion	C0037284	MYDGF	56005	Q969H8	myeloid derived growth factor		295	0,451	0,846	3,492E-06	0,02		1	2	0	2013	2017
Skin lesion	C0037284	BDNF	627	P23560	brain derived neurotrophic factor	Signaling	992	0,345	0,923	0,65626	0,02		1	2	0	2000	2018
Skin lesion	C0037284	PROC	5624	P04070	protein C, inactivator of coagulation factors Va and VIIIa	Enzyme	200	0,504	0,808	1,912E-05	0,02		1	2	0	2000	2004
Skin lesion	C0037284	LDHA	3939	P00338	lactate dehydrogenase A	Enzyme	185	0,507	0,808	0,069173	0,02		1	2	0	1986	1991
Skin lesion	C0037284	IFNB1	3456	P01574	interferon beta 1		426	0,421	0,846		0,02		1	2	0	2018	2018
Skin lesion	C0037284	SUMO4	387082	Q6EEV6	small ubiquitin like modifier 4		39	0,653	0,577		0,02		1	2	0	2011	2012
Skin lesion	C0037284	CCN1	3491	O00622	cellular communication network factor 1	Signaling	246	0,473	0,731	0,71388	0,02		1	2	0	2017	2017
Skin lesion	C0037284	PTGS2	5743	P35354	prostaglandin-endoperoxide synthase 2	Enzyme	1234	0,314	0,962	0,99597	0,02		1	2	0	2017	2020
Skin lesion	C0037284	IVL	3713	P07476	involucrin		55	0,626	0,5		0,02		1	2	0	2017	2019
Skin lesion	C0037284	PTPN6	5777	P29350	protein tyrosine phosphatase non-receptor type 6		218	0,485	0,769	0,99999	0,02		1	2	0	2006	2016
Skin lesion	C0037284	MAPK3	5595	P27361	mitogen-activated protein kinase 3	Kinase	647	0,379	0,885	0,036884	0,02		1	2	0	2016	2019
Skin lesion	C0037284	IL26	55801	Q9NPH9	interleukin 26		51	0,631	0,538	0,0005351	0,02		1	2	0	2019	2019
Skin lesion	C0037284	MSH6	2956	P52701	mutS homolog 6	Nucleic acid binding	296	0,462	0,731	3,671E-05	0,02		1	2	0	2005	2016
Skin lesion	C0037284	GZMB	3002	P10144	granzyme B	Enzyme	290	0,453	0,808	3,667E-14	0,02		1	2	0	2001	2018
Skin lesion	C0037284	MMP9	4318	P14780	matrix metallopeptidase 9	Enzyme	1337	0,305	0,923	1,887E-17	0,02		1	2	0	2003	2007
Skin lesion	C0037284	MEN1	4221	O00255	menin 1		364	0,444	0,808	0,99971	0,02		1	2	0	1997	1998
Skin lesion	C0037284	CDH1	999	P12830	cadherin 1		508	0,401	0,808	0,14631	0,02		1	2	3	2003	2012
Skin lesion	C0037284	PNP	4860	P00491	purine nucleoside phosphorylase	Enzyme	161	0,527	0,885	6,999E-06	0,02		1	2	1	2008	2018
Skin lesion	C0037284	CCL20	6364	P78556	C-C motif chemokine ligand 20	Signaling	242	0,474	0,846	0,0002424	0,02		1	2	0	2017	2017
Skin lesion	C0037284	HFE	3077	Q30201	homeostatic iron regulator		415	0,436	0,846	2,559E-08	0,02		1	2	1	2000	2006
Skin lesion	C0037284	MDM2	4193	Q00987	MDM2 proto-oncogene	Nucleic acid binding	702	0,362	0,846	0,99981	0,02		1	2	0	1997	2012
Skin lesion	C0037284	MCAM	4162	P43121	melanoma cell adhesion molecule	Cell adhesion	169	0,514	0,731	0,0001595	0,02		1	2	0	2016	2019
Skin lesion	C0037284	MBL2	4153	P11226	mannose binding lectin 2	Receptor	563	0,39	0,846	0,0026836	0,02		1	2	0	2010	2011
Skin lesion	C0037284	HLA-DMA	3108	P28067	major histocompatibility complex, class II, DM alpha	Immune response	63	0,608	0,654	0,002381	0,02		0,5	2	0	2007	2018
Skin lesion	C0037284	HLCS	3141	P50747	holocarboxylase synthetase	Enzyme	63	0,65	0,654	1,921E-08	0,02		1	2	0	1995	2000
Skin lesion	C0037284	IL16	3603	Q14005	interleukin 16	Signaling	193	0,501	0,846	1,245E-10	0,02		1	2	0	1998	1999
Skin lesion	C0037284	TAC1	6863	P20366	tachykinin precursor 1		478	0,424	0,923	0,74608	0,02		1	2	0	2017	2018
Skin lesion	C0037284	CLEC4C	170482	Q8WTT0	C-type lectin domain family 4 member C	Receptor	30	0,678	0,5	5,771E-07	0,02		1	2	0	2017	2019
Skin lesion	C0037284	TNFSF13B	10673	Q9Y275	TNF superfamily member 13b		282	0,46	0,731	0,98193	0,02		1	2	0	2009	2012
Skin lesion	C0037284	SERPINH1	871	P50454	serpin family H member 1	Enzyme modulator	148	0,545	0,769	0,027553	0,02		1	2	0	2002	2015
Skin lesion	C0037284	TNFRSF1A	7132	P19438	TNF receptor superfamily member 1A		487	0,409	0,923	0,9949	0,02		1	2	0	2006	2020
Skin lesion	C0037284	DSG3	1830	P32926	desmoglein 3	Cell adhesion	78	0,603	0,654	1,458E-20	0,02		1	2	0	1998	2007

(continued)

Table S2. (continued)

Disease	Disease_id	Gene	Gene_id	UniProt	Gene_Full_Name	Protein_Class	N_diseases_g	DSI_g	DPI_g	pLI	Score_gda	EL_gda	EI_gda	N_PMIDs	N_SNPs_gda	First_Ref	Last_Ref
Skin lesion	C0037284	GNLY	10578	P22749	granulysin		88	0,584	0,692	9,69E-09	0,02		1	2	0	2013	2019
Skin lesion	C0037284	H3P10	115482713		H3 histone pseudogene 10		769	0,35	0,846		0,02		1	2	0	2007	2013
Skin lesion	C0037284	CCN2	1490	P29279	cellular communication network factor 2	Signaling	518	0,399	0,846	0,000502	0,02		1	2	0	2018	2019
Skin lesion	C0037284	CETN1	1068	Q12798	centrin 1	Calcium-binding protein	82	0,584	0,654	0,21511	0,02		1	2	0	2008	2017
Skin lesion	C0037284	FLCN	201163	Q8NFG4	folliculin		160	0,537	0,885	0,78892	0,02		1	2	0	2010	2012
Skin lesion	C0037284	EBP	10682	Q15125	EBP cholestenol delta-isomerase	Enzyme	243	0,494	0,846	0,93645	0,02		0,5	2	0	2011	2019
Skin lesion	C0037284	CYP1A1	1543	P04798	cytochrome P450 family 1 subfamily A member 1	Enzyme	379	0,436	0,846	1,064E-17	0,02		0,5	2	0	2006	2018
Skin lesion	C0037284	VEGFA	7422	P15692	vascular endothelial growth factor A	Signaling	1899	0,266	0,923	2,409E-05	0,02		1	2	0	2014	2016
Skin lesion	C0037284	VCAM1	7412	P19320	vascular cell adhesion molecule 1		406	0,422	0,808	0,79791	0,02		1	2	0	2010	2010
Skin lesion	C0037284	XPA	7507	P23025	XPA, DNA damage recognition and repair factor	Nucleic acid binding	209	0,52	0,846	7,865E-05	0,02		1	2	1	1996	2010
Skin lesion	C0037284	DUSP1	1843	P28562	dual specificity phosphatase 1		214	0,491	0,808	0,010151	0,02		1	2	0	2013	2015
Skin lesion	C0037284	XPC	7508	Q01831	XPC complex subunit, DNA damage recognition and repair factor	Nucleic acid binding	211	0,504	0,808	3,687E-11	0,02		1	2	1	2015	2017
Skin lesion	C0037284	SIRT1	23411	Q96EB6	sirtuin 1	Epigenetic regulator	675	0,378	0,885	0,087326	0,02		1	2	0	2015	2017
Skin lesion	C0037284	DEFB1	1672	P60022	defensin beta 1		177	0,509	0,808	0,4059	0,02		0,5	2	0	2011	2015
Skin lesion	C0037284	ELN	2006	P15502	elastin		545	0,415	0,885	2,143E-14	0,02		1	2	0	1981	1992
Skin lesion	C0037284	CSF2	1437	P04141	colony stimulating factor 2	Signaling	1028	0,33	0,962	0,83468	0,02		1	2	0	2010	2017
Skin lesion	C0037284	AIM2	9447	O14862	absent in melanoma 2		167	0,521	0,769	2,194E-09	0,02		1	2	0	2013	2019
Skin lesion	C0037284	CDR3	8163		Cerebellar degeneration-related autoantigen-3		233	0,472	0,808		0,02		1	2	0	1999	2002
Skin lesion	C0037284	CD40	958	P25942	CD40 molecule		528	0,396	0,846	0,84603	0,02		1	2	1	2000	2015
Skin lesion	C0037284	CCR3	1232	P51677	C-C motif chemokine receptor 3	G-protein coupled receptor	149	0,527	0,808	0,0001264	0,02		1	2	0	2001	2017
Skin lesion	C0037284	ADAM17	6868	P78536	ADAM metallopeptidase domain 17		316	0,453	0,808	0,99528	0,02		1	2	0	2014	2015
Skin lesion	C0037284	TAP1	6890	Q03518	transporter 1, ATP binding cassette subfamily B member	Transporter	181	0,5	0,808	5,343E-06	0,02		1	2	0	2014	2018
Skin lesion	C0037284	PIK3CG	5294	P48736	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma	Kinase	1101	0,32	0,885	1,408E-06	0,02		1	2	0	2014	2019
Skin lesion	C0037284	TGFA	7039	P01135	transforming growth factor alpha	Signaling	376	0,432	0,885	0,71981	0,02		1	2	0	1998	2008
Skin lesion	C0037284	CCR5	1234	P51681	C-C motif chemokine receptor 5 (gene/pseudogene)	G-protein coupled receptor	508	0,398	0,885	4,309E-10	0,02		1	2	0	2016	2017
Skin lesion	C0037284	CD40LG	959	P29965	CD40 ligand	Signaling	453	0,414	0,846	0,72079	0,02		1	2	0	2000	2017
Skin lesion	C0037284	CCR6	1235	P51684	C-C motif chemokine receptor 6	G-protein coupled receptor	231	0,485	0,808	0,0057867	0,02		1	2	0	2017	2019
Skin lesion	C0037284	MAPK8	5599	P45983	mitogen-activated protein kinase 8	Kinase	520	0,397	0,885	0,99823	0,01		1	1	0	2018	2018
Skin lesion	C0037284	TNFRSF6B	8771	O95407	TNF receptor superfamily member 6b		145	0,528	0,731	3,874E-06	0,01		1	1	0	2011	2011
Skin lesion	C0037284	CCK	885	P06307	cholecystokinin		326	0,453	0,846	3,303E-05	0,01		1	1	0	2019	2019
Skin lesion	C0037284	TNFSF13	8741	O75888	TNF superfamily member 13		189	0,499	0,769	0,81724	0,01		1	1	0	2012	2012
Skin lesion	C0037284	MOK	5891	Q9UQ07	MOK protein kinase	Kinase	251	0,476	0,769	8,84E-22	0,01		1	1	0	2018	2018
Skin lesion	C0037284	KRIT1	889	O00522	KRIT1 ankyrin repeat containing		201	0,5	0,808	0,0006933	0,01		1	1	1	2007	2007
Skin lesion	C0037284	ACKR3	57007	P25106	atypical chemokine receptor 3	G-protein coupled receptor	400	0,428	0,885	0,39134	0,01		1	1	0	2014	2014
Skin lesion	C0037284	KYNU	8942	Q16719	kynureninase	Enzyme	88	0,617	0,692	4,181E-18	0,01		1	1	0	2004	2004
Skin lesion	C0037284	NLRP2	55655	Q9NX02	NLR family pyrin domain containing 2		155	0,515	0,731	1,42E-38	0,01		1	1	1	2013	2013
Skin lesion	C0037284	RAF1	5894	P04049	Raf-1 proto-oncogene, serine/threonine kinase	Kinase	470	0,418	0,885	0,85295	0,01		1	1	0	2016	2016
Skin lesion	C0037284	IL21	59067	Q9HBE4	interleukin 21		321	0,441	0,769	0,6254	0,01		1	1	0	2017	2017
Skin lesion	C0037284	TMEM11	8834	P17152	transmembrane protein 11		24	0,729	0,385	0,87922	0,01		1	1	0	2017	2017
Skin lesion	C0037284	MAP2K7	5609	O14733	mitogen-activated protein kinase kinase 7	Kinase	408	0,419	0,808	0,99552	0,01		1	1	0	2013	2013
Skin lesion	C0037284	PTX3	5806	P26022	pentraxin 3		296	0,457	0,808	6,983E-05	0,01		1	1	0	2017	2017
Skin lesion	C0037284	GFM1	85476	Q96RP9	G elongation factor mitochondrial 1		74	0,623	0,692	9,278E-13	0,01		1	1	0	2019	2019
Skin lesion	C0037284	IKBKG	8517	Q9Y6K9	inhibitor of nuclear factor kappa B kinase regulatory subunit gamma	Kinase	252	0,493	0,769	0,084853	0,01		1	1	0	2017	2017
Skin lesion	C0037284	USO1	8615	O60763	USO1 vesicle transport factor	Transporter	153	0,522	0,885	0,33417	0,01		1	1	0	2003	2003
Skin lesion	C0037284	PSMD9	5715	O00233	proteasome 26S subunit, non-ATPase 9	Enzyme modulator	344	0,435	0,846	4,86E-06	0,01		1	1	0	2017	2017
Skin lesion	C0037284	AKR1C3	8644	P42330	aldo-keto reductase family 1 member C3	Enzyme	142	0,529	0,769	7,581E-24	0,01		1	1	0	2018	2018
Skin lesion	C0037284	MMP23A	8511		matrix metallopeptidase 23A (pseudogene)		27	0,722	0,308		0,01		1	1	0	2006	2006
Skin lesion	C0037284	SLC12A9	56996	Q9BXP2	solute carrier family 12 member 9	Transporter	280	0,454	0,769	1,181E-15	0,01		1	1	0	1997	1997

(continued)

Table S2. (continued)

Disease	Disease_id	Gene	Gene_id	UniProt	Gene_Full_Name	Protein_Class	N_diseases_g	DSI_g	DPI_g	pLI	Score_gda	EL_gda	EI_gda	N_PMIDs	N_SNPs_gda	First_Ref	Last_Ref
Skin lesion	C0037284	B2M	567	P61769	beta-2-microglobulin	Immune response	352	0,447	0,846	0,56167	0,01		1	1	0	1993	1993
Skin lesion	C0037284	SOCS1	8651	O15524	suppressor of cytokine signaling 1	Enzyme modulator	315	0,445	0,808	0,58544	0,01		1	1	0	2015	2015
Skin lesion	C0037284	MMP23B	8510	O75900	matrix metallopeptidase 23B	Enzyme	32	0,695	0,346	0,11732	0,01		1	1	0	2006	2006
Skin lesion	C0037284	AICDA	57379	Q9GZX7	activation induced cytidine deaminase	Enzyme	265	0,463	0,885	9,21E-06	0,01		1	1	0	2011	2011
Skin lesion	C0037284	PRL	5617	P01236	prolactin	Signaling	506	0,406	0,885	2,902E-07	0,01		1	1	0	2018	2018
Skin lesion	C0037284	EIF2AK2	5610	P19525	eukaryotic translation initiation factor 2 alpha kinase 2	Kinase	142	0,538	0,769	0,017643	0,01		1	1	0	2003	2003
Skin lesion	C0037284	MIR202	574448		microRNA 202		82	0,579	0,769		0,01		1	1	0	2017	2017
Skin lesion	C0037284	UBASH3B	84959	Q8TF42	ubiquitin associated and SH3 domain containing B		104	0,561	0,769	4,705E-05	0,01		1	1	0	1998	1998
Skin lesion	C0037284	PTPRC	5788	P08575	protein tyrosine phosphatase receptor type C	Enzyme	366	0,435	0,808	1	0,01		1	1	0	2015	2015
Skin lesion	C0037284	RHOJ	57381	Q9H4E5	ras homolog family member J	Enzyme modulator	38	0,686	0,308	0,0064012	0,01		1	1	0	2017	2017
Skin lesion	C0037284	MEG3	55384		maternally expressed 3		239	0,471	0,846		0,01		1	1	0	2019	2019
Skin lesion	C0037284	SIRT7	51547	Q9NRC8	sirtuin 7	Epigenetic regulator	80	0,582	0,577	0,0005562	0,01		1	1	0	2019	2019
Skin lesion	C0037284	CD34	947	P28906	CD34 molecule		674	0,368	0,808	4,988E-06	0,01		1	1	0	2001	2001
Skin lesion	C0037284	ENPP1	5167	P22413	ectonucleotide pyrophosphatase/phosphodiesterase 1	Enzyme	247	0,498	0,808	4,994E-08	0,01		1	1	0	2012	2012
Skin lesion	C0037284	SUFU	51684	Q9UMX1	SUFU negative regulator of hedgehog signaling		272	0,493	0,769	0,99992	0,01		1	1	0	2015	2015
Skin lesion	C0037284	ABCB1	5243	P08183	ATP binding cassette subfamily B member 1	Transporter	933	0,344	0,885	1,256E-05	0,01		0	1	1	2014	2014
Skin lesion	C0037284	GSTO1	9446	P78417	glutathione S-transferase omega 1		136	0,541	0,769	5,092E-09	0,01		1	1	2	2018	2018
Skin lesion	C0037284	CD27	939	P26842	CD27 molecule		154	0,517	0,692	0,010011	0,01		0	1	0	2010	2010
Skin lesion	C0037284	SLIT2	9353	O94813	slit guidance ligand 2		177	0,511	0,769	1	0,01		1	1	0	2014	2014
Skin lesion	C0037284	HSPD1	3329	P10809	heat shock protein family D (Hsp60) member 1		398	0,432	0,808	0,99257	0,01		1	1	0	2007	2007
Skin lesion	C0037284	CD22	933	P20273	CD22 molecule		106	0,556	0,615	0,8044	0,01		1	1	0	2015	2015
Skin lesion	C0037284	GDF15	9518	Q99988	growth differentiation factor 15	Signaling	389	0,429	0,808	3,013E-07	0,01		1	1	0	2018	2018
Skin lesion	C0037284	TNFRSF12A	51330	Q9NP84	TNF receptor superfamily member 12A		173	0,509	0,692	0,017995	0,01		1	1	0	2020	2020
Skin lesion	C0037284	SIRT6	51548	Q8N6T7	sirtuin 6	Epigenetic regulator	195	0,496	0,846	0,039119	0,01		1	1	0	2019	2019
Skin lesion	C0037284	SDC1	6382	P18827	syndecan 1	Extracellular structure	323	0,445	0,769	0,0084118	0,01		1	1	0	2010	2010
Skin lesion	C0037284	TNFSF15	9966	O95150	TNF superfamily member 15	Signaling	143	0,531	0,692	0,0028159	0,01		1	1	0	2011	2011
Skin lesion	C0037284	CDC6	990	Q99741	cell division cycle 6		130	0,552	0,731	1,15E-09	0,01		1	1	0	2019	2019
Skin lesion	C0037284	TOX	9760	O94900	thymocyte selection associated high mobility group box		57	0,636	0,538	0,99869	0,01		1	1	0	2014	2014
Skin lesion	C0037284	CD74	972	P04233	CD74 molecule	Enzyme modulator	170	0,512	0,808	0,24889	0,01		1	1	0	2018	2018
Skin lesion	C0037284	CD69	969	Q07108	CD69 molecule		206	0,488	0,923	0,029691	0,01		1	1	0	2013	2013
Skin lesion	C0037284	CD68	968	P34810	CD68 molecule	Transporter	452	0,408	0,808	1,406E-06	0,01		1	1	0	2013	2013
Skin lesion	C0037284	CD63	967	P08962	CD63 molecule		128	0,542	0,731	0,017439	0,01		1	1	0	2018	2018
Skin lesion	C0037284	DMKN	93099	Q6E0U4	dermokine		20	0,729	0,308	8,345E-13	0,01		1	1	0	2017	2017
Skin lesion	C0037284	CD14	929	P08571	CD14 molecule		551	0,392	0,885	4,881E-05	0,01		1	1	0	2014	2014
Skin lesion	C0037284	KRT20	54474	P35900	keratin 20		559	0,388	0,846	9,078E-11	0,01		1	1	0	2020	2020
Skin lesion	C0037284	BAX	581	Q07812	BCL2 associated X, apoptosis regulator	Signaling	420	0,417	0,885	0,31746	0,01		1	1	0	2003	2003
Skin lesion	C0037284	TET2	54790	Q6N021	tet methylcytosine dioxygenase 2		362	0,458	0,808	4,333E-54	0,01		1	1	0	2018	2018
Skin lesion	C0037284	TESC	54997	Q96BS2	tescalcin		97	0,57	0,692	0,10778	0,01		1	1	0	2018	2018
Skin lesion	C0037284	CD1A	909	P06126	CD1a molecule		121	0,543	0,769	4,195E-24	0,01		1	1	0	2001	2001
Skin lesion	C0037284	OTULIN	90268	Q96BN8	OTU deubiquitinase with linear linkage specificity		26	0,751	0,346	0,2201	0,01		1	1	0	2019	2019
Skin lesion	C0037284	MCUB	55013	Q9NWR8	mitochondrial calcium uniporter dominant negative subunit beta		6	0,861	0,192	2,278E-08	0,01		1	1	0	2012	2012
Skin lesion	C0037284	TRPA1	8989	O75762	transient receptor potential cation channel subfamily A member 1	Ion channel	160	0,546	0,846	7,231E-35	0,01		1	1	0	2015	2015
Skin lesion	C0037284	SLC29A3	55315	Q9BZD2	solute carrier family 29 member 3	Transporter	123	0,578	0,769	1,293E-07	0,01		1	1	0	2012	2012
Skin lesion	C0037284	CD1B	910	P29016	CD1b molecule		28	0,722	0,423	5,356E-11	0,01		1	1	0	2001	2001
Skin lesion	C0037284	POLG	5428	P54098	DNA polymerase gamma, catalytic subunit	Enzyme	462	0,457	0,846	2,076E-09	0,01		1	1	0	2017	2017
Skin lesion	C0037284	PLCB3	5331	Q01970	phospholipase C beta 3	Enzyme	32	0,729	0,385	0,93999	0,01		1	1	0	2014	2014
Skin lesion	C0037284	PDLIM7	9260	Q9NR12	PDZ and LIM domain 7	Cellular structure	241	0,474	0,808	0,70838	0,01		1	1	0	2005	2005
Skin lesion	C0037284	IL1RL1	9173	Q01638	interleukin 1 receptor like 1	Receptor	117	0,547	0,731	1,441E-12	0,01		1	1	0	2016	2016
Skin lesion	C0037284	PLG	5340	P00747	plasminogen	Enzyme	586	0,389	0,923	0,010345	0,01		1	1	0	1999	1999
Skin lesion	C0037284	MYOM2	9172	P54296	myomesin 2		103	0,57	0,692	7,009E-85	0,01		1	1	0	2017	2017

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Table S2. (continued)

Disease	Disease_id	Gene	Gene_id	UniProt	Gene_Full_Name	Protein_Class	N_diseases_g	DSI_g	DPI_g	pLI	Score_gda	EL_gda	EI_gda	N_PMIDs	N_SNPs_gda	First_Ref	Last_Ref
Skin lesion	C0037284	PLXNA2	5362	O75051	plexin A2		307	0,447	0,808	1,077E-06	0,01		1	1	0	2018	2018
Skin lesion	C0037284	PMM2	5373	O15305	phosphomannomutase 2	Enzyme	214	0,535	0,769	1,407E-17	0,01		1	1	0	2017	2017
Skin lesion	C0037284	DUOX1	53905	Q9NRD9	dual oxidase 1	Enzyme	97	0,57	0,692	6,224E-33	0,01		1	1	0	2014	2014
Skin lesion	C0037284	TLR9	54106	Q9NR96	toll like receptor 9		457	0,411	0,885	9,812E-06	0,01		1	1	0	2007	2007
Skin lesion	C0037284	NAV3	89795	Q8IVL0	neuron navigator 3		46	0,653	0,615	1	0,01		1	1	0	2005	2005
Skin lesion	C0037284	CCR2	729230	P41597	C-C motif chemokine receptor 2		436	0,418	0,846	0,023412	0,01		1	1	0	2017	2017
Skin lesion	C0037284	TRPM2	7226	O94759	transient receptor potential cation channel subfamily M member 2	Ion channel	133	0,546	0,731	8,963E-44	0,01		1	1	0	2019	2019
Skin lesion	C0037284	BMP4	652	P12644	bone morphogenetic protein 4	Signaling	423	0,422	0,808	0,9564	0,01		1	1	0	2019	2019
Skin lesion	C0037284	BMP6	654	P22004	bone morphogenetic protein 6	Signaling	137	0,531	0,808	0,75947	0,01		1	1	0	2018	2018
Skin lesion	C0037284	SLC7A1	6541	P30825	solute carrier family 7 member 1	Transporter	46	0,678	0,5	0,99291	0,01		1	1	0	2008	2008
Skin lesion	C0037284	SLC7A2	6542	P52569	solute carrier family 7 member 2	Transporter	30	0,7	0,5	2,343E-11	0,01		1	1	0	2008	2008
Skin lesion	C0037284	OCM	654231	P0CE72	oncomodulin		24	0,751	0,423	1,089E-08	0,01		1	1	0	2018	2018
Skin lesion	C0037284	TLR2	7097	O60603	toll like receptor 2		749	0,361	0,923	1,015E-06	0,01		1	1	0	2007	2007
Skin lesion	C0037284	THY1	7070	P04216	Thy-1 cell surface antigen		197	0,496	0,808	0,049895	0,01		1	1	0	1989	1989
Skin lesion	C0037284	THBS1	7057	P07996	thrombospondin 1		480	0,407	0,885	0,99985	0,01		1	1	0	2004	2004
Skin lesion	C0037284	SEMA4A	64218	Q9H3S1	semaphorin 4A	Signaling	141	0,569	0,692	1,839E-05	0,01		1	1	0	2013	2013
Skin lesion	C0037284	XYLT2	64132	Q9H1B5	xylosyltransferase 2		138	0,566	0,808	0,92576	0,01		1	1	2	2006	2006
Skin lesion	C0037284	TNFSF4	7292	P23510	TNF superfamily member 4	Signaling	129	0,54	0,808	0,049378	0,01		1	1	0	2018	2018
Skin lesion	C0037284	SEA	6395		S13 erythroblastosis (avian) oncogene homolog		65	0,606	0,615		0,01		1	1	0	2019	2019
Skin lesion	C0037284	C5AR1	728	P21730	complement C5a receptor 1	G-protein coupled receptor	179	0,513	0,808	0,40249	0,01		1	1	0	2019	2019
Skin lesion	C0037284	C5	727	P01031	complement C5	Enzyme modulator	129	0,55	0,731	8,079E-24	0,01		1	1	0	2019	2019
Skin lesion	C0037284	TSHR	7253	P16473	thyroid stimulating hormone receptor	G-protein coupled receptor	250	0,486	0,808	3,045E-15	0,01		1	1	0	1996	1996
Skin lesion	C0037284	ERVK-6	64006		endogenous retrovirus group K member 6, envelope		162	0,521	0,808		0,01		1	1	0	2017	2017
Skin lesion	C0037284	SELPLG	6404	Q14242	selectin P ligand		113	0,564	0,692	0,1768	0,01		0	1	0	2010	2010
Skin lesion	C0037284	GOLPH3	64083	Q9H4A6	golgi phosphoprotein 3		140	0,53	0,808	0,23586	0,01		1	1	0	2013	2013
Skin lesion	C0037284	BLM	641	P54132	BLM RecQ like helicase		158	0,535	0,808	1,538E-15	0,01		1	1	0	2015	2015
Skin lesion	C0037284	SMARCA1	6594	P28370	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	Enzyme	183	0,504	0,808	1	0,01		1	1	0	2011	2011
Skin lesion	C0037284	SNAI1	6615	O95863	snail family transcriptional repressor 1		243	0,474	0,808	0,21754	0,01		1	1	0	2017	2017
Skin lesion	C0037284	BTK	695	Q06187	Bruton tyrosine kinase	Kinase	290	0,464	0,808	0,99996	0,01		1	1	0	2018	2018
Skin lesion	C0037284	SRY	6736	Q05066	sex determining region Y	Transcription factor	315	0,456	0,808		0,01		1	1	0	2018	2018
Skin lesion	C0037284	TCF4	6925	P15884	transcription factor 4	Transcription factor	378	0,464	0,846	0,99981	0,01		1	1	0	2018	2018
Skin lesion	C0037284	TAT	6898	P17735	tyrosine aminotransferase		230	0,492	0,846	0,0068998	0,01		1	1	0	2017	2017
Skin lesion	C0037284	TAP2	6891	Q03519	transporter 2, ATP binding cassette subfamily B member	Transporter	155	0,517	0,808	6,891E-11	0,01		1	1	0	2014	2014
Skin lesion	C0037284	TACR1	6869	P25103	tachykinin receptor 1	G-protein coupled receptor	217	0,502	0,885	0,0003844	0,01		1	1	0	2017	2017
Skin lesion	C0037284	STAT5A	6776	P42229	signal transducer and activator of transcription 5A	Nucleic acid binding	318	0,445	0,808	0,99994	0,01		1	1	0	2018	2018
Skin lesion	C0037284	STAT5B	6777	P51692	signal transducer and activator of transcription 5B	Nucleic acid binding	357	0,442	0,808	0,99988	0,01		1	1	0	2018	2018
Skin lesion	C0037284	STAT6	6778	P42226	signal transducer and activator of transcription 6	Nucleic acid binding	281	0,475	0,808	0,98849	0,01		1	1	0	2002	2002
Skin lesion	C0037284	PRDX2	7001	P32119	peroxiredoxin 2	Enzyme	243	0,474	0,885	0,086513	0,01		1	1	0	2011	2011
Skin lesion	C0037284	SRF	6722	P11831	serum response factor	Transcription factor	147	0,534	0,808	0,97545	0,01		1	1	0	2009	2009
Skin lesion	C0037284	TGM2	7052	P21980	transglutaminase 2	Enzyme	315	0,445	0,808	6,812E-18	0,01		1	1	0	2017	2017
Skin lesion	C0037284	SOX9	6662	P48436	SRY-box transcription factor 9		466	0,419	0,846	0,99772	0,01		1	1	0	2018	2018
Skin lesion	C0037284	TGFBR2	7048	P37173	transforming growth factor beta receptor 2	Kinase	502	0,413	0,846	0,12535	0,01		1	1	0	2016	2016
Skin lesion	C0037284	SOX11	6664	P35716	SRY-box transcription factor 11	Transcription factor	246	0,494	0,808	0,85844	0,01		1	1	0	2013	2013
Skin lesion	C0037284	DST	667	Q03001	dystonin	Cellular structure	147	0,552	0,846	1	0,01		1	1	0	2019	2019
Skin lesion	C0037284	SPP1	6696	P10451	secreted phosphoprotein 1		824	0,353	0,885	2,146E-06	0,01		1	1	0	2011	2011
Skin lesion	C0037284	TEK	7010	Q02763	TEK receptor tyrosine kinase	Kinase	300	0,462	0,692	1	0,01		1	1	0	2011	2011
Skin lesion	C0037284	SPRR1A	6698	P35321	small proline rich protein 1A		16	0,729	0,269	0,0060385	0,01		1	1	0	2010	2010
Skin lesion	C0037284	SPRR3	6707	Q9UBC9	small proline rich protein 3		23	0,736	0,269		0,01		1	1	0	1997	1997
Skin lesion	C0037284	BSG	682	P35613	basigin (Ok blood group)		287	0,458	0,769	2,587E-05	0,01		1	1	0	2017	2017

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Table S2. (continued)

Disease	Disease_id	Gene	Gene_id	UniProt	Gene_Full_Name	Protein_Class	N_diseases_g	DSI_g	DPI_g	pLI	Score_gda	EL_gda	EI_gda	N_PMIDs	N_SNPs_gda	First_Ref	Last_Ref
Skin lesion	C0037284	TYMS	7298	P04818	thymidylate synthetase	Enzyme	406	0,425	0,846	0,72247	0,01		1	1	1	2018	2018
Skin lesion	C0037284	RARRES2	5919	Q99969	retinoic acid receptor responder 2		180	0,519	0,731	2,716E-05	0,01		1	1	0	2009	2009
Skin lesion	C0037284	USP9X	8239	Q93008	ubiquitin specific peptidase 9 X-linked		255	0,502	0,846	1	0,01		1	1	0	2017	2017
Skin lesion	C0037284	SHARPIN	81858	Q9H0F6	SHANK associated RH domain interactor	Enzyme	53	0,638	0,615	2,312E-05	0,01		1	1	0	2011	2011
Skin lesion	C0037284	FGF23	8074	Q9GZV9	fibroblast growth factor 23	Signaling	305	0,46	0,731	0,031014	0,01		1	1	0	2012	2012
Skin lesion	C0037284	PPP1R2C	80316	O14990	PPP1R2C family member C	Enzyme modulator	231	0,478	0,846		0,01		1	1	0	2014	2014
Skin lesion	C0037284	REL	5966	Q04864	REL proto-oncogene, NF-kB subunit	Transcription factor	90	0,579	0,692	0,99836	0,01		1	1	1	2016	2016
Skin lesion	C0037284	REG1A	5967	P05451	regenerating family member 1 alpha		264	0,467	0,846	1,35E-05	0,01		1	1	0	2008	2008
Skin lesion	C0037284	BCL3	602	P20749	BCL3 transcription coactivator		136	0,541	0,731	0,98871	0,01		1	1	0	2018	2018
Skin lesion	C0037284	BCL6	604	P41182	BCL6 transcription repressor		309	0,444	0,808	0,96038	0,01		1	1	0	2012	2012
Skin lesion	C0037284	ZC3H12A	80149	Q5D1E8	zinc finger CCCH-type containing 12A	Nucleic acid binding	88	0,578	0,654	0,14015	0,01		1	1	0	2017	2017
Skin lesion	C0037284	CCND1	595	P24385	cyclin D1	Enzyme modulator	859	0,344	0,923	0,89057	0,01		1	1	0	2010	2010
Skin lesion	C0037284	CAST	831	P20810	calpastatin		141	0,541	0,846	4,122E-12	0,01		1	1	0	2020	2020
Skin lesion	C0037284	PLAAT4	5920	Q9UL19	phospholipase A and acyltransferase 4		190	0,5	0,808	1,223E-07	0,01		1	1	0	2007	2007
Skin lesion	C0037284	CAT	847	P04040	catalase	Enzyme	794	0,359	0,962	1,626E-10	0,01		1	1	0	2003	2003
Skin lesion	C0037284	GLIS2	84662	Q9BZE0	GLIS family zinc finger 2	Transcription factor	67	0,608	0,462	0,85834	0,01		1	1	0	2001	2001
Skin lesion	C0037284	IL1F10	84639	Q8WWZ1	interleukin 1 family member 10		57	0,636	0,462	2,023E-06	0,01		1	1	0	2017	2017
Skin lesion	C0037284	NR0B2	8431	Q15466	nuclear receptor subfamily 0 group B member 2	Nuclear receptor	251	0,474	0,808	8,338E-06	0,01		1	1	0	2006	2006
Skin lesion	C0037284	CASP5	838	P51878	caspase 5	Enzyme	47	0,653	0,5	1,752E-16	0,01		1	1	0	2017	2017
Skin lesion	C0037284	ACE2	59272	Q9BYF1	angiotensin I converting enzyme 2	Enzyme	253	0,477	0,769	0,99769	0,01		1	1	0	2013	2013
Skin lesion	C0037284	RBP2	5948	P50120	retinol binding protein 2		60	0,615	0,615	0,22089	0,01		1	1	0	2016	2016
Skin lesion	C0037284	CASP3	836	P42574	caspase 3	Enzyme	819	0,351	0,923	0,10017	0,01		1	1	0	2019	2019
Skin lesion	C0037284	TNFRSF17	608	Q02223	TNF receptor superfamily member 17	Receptor	81	0,588	0,692	1,372E-06	0,01		1	1	0	2012	2012
Skin lesion	C0037284	EHMT1	79813	Q9H9B1	euchromatic histone lysine methyltransferase 1	Epigenetic regulator	371	0,46	0,808	1	0,01		1	1	0	2019	2019
Skin lesion	C0037284	CCL3	6348	P10147	C-C motif chemokine ligand 3	Signaling	282	0,46	0,885	0,34981	0,01		1	1	0	2017	2017
Skin lesion	C0037284	CCL4	6351	P13236;Q8NHW4	C-C motif chemokine ligand 4	Signaling	276	0,466	0,923	0,24134	0,01		1	1	0	2017	2017
Skin lesion	C0037284	WT1	7490	P19544	WT1 transcription factor	Nucleic acid binding	446	0,422	0,808	0,99648	0,01		1	1	0	2018	2018
Skin lesion	C0037284	TRPV1	7442	Q8NER1	transient receptor potential cation channel subfamily V member 1	Ion channel	404	0,446	0,885	1,01E-16	0,01		1	1	0	2018	2018
Skin lesion	C0037284	CCL11	6356	P51671	C-C motif chemokine ligand 11	Signaling	250	0,473	0,885	0,010211	0,01		1	1	0	2000	2000
Skin lesion	C0037284	CCL13	6357	Q99616	C-C motif chemokine ligand 13	Signaling	50	0,628	0,692	0,040987	0,01		1	1	0	2000	2000
Skin lesion	C0037284	UROS	7390	P10746	uroporphyrinogen III synthase	Enzyme	58	0,678	0,462	0,031627	0,01		1	1	0	2012	2012
Skin lesion	C0037284	CCL18	6362	P55774	C-C motif chemokine ligand 18	Signaling	200	0,489	0,846	0,0091743	0,01		1	1	0	2013	2013
Skin lesion	C0037284	UBE2B	7320	P63146	ubiquitin conjugating enzyme E2 B		59	0,644	0,615	0,19663	0,01		1	1	0	2018	2018
Skin lesion	C0037284	SLC12A3	6559	P55017	solute carrier family 12 member 3	Transporter	252	0,493	0,808	3,032E-32	0,01		1	1	0	2018	2018
Skin lesion	C0037284	CEACAM1	634	P13688	CEA cell adhesion molecule 1		167	0,525	0,731	0,0007882	0,01		1	1	0	2015	2015
Skin lesion	C0037284	VASH2	79805	Q86V25	vasohibin 2		45	0,678	0,423	0,24217	0,01		1	1	0	2016	2016
Skin lesion	C0037284	BCR	613	P11274	BCR activator of RhoGEF and GTPase	Enzyme modulator	392	0,431	0,885	0,98761	0,01		1	1	0	1999	1999
Skin lesion	C0037284	CARD14	79092	Q9BXL6	caspase recruitment domain family member 14		126	0,546	0,846	1,205E-19	0,01		1	1	0	2018	2018
Skin lesion	C0037284	CACNA1A	773	O00555	calcium voltage-gated channel subunit alpha1 A	Ion channel	320	0,489	0,769	1	0,01		1	1	0	2019	2019
Skin lesion	C0037284	S100A4	6275	P26447	S100 calcium binding protein A4	Calcium-binding protein	308	0,448	0,769	0,0061838	0,01		0	1	0	2009	2009
Skin lesion	C0037284	YWHAZ	7534	P63104	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta	Chaperone	247	0,475	0,846	0,93965	0,01		1	1	0	2017	2017
Skin lesion	C0037284	S100A8	6279	P05109	S100 calcium binding protein A8	Calcium-binding protein	369	0,43	0,962	0,13761	0,01		1	1	0	2016	2016
Skin lesion	C0037284	XRCC1	7515	P18887	X-ray repair cross complementing 1		410	0,421	0,923	6,339E-09	0,01		1	1	2	2007	2007
Skin lesion	C0037284	S100A9	6280	P06702	S100 calcium binding protein A9	Calcium-binding protein	363	0,433	0,885	0,4777	0,01		1	1	0	2016	2016
Skin lesion	C0037284	TYR	7299	P14679	tyrosinase	Enzyme	281	0,473	0,808	4,986E-32	0,01		1	1	0	2017	2017
Skin lesion	C0037284	DEFB104A	140596	Q8WTQ1	defensin beta 104A		43	0,638	0,692	0,093748	0,01		1	1	0	2019	2019
Skin lesion	C0037284	DHFR	1719	P00374	dihydrofolate reductase	Enzyme	191	0,513	0,808	0,0343	0,01		1	1	1	2015	2015
Skin lesion	C0037284	AFP	174	P02771	alpha fetoprotein	Transporter	392	0,429	0,885	1,138E-11	0,01		1	1	0	2006	2006
Skin lesion	C0037284	AGER	177	Q15109	advanced glycosylation end-product specific receptor	Receptor	450	0,42	0,885	6,353E-16	0,01		1	1	0	2018	2018

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Table S2. (continued)

Disease	Disease_id	Gene	Gene_id	UniProt	Gene_Full_Name	Protein_Class	N_diseases_g	DSI_g	DPI_g	pLI	Score_gda	EL_gda	EI_gda	N_PMIDs	N_SNPs_gda	First_Ref	Last_Ref
Skin lesion	C0037284	ECM1	1893	Q16610	extracellular matrix protein 1		120	0,576	0,731	4,663E-14	0,01		1	1	0	2016	2016
Skin lesion	C0037284	EDN1	1906	P05305	endothelin 1	Signaling	679	0,38	0,846	0,45504	0,01		1	1	0	2015	2015
Skin lesion	C0037284	AHCY	191	P23526	adenosylhomocysteinase	Enzyme	107	0,582	0,692	0,035922	0,01		1	1	0	2018	2018
Skin lesion	C0037284	EDNRB	1910	P24530	endothelin receptor type B	G-protein coupled receptor	300	0,47	0,846	0,0092419	0,01		1	1	0	2013	2013
Skin lesion	C0037284	EGR1	1958	P18146	early growth response 1	Nucleic acid binding	378	0,433	0,923	0,3509	0,01		1	1	0	2014	2014
Skin lesion	C0037284	AIF1	199	P55008	allograft inflammatory factor 1	Calcium-binding protein	166	0,521	0,808	1,879E-06	0,01		1	1	0	2006	2006
Skin lesion	C0037284	APOBEC3A	200315	P31941	apolipoprotein B mRNA editing enzyme catalytic subunit 3A		68	0,612	0,692	0,0010454	0,01		1	1	0	2013	2013
Skin lesion	C0037284	SPRED2	200734	Q7Z698	sprouty related EVH1 domain containing 2	Receptor	38	0,711	0,577	2,868E-07	0,01		1	1	0	2018	2018
Skin lesion	C0037284	EPHA4	2043	P54764	EPH receptor A4	Kinase	118	0,566	0,846	1	0,01		1	1	0	2004	2004
Skin lesion	C0037284	AKR1C1	1645	Q04828	aldo-keto reductase family 1 member C1	Enzyme	80	0,593	0,615	3,524E-15	0,01		1	1	0	2018	2018
Skin lesion	C0037284	ACE	1636	P12821	angiotensin I converting enzyme	Enzyme	1082	0,328	0,923	1,034E-37	0,01		1	1	0	2013	2013
Skin lesion	C0037284	HT	140805		Hashimoto thyroiditis		170	0,505	0,731		0,01		1	1	0	2016	2016
Skin lesion	C0037284	LACC1	144811	Q8IV20	laccase domain containing 1		35	0,7	0,423	1,166E-05	0,01		1	1	0	2018	2018
Skin lesion	C0037284	TMC8	147138	Q8IU68	transmembrane channel like 8	Ion channel	35	0,705	0,231	1,14E-14	0,01		1	1	0	2018	2018
Skin lesion	C0037284	IL23R	149233	Q5VWK5	interleukin 23 receptor	Signaling	306	0,466	0,769	0,0005596	0,01		1	1	0	2013	2013
Skin lesion	C0037284	CTNND1	1500	O60716	catenin delta 1	Cellular structure	196	0,5	0,808	0,99999	0,01		1	1	0	2019	2019
Skin lesion	C0037284	CTSE	1510	P14091	cathepsin E	Enzyme	56	0,631	0,615	1,437E-14	0,01		1	1	0	2003	2003
Skin lesion	C0037284	PLB1	151056	Q6P1J6	phospholipase B1		219	0,488	0,846	1,732E-72	0,01		1	1	0	2017	2017
Skin lesion	C0037284	CTSK	1513	P43235	cathepsin K	Enzyme	221	0,497	0,808	3,099E-05	0,01		1	1	0	2013	2013
Skin lesion	C0037284	AMOT	154796	Q4VCS5	angiomotin		52	0,641	0,538	0,99666	0,01		1	1	0	2016	2016
Skin lesion	C0037284	DAPK1	1612	P53355	death associated protein kinase 1	Kinase	249	0,472	0,808	0,99767	0,01		1	1	0	2013	2013
Skin lesion	C0037284	TRPV3	162514	Q8NET8	transient receptor potential cation channel subfamily V member 3	Ion channel	73	0,61	0,577	4,601E-20	0,01		1	1	0	2019	2019
Skin lesion	C0037284	DCN	1634	P07585	decorin		297	0,457	0,808	0,31231	0,01		1	1	0	2009	2009
Skin lesion	C0037284	ERBB2	2064	P04626	erb-b2 receptor tyrosine kinase 2	Kinase	995	0,328	0,923	0,0059892	0,01		1	1	0	2017	2017
Skin lesion	C0037284	ERCC1	2067	P07992	ERCC excision repair 1, endonuclease non-catalytic subunit	Enzyme	345	0,445	0,846	1,593E-07	0,01		1	1	0	2017	2017
Skin lesion	C0037284	STAB1	23166	Q9NY15	stabilin 1		69	0,619	0,692	8,679E-50	0,01		1	1	0	2016	2016
Skin lesion	C0037284	FLNB	2317	O75369	filamin B		374	0,458	0,923	6,051E-10	0,01		1	1	0	2003	2003
Skin lesion	C0037284	FLT3	2322	P36888	fms related receptor tyrosine kinase 3	Kinase	270	0,462	0,654	0,60777	0,01		1	1	0	2018	2018
Skin lesion	C0037284	FLT4	2324	P35916	fms related receptor tyrosine kinase 4	Kinase	306	0,457	0,808	1	0,01		1	1	0	1998	1998
Skin lesion	C0037284	FN1	2335	P02751	fibronectin 1	Signaling	724	0,365	0,962	0,0014045	0,01		1	1	0	2014	2014
Skin lesion	C0037284	NCSTN	23385	Q92542	nicastrin		40	0,666	0,462	0,99942	0,01		1	1	0	2010	2010
Skin lesion	C0037284	ZGLP1	100125288	P0C6A0	zinc finger GATA like protein 1		186	0,512	0,808	0,3868	0,01		1	1	0	2019	2019
Skin lesion	C0037284	FOLR1	2348	P15328	folate receptor alpha		174	0,522	0,885	0,12642	0,01		1	1	1	2018	2018
Skin lesion	C0037284	TNFRSF13B	23495	O14836	TNF receptor superfamily member 13B		137	0,558	0,769	2,091E-15	0,01		1	1	0	2012	2012
Skin lesion	C0037284	MMD	23531	Q15546	monocyte to macrophage differentiation associated	Receptor	58	0,647	0,577	0,0001344	0,01		1	1	0	2007	2007
Skin lesion	C0037284	SEC14L2	23541	O76054	SEC14 like lipid binding 2		198	0,494	0,885	2,92E-08	0,01		1	1	0	2003	2003
Skin lesion	C0037284	LEMD3	23592	Q9Y2U8	LEM domain containing 3		112	0,582	0,731	0,99877	0,01		1	1	0	2019	2019
Skin lesion	C0037284	FLNA	2316	P21333	filamin A		571	0,419	0,846	1	0,01		1	1	0	2015	2015
Skin lesion	C0037284	TBC1D9	23158	Q6ZT07	TBC1 domain family member 9	Enzyme	491	0,399	0,846	2,804E-05	0,01		0	1	0	2014	2014
Skin lesion	C0037284	AKT1	207	P31749	AKT serine/threonine kinase 1	Kinase	1250	0,311	0,962	0,9759	0,01		1	1	0	2014	2014
Skin lesion	C0037284	ETS1	2113	P14921	ETS proto-oncogene 1, transcription factor	Transcription factor	327	0,444	0,731	0,7816	0,01		1	1	0	2017	2017
Skin lesion	C0037284	F2	2147	P00734	coagulation factor II, thrombin	Enzyme	490	0,415	0,885	0,0011118	0,01		1	1	0	2008	2008
Skin lesion	C0037284	F9	2158	P00740	coagulation factor IX	Enzyme	276	0,465	0,885	0,99776	0,01		1	1	0	2008	2008
Skin lesion	C0037284	FAT1	2195	Q14517	FAT atypical cadherin 1		178	0,508	0,808	1,197E-12	0,01		1	1	0	2018	2018
Skin lesion	C0037284	FCGR3A	2214	P08637	Fc fragment of IgG receptor IIIa	Cell adhesion	352	0,432	0,962	3,696E-06	0,01		1	1	0	2014	2014
Skin lesion	C0037284	FCGR3B	2215	O75015	Fc fragment of IgG receptor IIIb	Cell adhesion	291	0,452	0,962	3,029E-07	0,01		1	1	0	2014	2014
Skin lesion	C0037284	THSD7A	221981	Q9UPZ6	thrombospondin type 1 domain containing 7A	Extracellular structure	51	0,644	0,654	1	0,01		1	1	0	2018	2018
Skin lesion	C0037284	FGF2	2247	P09038	fibroblast growth factor 2	Signaling	635	0,383	0,923	0,0184	0,01		1	1	0	2004	2004
Skin lesion	C0037284	FGFR3	2261	P22607	fibroblast growth factor receptor 3	Kinase	654	0,391	0,846	1,643E-05	0,01		1	1	0	2007	2007
Skin lesion	C0037284	NLRP1	22861	Q9C000	NLR family pyrin domain containing 1		200	0,502	0,769	4,969E-19	0,01		1	1	0	2019	2019

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Table S2. (continued)

Disease	Disease_id	Gene	Gene_id	UniProt	Gene_Full_Name	Protein_Class	N_diseases_g	DSI_g	DPI_g	pLI	Score_gda	EL_gda	EI_gda	N_PMIDs	N_SNPs_gda	First_Ref	Last_Ref
Skin lesion	C0037284	ZHX2	22882	Q9Y6X8	zinc fingers and homeoboxes 2	Transcription factor	172	0,51	0,654	0,03372	0,01		1	1	0	2016	2016
Skin lesion	C0037284	CADM1	23705	Q9BY67	cell adhesion molecule 1		205	0,491	0,769	0,66216	0,01		1	1	0	2012	2012
Skin lesion	C0037284	HLP	100188397		hyperkeratosis lenticularis perstans		29	0,691	0,346		0,01		1	1	0	2016	2016
Skin lesion	C0037284	LINC02210-CRHR1	104909134	P34998	LINC02210-CRHR1 readthrough		123	0,57	0,692		0,01		1	1	0	2017	2017
Skin lesion	C0037284	CIB1	10519	Q99828	calcium and integrin binding 1		275	0,458	0,769	0,0003261	0,01		1	1	0	2000	2000
Skin lesion	C0037284	CEBPD	1052	P49716	CCAAT enhancer binding protein delta	Transcription factor	97	0,57	0,769	0,61219	0,01		1	1	0	2019	2019
Skin lesion	C0037284	ZNRD2	10534	O60232	zinc ribbon domain containing 2		311	0,443	0,769	1,843E-07	0,01		1	1	0	2017	2017
Skin lesion	C0037284	LINC01638	105372978		long intergenic non-protein coding RNA 1638		25	0,722	0,346		0,01		1	1	0	2019	2019
Skin lesion	C0037284	ANP32B	10541	Q92688	acidic nuclear phosphoprotein 32 family member B	Enzyme modulator	120	0,541	0,731	0,95827	0,01		1	1	0	2012	2012
Skin lesion	C0037284	POSTN	10631	Q15063	periostin	Signaling	378	0,428	0,885	1,067E-09	0,01		1	1	0	2019	2019
Skin lesion	C0037284	KHDRBS1	10657	Q07666	KH RNA binding domain containing, signal transduction associated 1	Nucleic acid binding	289	0,457	0,846	0,99423	0,01		1	1	0	2019	2019
Skin lesion	C0037284	DCTN6	10671	O00399	dynactin subunit 6	Cellular structure	315	0,442	0,769	0,055741	0,01		1	1	0	2017	2017
Skin lesion	C0037284	MTCO2P12	107075310		MT-CO2 pseudogene 12		703	0,368	0,962		0,01		1	1	0	2017	2017
Skin lesion	C0037284	CCL27	10850	Q9Y4X3	C-C motif chemokine ligand 27	Signaling	185	0,502	0,846	0,013511	0,01		1	1	0	2018	2018
Skin lesion	C0037284	LYVE1	10894	Q9Y5Y7	lymphatic vessel endothelial hyaluronan receptor 1		80	0,587	0,731	4,719E-07	0,01		1	1	0	2016	2016
Skin lesion	C0037284	NXF1	10482	Q9UBU9	nuclear RNA export factor 1	Nucleic acid binding	141	0,531	0,885	0,9763	0,01		1	1	0	2003	2003
Skin lesion	C0037284	SLC9A6	10479	Q92581	solute carrier family 9 member A6	Transporter	210	0,516	0,846	0,99833	0,01		1	1	0	2018	2018
Skin lesion	C0037284	TMED7-TICAM2	100302736	Q86XR7;Q9Y3B3	TMED7-TICAM2 readthrough		329	0,438	0,769	0,0025936	0,01		1	1	0	2017	2017
Skin lesion	C0037284	MICA	100507436	Q29983	MHC class I polypeptide-related sequence A		248	0,473	0,846	0,0049697	0,01		1	1	0	2003	2003
Skin lesion	C0037284	NR1H3	10062	Q13133	nuclear receptor subfamily 1 group H member 3	Nuclear receptor	102	0,566	0,692	0,90374	0,01		1	1	0	2010	2010
Skin lesion	C0037284	EDIL3	10085	O43854	EGF like repeats and discoidin domains 3	Enzyme	104	0,564	0,769	0,0001458	0,01		1	1	0	2016	2016
Skin lesion	C0037284	APOBEC3A_B	100913187	P31941	APOBEC3A and APOBEC3B deletion hybrid		40	0,663	0,5		0,01		1	1	0	2013	2013
Skin lesion	C0037284	CDKN1A	1026	P38936	cyclin dependent kinase inhibitor 1A		490	0,403	0,769	0,0018575	0,01		1	1	0	1997	1997
Skin lesion	C0037284	CDKN1B	1027	P46527	cyclin dependent kinase inhibitor 1B		454	0,409	0,769	0,62376	0,01		1	1	0	2000	2000
Skin lesion	C0037284	ADAR	103	P55265	adenosine deaminase RNA specific	Enzyme	256	0,501	0,808	0,026282	0,01		1	1	0	2008	2008
Skin lesion	C0037284	CDKN2D	1032	P55273	cyclin dependent kinase inhibitor 2D		110	0,547	0,769	0,49473	0,01		1	1	0	2008	2008
Skin lesion	C0037284	CCL26	10344	Q9Y258	C-C motif chemokine ligand 26	Signaling	60	0,617	0,654	0,010114	0,01		1	1	0	2010	2010
Skin lesion	C0037284	PEMT	10400	Q9UBM1	phosphatidylethanolamine N-methyltransferase		43	0,653	0,538	0,23456	0,01		1	1	2	2015	2015
Skin lesion	C0037284	CD52	1043	P31358	CD52 molecule		60	0,615	0,5	0,40282	0,01		1	1	0	2000	2000
Skin lesion	C0037284	ERVK-32	110006328		endogenous retrovirus group K member 32, envelope		158	0,522	0,692		0,01		1	1	0	2017	2017
Skin lesion	C0037284	SPINK5	11005	Q9NQ38	serine peptidase inhibitor Kazal type 5	Enzyme modulator	93	0,604	0,654	4,846E-28	0,01		1	1	0	2019	2019
Skin lesion	C0037284	CLU	1191	P10909	clusterin		412	0,426	0,885	7,807E-05	0,01		1	1	0	2017	2017
Skin lesion	C0037284	GSTO2	119391	Q9H4Y5	glutathione S-transferase omega 2		53	0,631	0,692	2,613E-09	0,01		1	1	3	2018	2018
Skin lesion	C0037284	CCR1	1230	P32246	C-C motif chemokine receptor 1	G-protein coupled receptor	192	0,531	0,769	0,38775	0,01		1	1	0	2017	2017
Skin lesion	C0037284	CCR7	1236	P32248	C-C motif chemokine receptor 7	G-protein coupled receptor	320	0,443	0,769	0,057623	0,01		0	1	0	2010	2010
Skin lesion	C0037284	GJB4	127534	Q9NTQ9	gap junction protein beta 4	Cell-cell junction	50	0,691	0,462	0,0005511	0,01		1	1	0	2005	2005
Skin lesion	C0037284	NAXE	128240	Q8NCW5	NAD(P)HX epimerase		41	0,743	0,346	2,444E-06	0,01		1	1	0	2016	2016
Skin lesion	C0037284	COL17A1	1308	Q9UMD9	collagen type XVII alpha 1 chain		138	0,545	0,769	2,287E-27	0,01		1	1	0	2019	2019
Skin lesion	C0037284	ADM	133	P35318	adrenomedullin	Signaling	405	0,436	0,808	0,040831	0,01		1	1	0	2012	2012
Skin lesion	C0037284	COX7B	1349	P24311	cytochrome c oxidase subunit 7B		104	0,595	0,654	0,67459	0,01		1	1	0	2012	2012
Skin lesion	C0037284	SGCZ	137868	Q96LD1	sarcoglycan zeta	Cellular structure	22	0,751	0,385	6,4E-09	0,01		1	1	0	2017	2017
Skin lesion	C0037284	CRABP2	1382	P29373	cellular retinoic acid binding protein 2		79	0,593	0,615	0,0015096	0,01		1	1	0	2016	2016
Skin lesion	C0037284	CRHR1	1394	P34998	corticotropin releasing hormone receptor 1		183	0,517	0,769	3,786E-05	0,01		1	1	0	2017	2017
Skin lesion	C0037284	BORCS7	119032	Q96B45	BLOC-1 related complex subunit 7		10	0,89	0,115	2,292E-07	0,01		1	1	1	2016	2016
Skin lesion	C0037284	MMP21	118856	Q8N119	matrix metallopeptidase 21	Enzyme	59	0,621	0,385	1,321E-09	0,01		1	1	0	2006	2006
Skin lesion	C0037284	CD160	11126	O95971	CD160 molecule		87	0,59	0,615	6,843E-05	0,01		1	1	0	2007	2007
Skin lesion	C0037284	CHI3L1	1116	P36222	chitinase 3 like 1		420	0,419	0,885	1,113E-05	0,01		1	1	0	2019	2019
Skin lesion	C0037284	WDHD1	11169	O75717	WD repeat and HMG-box DNA binding protein 1	Nucleic acid binding	161	0,529	0,846	4,369E-18	0,01		1	1	0	2018	2018
Skin lesion	C0037284	PADI2	11240	Q9Y2J8	peptidyl arginine deiminase 2		67	0,61	0,615	4,947E-11	0,01		1	1	0	2014	2014

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Table S2. (continued)

Disease	Disease_id	Gene	Gene_id	UniProt	Gene_Full_Name	Protein_Class	N_diseases_g	DSI_g	DPI_g	pLI	Score_gda	EL_gda	EI_gda	N_PMIDs	N_SNPs_gda	First_Ref	Last_Ref
Skin lesion	C0037284	TREX1	11277	Q9NSU2	three prime repair exonuclease 1		241	0,517	0,808	0,57528	0,01		1	1	0	2017	2017
Skin lesion	C0037284	LINC02605	112935892		long intergenic non-protein coding RNA 2605		203	0,49	0,769		0,01		1	1	0	2006	2006
Skin lesion	C0037284	TMC6	11322	Q7Z403	transmembrane channel like 6	Ion channel	41	0,705	0,308	5,856E-10	0,01		1	1	0	2018	2018
Skin lesion	C0037284	NLRP3	114548	Q96P20	NLR family pyrin domain containing 3		805	0,361	0,962	0,000811	0,01		1	1	0	2013	2013
Skin lesion	C0037284	H3P13	115482685		H3 histone pseudogene 13		78	0,584	0,769		0,01		1	1	0	2008	2008
Skin lesion	C0037284	H3P23	115482696		H3 histone pseudogene 23		310	0,443	0,769		0,01		1	1	0	2017	2017
Skin lesion	C0037284	H3P29	115482721		H3 histone pseudogene 29		12	0,78	0,346		0,01		1	1	0	2008	2008
Skin lesion	C0037284	DCD	117159	P81605	dermcidin		64	0,619	0,654	0,0001578	0,01		1	1	0	2004	2004
Skin lesion	C0037284	CRP	1401	P02741	C-reactive protein		1483	0,299	0,962	0,0036969	0,01		1	1	0	2019	2019
Skin lesion	C0037284	INPP5A	3632	Q14642	inositol polyphosphate-5-phosphatase A	Enzyme	22	0,743	0,385	0,98121	0,01		1	1	1	2015	2015
Skin lesion	C0037284	C10orf99	387695	Q6UWK7	chromosome 10 open reading frame 99		5	0,931	0,038	0,21211	0,01		1	1	0	2018	2018
Skin lesion	C0037284	LAMC2	3918	Q13753	laminin subunit gamma 2	Enzyme modulator	602	0,389	0,923	2,879E-12	0,01		1	1	0	2017	2017
Skin lesion	C0037284	LCN2	3934	P80188	lipocalin 2	Enzyme	497	0,405	0,885	1,14E-09	0,01		1	1	0	2018	2018
Skin lesion	C0037284	LDLR	3949	P01130	low density lipoprotein receptor		336	0,449	0,885	9,841E-24	0,01		1	1	0	2018	2018
Skin lesion	C0037284	LGALS3	3958	P17931	galectin 3	Signaling	557	0,392	0,846	2,321E-05	0,01		0	1	0	2018	2018
Skin lesion	C0037284	SH2D1A	4068	O60880	SH2 domain containing 1A		160	0,525	0,731	0,38935	0,01		1	1	0	2012	2012
Skin lesion	C0037284	MIRLET7B	406884		microRNA let-7b		186	0,493	0,769		0,01		1	1	0	2019	2019
Skin lesion	C0037284	LYZ	4069	P61626	lysozyme		178	0,526	0,846	3,411E-06	0,01		0	1	0	2015	2015
Skin lesion	C0037284	CRH	1392	P06850	corticotropin releasing hormone	Signaling	402	0,439	0,808	0,71614	0,01		1	1	0	2017	2017
Skin lesion	C0037284	MIR210	406992		microRNA 210		277	0,46	0,846		0,01		1	1	0	2020	2020
Skin lesion	C0037284	MIR223	407008		microRNA 223		348	0,433	0,808		0,01		1	1	0	2019	2019
Skin lesion	C0037284	MIR31	407035		microRNA 31		235	0,471	0,769		0,01		1	1	0	2014	2014
Skin lesion	C0037284	KRT16	3868	P08779	keratin 16		97	0,565	0,769	1,501E-14	0,01		1	1	0	2013	2013
Skin lesion	C0037284	KRT5	3852	P13647	keratin 5		203	0,512	0,731	0,64172	0,01		1	1	0	2004	2004
Skin lesion	C0037284	IRAK1	3654	P51617	interleukin 1 receptor associated kinase 1	Kinase	200	0,506	0,808	0,98774	0,01		1	1	0	2012	2012
Skin lesion	C0037284	IRF6	3664	O14896	interferon regulatory factor 6	Transcription factor	233	0,486	0,769	0,99961	0,01		1	1	0	2015	2015
Skin lesion	C0037284	IRS1	3667	P35568	insulin receptor substrate 1		233	0,488	0,769	0,023645	0,01		1	1	0	2014	2014
Skin lesion	C0037284	ITGA4	3676	P13612	integrin subunit alpha 4		123	0,558	0,769	0,0001007	0,01		1	1	0	2010	2010
Skin lesion	C0037284	ITGAE	3682	P38570	integrin subunit alpha E		95	0,579	0,692	3,92E-20	0,01		0	1	0	2016	2016
Skin lesion	C0037284	ITGAM	3684	P11215	integrin subunit alpha M		343	0,443	0,808	3,315E-11	0,01		1	1	0	2002	2002
Skin lesion	C0037284	ITGAX	3687	P20702	integrin subunit alpha X		170	0,504	0,769	1,367E-15	0,01		1	1	0	2018	2018
Skin lesion	C0037284	ITIH4	3700	Q14624	inter-alpha-trypsin inhibitor heavy chain 4	Enzyme modulator	129	0,559	0,769	6,435E-13	0,01		1	1	0	2002	2002
Skin lesion	C0037284	JUN	3725	P05412	Jun proto-oncogene, AP-1 transcription factor subunit	Transcription factor	344	0,442	0,885	0,05962	0,01		1	1	0	2006	2006
Skin lesion	C0037284	KISS1	3814	Q15726	KiSS-1 metastasis suppressor		179	0,507	0,808	0,49039	0,01		1	1	0	2004	2004
Skin lesion	C0037284	ARG1	383	P05089	arginase 1	Enzyme	273	0,476	0,846	0,0003594	0,01		1	1	0	2019	2019
Skin lesion	C0037284	KRAS	3845	P01116	KRAS proto-oncogene, GTPase	Enzyme modulator	1213	0,32	0,923	0,000788	0,01		1	1	1	2017	2017
Skin lesion	C0037284	SMAD3	4088	P84022	SMAD family member 3	Transcription factor	470	0,415	0,923	0,79796	0,01		1	1	0	2019	2019
Skin lesion	C0037284	MAS1	4142	P04201	MAS1 proto-oncogene, G protein-coupled receptor	G-protein coupled receptor	142	0,533	0,769	8,252E-05	0,01		1	1	0	2006	2006
Skin lesion	C0037284	NGF	4803	P01138	nerve growth factor	Signaling	616	0,391	0,885	0,82026	0,01		1	1	0	2018	2018
Skin lesion	C0037284	NOS2	4843	P35228	nitric oxide synthase 2		783	0,364	0,923	4,028E-15	0,01		1	1	0	2003	2003
Skin lesion	C0037284	NOS3	4846	P29474	nitric oxide synthase 3		706	0,378	0,885	6,725E-07	0,01		1	1	1	2008	2008
Skin lesion	C0037284	NRAS	4893	P01111	NRAS proto-oncogene, GTPase	Enzyme modulator	611	0,39	0,808	0,49009	0,01		1	1	0	2014	2014
Skin lesion	C0037284	OGG1	4968	O15527	8-oxoguanine DNA glycosylase		313	0,453	0,808	3,931E-12	0,01		1	1	2	2007	2007
Skin lesion	C0037284	CRNN	49860	Q9UBG3	cornulin	Calcium-binding protein	22	0,736	0,308	0,0001258	0,01		1	1	0	2019	2019
Skin lesion	C0037284	DEFB104B	503618	Q8WTQ1	defensin beta 104B		42	0,638	0,692	0,33176	0,01		1	1	0	2019	2019
Skin lesion	C0037284	REG3A	5068	Q06141	regenerating family member 3 alpha		148	0,522	0,769	0,000629	0,01		1	1	0	2012	2012
Skin lesion	C0037284	TMED7	51014	Q86XR7;Q9Y3B3	transmembrane p24 trafficking protein 7	Transporter	336	0,436	0,808	0,47966	0,01		1	1	0	2017	2017
Skin lesion	C0037284	CKLF	51192	Q9UBR5	chemokine like factor		36	0,682	0,538	0,0049483	0,01		1	1	0	2013	2013
Skin lesion	C0037284	TLR7	51284	Q9NYK1	toll like receptor 7		276	0,464	0,885	0,97912	0,01		1	1	0	2018	2018
Skin lesion	C0037284	TLR8	51311	Q9NR97	toll like receptor 8		122	0,543	0,769	0,32401	0,01		1	1	0	2017	2017

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Table S2. (continued)

Disease	Disease_id	Gene	Gene_id	UniProt	Gene_Full_Name	Protein_Class	N_diseases_g	DSI_g	DPI_g	pLI	Score_gda	EL_gda	EI_gda	N_PMIDs	N_SNPs_gda	First_Ref	Last_Ref
Skin lesion	C0037284	ATF1	466	P18846	activating transcription factor 1		88	0,588	0,577	0,63426	0,01		1	1	0	2019	2019
Skin lesion	C0037284	MYC	4609	P01106	MYC proto-oncogene, bHLH transcription factor	Transcription factor	821	0,344	0,923	0,99801	0,01		1	1	0	2017	2017
Skin lesion	C0037284	MC1R	4157	Q01726	melanocortin 1 receptor	G-protein coupled receptor	183	0,524	0,808	8,108E-11	0,01		1	1	0	2001	2001
Skin lesion	C0037284	MCL1	4170	Q07820	MCL1 apoptosis regulator, BCL2 family member	Signaling	375	0,43	0,808	0,96349	0,01		1	1	0	2003	2003
Skin lesion	C0037284	MET	4233	P08581	MET proto-oncogene, receptor tyrosine kinase	Kinase	594	0,38	0,846	0,96998	0,01		1	1	0	2016	2016
Skin lesion	C0037284	MFAP4	4239	P55083	microfibril associated protein 4	Signaling	31	0,691	0,462	0,11416	0,01		1	1	0	2019	2019
Skin lesion	C0037284	MKI67	4288	P46013	marker of proliferation Ki-67		351	0,431	0,808	1,26E-28	0,01		1	1	0	2013	2013
Skin lesion	C0037284	MME	4311	P08473	membrane metalloendopeptidase	Enzyme	470	0,407	0,808	1,465E-18	0,01		1	1	0	2019	2019
Skin lesion	C0037284	MMP1	4312	P03956	matrix metallopeptidase 1	Enzyme	589	0,385	0,885	7,72E-18	0,01		1	1	0	2003	2003
Skin lesion	C0037284	MPI	4351	P34949	mannose phosphate isomerase	Enzyme	101	0,585	0,654	1,172E-07	0,01		1	1	0	2017	2017
Skin lesion	C0037284	MPO	4353	P05164	myeloperoxidase	Enzyme	653	0,377	0,923	7,105E-15	0,01		1	1	0	2003	2003
Skin lesion	C0037284	COX2	4513	P00403	cytochrome c oxidase subunit II	Enzyme	875	0,352	0,962		0,01		1	1	0	2017	2017
Skin lesion	C0037284	MTRR	4552	Q9UBK8	5-methyltetrahydrofolate-homocysteine methyltransferase reductase		207	0,502	0,808	2,179E-14	0,01		1	1	1	2018	2018
Skin lesion	C0037284	MX1	4599	P20591	MX dynamin like GTPase 1	Enzyme modulator	71	0,599	0,731	3,421E-18	0,01		1	1	0	2019	2019
Skin lesion	C0037284	PDCD1	5133	Q15116	programmed cell death 1		497	0,402	0,846	0,41706	0,01		1	1	0	2018	2018
Skin lesion	C0037284	ALOX5	240	P09917	arachidonate 5-lipoxygenase	Enzyme	342	0,447	0,885	1,206E-06	0,01		1	1	0	2001	2001
Skin lesion	C0037284	GLI2	2736	P10070	GLI family zinc finger 2		351	0,446	0,846	0,97303	0,01		1	1	0	2019	2019
Skin lesion	C0037284	GLO1	2739	Q04760	glyoxalase I		137	0,537	0,769	9,672E-07	0,01		1	1	0	2018	2018
Skin lesion	C0037284	GLP1R	2740	P43220	glucagon like peptide 1 receptor	G-protein coupled receptor	288	0,471	0,846	0,29347	0,01		1	1	0	2019	2019
Skin lesion	C0037284	GNAS	2778	O95467;P63092;P84996;Q5JWF2	GNAS complex locus	Enzyme modulator	536	0,42	0,885	0,68076	0,01		0	1	0	2004	2004
Skin lesion	C0037284	SFN	2810	P31947	stratifin	Chaperone	105	0,561	0,769	0,36544	0,01		1	1	0	2011	2011
Skin lesion	C0037284	PGP	283871	A6NDG6	phosphoglycolate phosphatase	Enzyme	77	0,606	0,808	0,16263	0,01		1	1	0	2018	2018
Skin lesion	C0037284	ENDOV	284131	Q8N8Q3	endonuclease V		10	0,805	0,385	1,013E-09	0,01		1	1	0	2001	2001
Skin lesion	C0037284	MIF-AS1	284889		MIF antisense RNA 1		38	0,663	0,577		0,01		1	1	0	2018	2018
Skin lesion	C0037284	GPER1	2852	Q99527	G protein-coupled estrogen receptor 1	G-protein coupled receptor	180	0,505	0,731	0,57434	0,01		1	1	0	2017	2017
Skin lesion	C0037284	DPH3	285381	Q96FX2	diphthamide biosynthesis 3		10	0,821	0,077	0,066294	0,01		1	1	0	2015	2015
Skin lesion	C0037284	GRN	2896	P28799	granulin precursor		412	0,435	0,846	0,069666	0,01		1	1	0	2019	2019
Skin lesion	C0037284	CXCL1	2919	P09341	C-X-C motif chemokine ligand 1	Signaling	315	0,449	0,923	0,11845	0,01		1	1	0	2017	2017
Skin lesion	C0037284	ADAMDEC1	27299	O15204	ADAM like decysin 1	Enzyme	18	0,76	0,423	3,63E-16	0,01		1	1	0	2020	2020
Skin lesion	C0037284	IL17C	27189	Q9P0M4	interleukin 17C		61	0,619	0,692	0,0001243	0,01		1	1	0	2014	2014
Skin lesion	C0037284	VAMAS6	246319		Vitiligo		23	0,729	0,269		0,01		1	1	0	2020	2020
Skin lesion	C0037284	FUCA1	2517	P04066	alpha-L-fucosidase 1		103	0,623	0,577	2,696E-08	0,01		1	1	0	2018	2018
Skin lesion	C0037284	SETBP1	26040	Q9Y6X0	SET binding protein 1		257	0,503	0,808	1	0,01		1	1	0	2019	2019
Skin lesion	C0037284	PRPF31	26121	Q8WWY3	pre-mRNA processing factor 31	Nucleic acid binding	150	0,531	0,731	0,98313	0,01		1	1	0	2017	2017
Skin lesion	C0037284	ZNF658	26149	Q5TYW1	zinc finger protein 658	Transcription factor	2			9,041E-14	0,01		1	1	0	2017	2017
Skin lesion	C0037284	GATA2	2624	P23769	GATA binding protein 2		229	0,496	0,654	0,97927	0,01		1	1	0	2018	2018
Skin lesion	C0037284	GCGR	2642	P47871	glucagon receptor	G-protein coupled receptor	47	0,656	0,308	2,215E-06	0,01		1	1	0	2017	2017
Skin lesion	C0037284	NUPR1	26471	O60356	nuclear protein 1, transcriptional regulator		68	0,606	0,615	0,0041502	0,01		1	1	0	2019	2019
Skin lesion	C0037284	NPTN	27020	Q9Y639	neuroplastin	Receptor	40	0,67	0,5	0,99304	0,01		1	1	0	2019	2019
Skin lesion	C0037284	GJB3	2707	O75712	gap junction protein beta 3	Cell-cell junction	79	0,621	0,462	0,0021767	0,01		1	1	0	2005	2005
Skin lesion	C0037284	FOXP1	27086	Q9H334	forkhead box P1		317	0,46	0,808	0,99998	0,01		1	1	0	2014	2014
Skin lesion	C0037284	IL37	27178	Q9NZH6	interleukin 37		280	0,459	0,846	0,0001234	0,01		1	1	0	2018	2018
Skin lesion	C0037284	IL19	29949	Q9UHD0	interleukin 19		103	0,558	0,769	4,325E-05	0,01		1	1	0	2005	2005
Skin lesion	C0037284	HCCS	3052	P53701	holocytochrome c synthase	Enzyme	135	0,559	0,731	0,88624	0,01		1	1	0	2018	2018
Skin lesion	C0037284	IFI16	3428	Q16666	interferon gamma inducible protein 16	Transcription factor	79	0,603	0,769	1,78E-11	0,01		1	1	0	2013	2013
Skin lesion	C0037284	IFI27	3429	P40305	interferon alpha inducible protein 27		332	0,437	0,769	0,010698	0,01		1	1	0	2017	2017
Skin lesion	C0037284	IFNAR1	3454	P17181	interferon alpha and beta receptor subunit 1	Receptor	142	0,532	0,769	3,25E-12	0,01		1	1	0	2018	2018
Skin lesion	C0037284	IGF1	3479	P05019	insulin like growth factor 1		1206	0,318	0,885	0,2716	0,01		1	1	0	2018	2018
Skin lesion	C0037284	IGH	3492		immunoglobulin heavy locus		238	0,473	0,654		0,01		1	1	0	2018	2018

(continued)

Table S2. (continued)

Disease	Disease_id	Gene	Gene_id	UniProt	Gene_Full_Name	Protein_Class	N_diseases_g	DSI_g	DPI_g	pLI	Score_gda	EL_gda	EI_gda	N_PMIDs	N_SNPs_gda	First_Ref	Last_Ref
Skin lesion	C0037284	IGHG3	3502	P01860	immunoglobulin heavy constant gamma 3 (G3m marker)		161	0,513	0,769		0,01		1	1	0	2019	2019
Skin lesion	C0037284	TICAM2	353376	Q86XR7;Q9Y3B3	toll like receptor adaptor molecule 2		332	0,438	0,769	0,0025936	0,01		1	1	0	2017	2017
Skin lesion	C0037284	FAS	355	P25445	Fas cell surface death receptor		754	0,372	0,923	0,8117	0,01		1	1	0	2005	2005
Skin lesion	C0037284	IL2RB	3560	P14784	interleukin 2 receptor subunit beta	Receptor	226	0,491	0,846	0,29095	0,01		1	1	0	2018	2018
Skin lesion	C0037284	IL7	3574	P13232	interleukin 7		275	0,464	0,808	0,92574	0,01		1	1	0	2006	2006
Skin lesion	C0037284	IL11	3589	P20809	interleukin 11		244	0,481	0,808	0,0003177	0,01		1	1	0	2019	2019
Skin lesion	C0037284	IL12RB1	3594	P42701	interleukin 12 receptor subunit beta 1	Signaling	118	0,555	0,731	9,357E-15	0,01		1	1	0	2013	2013
Skin lesion	C0037284	IDH1	3417	O75874	isocitrate dehydrogenase (NADP(+)) 1		399	0,424	0,808	2,624E-12	0,01		1	1	0	2018	2018
Skin lesion	C0037284	STING1	340061	Q86WV6	stimulator of interferon response cGAMP interactor 1		159	0,522	0,769	0,0012067	0,01		1	1	0	2018	2018
Skin lesion	C0037284	HDAC1	3065	Q13547	histone deacetylase 1	Epigenetic regulator	277	0,46	0,846	0,61427	0,01		1	1	0	2012	2012
Skin lesion	C0037284	HDAC2	3066	Q92769	histone deacetylase 2	Epigenetic regulator	257	0,476	0,846	0,99997	0,01		1	1	0	2012	2012
Skin lesion	C0037284	HHEX	3087	Q03014	hematopoietically expressed homeobox		73	0,599	0,692	0,54289	0,01		1	1	0	2015	2015
Skin lesion	C0037284	ANXA6	309	P08133	annexin A6		156	0,514	0,846	1,08E-08	0,01		1	1	0	1998	1998
Skin lesion	C0037284	HLA-A	3105	P04439	major histocompatibility complex, class I, A		672	0,37	0,846	0,0013299	0,01		1	1	0	2011	2011
Skin lesion	C0037284	HLA-B	3106	P01889	major histocompatibility complex, class I, B		706	0,379	0,885	3,864E-05	0,01		1	1	1	2019	2019
Skin lesion	C0037284	HMGA1	3159	P17096	high mobility group AT-hook 1	Nucleic acid binding	206	0,494	0,769	0,83209	0,01		1	1	0	2018	2018
Skin lesion	C0037284	APEX1	328	P27695	apurinic/apyrimidinic endodeoxyribonuclease 1		305	0,458	0,846	1,919E-07	0,01		1	1	1	2007	2007
Skin lesion	C0037284	XIAP	331	P98170	X-linked inhibitor of apoptosis	Enzyme modulator	321	0,447	0,808	0,91837	0,01		1	1	0	2015	2015
Skin lesion	C0037284	HSP90AA1	3320	P07900	heat shock protein 90 alpha family class A member 1	Chaperone	455	0,411	0,923	0,86025	0,01		1	1	0	2018	2018
Skin lesion	C0037284	HTR7	3363	P34969	5-hydroxytryptamine receptor 7	G-protein coupled receptor	103	0,592	0,5	0,045409	0,01		1	1	0	2015	2015
Skin lesion	C0037284	TNC	3371	P24821	tenascin C		369	0,433	0,846	1,259E-07	0,01		1	1	0	2005	2005
Skin lesion	C0037284	CXCL10	3627	P02778	C-X-C motif chemokine ligand 10	Signaling	631	0,378	0,885	0,36865	0,01		1	1	0	2017	2017