

Identification of TNF-related apoptosis-inducing ligand and other molecules that distinguish inflammatory from resident dendritic cells in patients with psoriasis

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Background: Previous work has identified CD11c⁺CD1c⁻ dendritic cells (DCs) as the major “inflammatory” dermal DC population in patients with psoriasis vulgaris and CD1c⁺ DCs as the “resident” cutaneous DC population.

Objective: We sought to further define molecular differences between these 2 myeloid dermal DC populations.

Methods: Inflammatory and resident DCs were single-cell sorted from lesional skin biopsy specimens of patients with psoriasis, and the transcriptome of CD11c⁺CD1c⁻ versus CD1c⁺ DCs was determined. Results were confirmed with RT-PCR, flow cytometry, immunohistochemistry, and double-labeled immunofluorescence. Human keratinocytes were cultured for functional studies.

Results: TNF-related apoptosis-inducing ligand (TRAIL), Toll-like receptors 1 and 2, S100A12/ENRAGE, CD32, and many other inflammatory products were differentially expressed in inflammatory DCs compared with resident DCs. Flow cytometry and immunofluorescence confirmed higher protein expression on CD1c⁻ versus CD1c⁺ DCs. TRAIL receptors, death receptor 4, and decoy receptor 2 were expressed in keratinocytes and dermal cells. *In vitro* culture of keratinocytes with TRAIL induced CCL20 chemokine.

Conclusions: CD11c⁺CD1c⁻ inflammatory DCs in psoriatic lesional skin express a wide range of inflammatory molecules compared with skin-resident CD1c⁺ DCs. Some molecules made by inflammatory DCs, including TRAIL, could have direct

effects on keratinocytes or other skin cell types to promote disease pathogenesis. (J Allergy Clin Immunol 2010;■■■:■■■-■■■.)

Key words: TRAIL, psoriasis, dendritic cell, inflammation, CCL20, Toll-like receptor 1, Toll-like receptor 2, S100A12, CD32

In normal human skin CD11c⁺ myeloid dendritic cells (DCs) express the MHC class II–like lipid recognition protein CD1c/blood dendritic cell antigen 1.¹ However, CD1c is not a sensitive marker for cutaneous myeloid DCs during inflammation. We have recently characterized a population of “inflammatory” dermal CD1c⁻ myeloid DCs that infiltrate cutaneous lesions of patients with psoriasis, which is a prototypic inflammatory disease of the skin.² CD1c⁻ DCs are phenotypically immature and produce cytokines and inflammatory mediators, including TNF, inducible nitric oxide synthase (iNOS), IL-20,³ IL-23p19, and IL-12/IL-23p40.^{4,5} In addition, these inflammatory myeloid DCs induce allogeneic T-cell proliferation and polarize T cells toward T_H17 and T_H1, 2 types of T cells implicated in psoriasis.^{2,6,7}

Myeloid DCs are important bridges between the innate and adaptive immune systems, but their functions in many inflammatory diseases are still not entirely clear. In this study these inflammatory CD1c⁻ myeloid DCs were single-cell sorted from psoriatic lesional dermis and further characterized by means of microarray analysis to elucidate molecules associated with CD1c⁻ versus CD1c⁺ DCs and to determine what inflammatory mediators these cells might be producing. We are also seeking a more useful “positive” marker to be able to study these cells specifically rather than relying on a “negative” (CD1c⁻) definition.

In this study, we identified several differentially expressed gene products, including TNF-related apoptosis-inducing ligand (TRAIL), as selective markers for inflammatory myeloid DCs. TRAIL is a member of the TNF superfamily of cytokines that is involved in different kinds of inflammatory responses.⁸ TRAIL is a type II transmembrane protein, which can be cleaved at its C-terminus to form a soluble ligand, and both the membrane-bound and soluble forms can induce apoptosis.⁹ Multiple cell types at different stages of activation express TRAIL, including myeloid lineage cells (monocytes, DCs, and macrophages),¹⁰ plasmacytoid DCs,¹¹ natural killer (NK) T cells,¹² and T cells.¹³ Five TRAIL receptors have been identified in human subjects.^{14–16} Although TRAIL is best known for induction of apoptosis in tumor cells while sparing normal tissue,¹² it has also been implicated in inflammatory disease processes, including allergic asthma¹⁷ and

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Abbreviations used

DC:	Dendritic cell
DcR2:	Decoy receptor 2
DR4:	Death receptor 4
DR5:	Death receptor 5
iDC:	Immature dendritic cell
iNOS:	Inducible nitric oxide synthase
TLR:	Toll-like receptor
TRAIL:	TNF-related apoptosis-inducing ligand

atopic dermatitis.¹⁸ In this article we demonstrate that inflammatory DCs in patients with psoriasis vulgaris express TRAIL, lesional epidermal and dermal cells coexpress TRAIL receptors, and the addition of TRAIL to keratinocytes induces CCL20. Thus, TRAIL and other differentially expressed molecules identified in inflammatory DCs might be direct inflammatory mediators in the skin. In addition, these markers provide a means to isolate different DC populations for future functional studies.

METHODS**Skin samples**

Skin biopsy specimens were obtained from healthy volunteers and patients with psoriasis under a Rockefeller University Institutional Review Board–approved protocol. Written informed consent was obtained, and the study was performed in adherence with the Declaration of Helsinki principles. Lesional and nonlesional psoriasis punch biopsy skin samples were used for immunohistochemistry and immunofluorescence. Dermal single-cell suspensions from shave biopsy specimens of patients with psoriasis were obtained after removing the epidermis with dispase and culturing the dermis for 2 to 3 days, as previously described.²

FACS

FACS sorting of dermal single-cell suspensions was performed as previously described² by using a FACS Aria (BD Biosciences, San Jose, Calif). Dermal cells were sorted into 2 populations, CD11c⁺CD163[−]HLA-DR⁺CD1c⁺ and CD11c⁺CD163[−]HLA-DR⁺CD1c[−] (n = 4), to 99% purity. Seven psoriatic DC samples were obtained: 3 paired CD1c^{+/−} DC samples and an additional unpaired CD1c[−] sample. FACS-sorted cells were processed for microarray as biological replicates. FACS phenotyping of dermal single-cell suspensions was performed on an LSR-II (BD Biosciences; n = 3). Antibodies used are outlined in Table E1 in this article's Online Repository at www.jacionline.org.

Cell culture of myeloid cells to determine their transcriptome

We have previously published the transcriptomes of the myeloid cells used for principal component analysis (see Fig E1 in this article's Online Repository at www.jacionline.org).¹⁹ Macrophages, immature dendritic cells (iDCs), and mature DCs were prepared in a standard manner from monocytes and RNA hybridized to HGU95 chips. To apply principal component analysis to our experimental samples on an Affymetrix Hu133A2.0 platform and previously published cell lineage data on an Affymetrix HGU95av2 platform,¹⁹ probe sets were averaged to obtain a unique expression for each gene.

Microarray hybridization

CD1c⁺ and CD1c[−] DCs were FACS sorted directly into Trizol (Invitrogen, Carlsbad, Calif). RNA was extracted with the RNeasy Mini Kit (Qiagen, Hilden, Germany), the GeneChip 2-cycle target labeling kit (Affymetrix, Santa Clara, Calif) was used, and fragmented cRNA were then

hybridized to HGU133A Affymetrix gene chips, as previously described.²⁰ The data discussed in this publication have been deposited in the National Center for Biotechnology Information's Gene Expression Omnibus and are accessible through Gene Expression Omnibus Series accession number GSE20264.

RT-PCR

RT-PCR was performed with EZ PCR core reagents, primers, and probes (Applied Biosystems, Foster City, Calif), as previously published.²¹ Primer and probe sets used were Toll-like receptor (TLR) 1 (Hs00413978_m1), TLR2 (Hs00152932_m1), TRAIL (Hs00234355_m1), S100A12 (Hs00194525_m1), CD32 (Hs00234969_m1), and CCL20 (Hs00171125_m1). A custom probe for human acidic ribosomal protein was used as a housekeeping gene.²¹

Immunohistochemistry and immunofluorescence

These techniques were performed in a standard manner, as previously described.⁴ Each staining was performed on 3 to 5 patient samples. Antibodies used are outlined in Table E1. All immunofluorescence images are from lesional skin. In all immunofluorescence figures, single-stained controls are above the merged image, the white line denotes the dermoepidermal junction, dermal collagen fibers produce green autofluorescence, and antibodies conjugated with a fluorochrome often produce background epidermal fluorescence.

CCL20 detection in TRAIL-treated cultured keratinocytes

Primary pooled human keratinocytes (n = 4) were obtained from the Yale Skin Diseases Research Center core facility. Keratinocytes were cultured in EpiLife medium with defined growth supplement (Cascade Biologics, Portland, Ore) at 37°C. Once 80% confluent, cytokines were added to keratinocytes and harvested after 24 hours. Cytokines added were rh-TRAIL (Peprotech, Inc, Rocky Hill, NJ) at 0.1, 1, 10, and 100 ng/mL, TNF (R&D Systems, Minneapolis, Minn) at 10 ng/mL, and etanercept (Enbrel; Amgen, Thousand Oaks, Calif) at 10 µg/mL. Concentrations of CCL20 in cell-free supernatants of TRAIL-treated keratinocytes were measured with the Quantikine Human CCL20/macrophage inflammatory protein 3α ELISA (R&D Systems).

Statistics

The 2-tailed Wilcoxon signed rank test was used to compare lesional versus nonlesional mRNA expression and control versus TNF- or TRAIL-treated keratinocytes. A *t* test was also used to compare the effects of TRAIL and other mediators on CCL20 protein. Effect size was calculated by subtracting control CCL20 protein from the mediator added. A moderated paired *t* test, which is available in limma package from R/Bioconductor (<http://www.bioconductor.org/>), was used to compare microarray data from CD1c[−] with CD1c⁺ DCs. For multiple hypotheses testing, the false discovery rate was controlled by using the Benjamini-Hochberg procedure. Genes were considered significant if they had a fold change of greater than 3 and a false discovery rate of less than 0.2 (maximum observed *P* value = .03, using ENTREZ identifiers) and then matched between the 2 platforms.

RESULTS**CD11c⁺CD1c[−] inflammatory DCs were closely related to CD1c⁺ resident DCs and *in vitro*-derived immature DCs**

We analyzed the transcriptome of these CD1c[−] DCs from psoriatic lesions together with the transcriptomes of other *in vitro*-derived myeloid cells¹⁹ using principal component analysis. Principal component analysis is a data analysis algorithm to

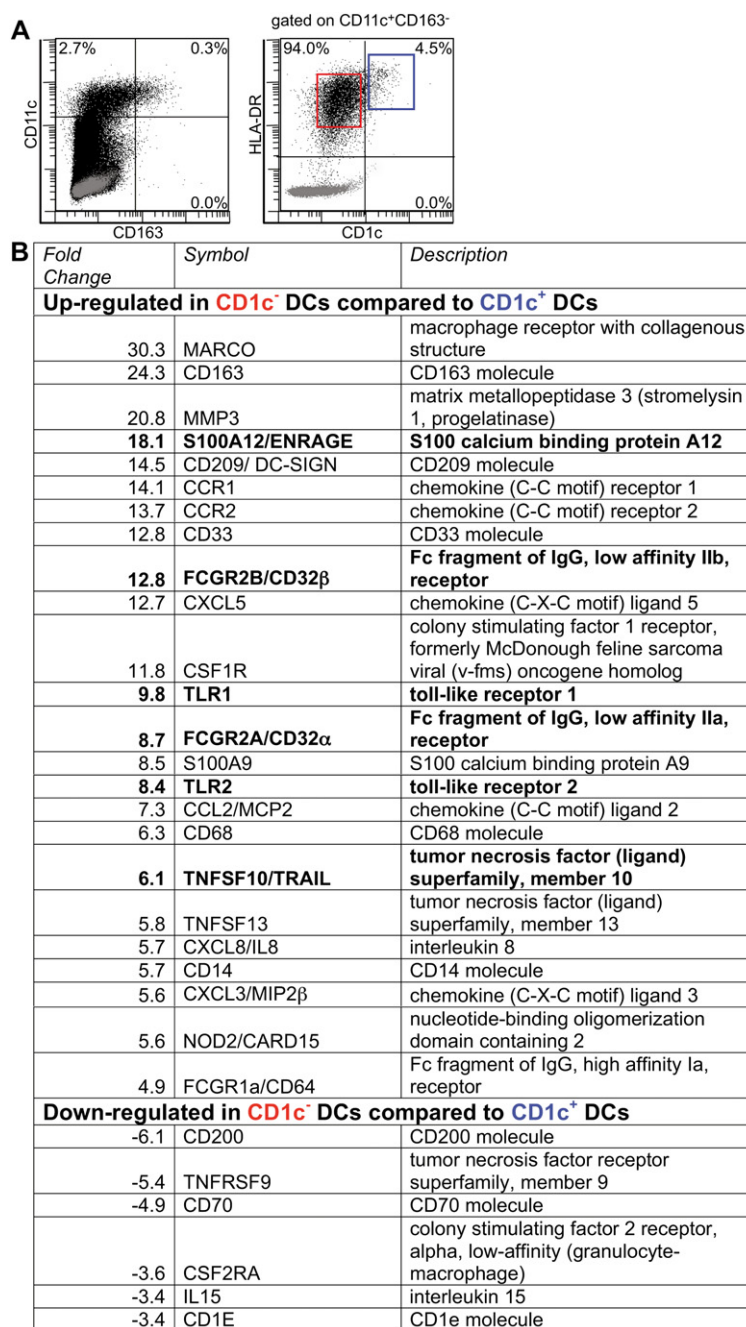


FIG 1. Transcriptome of CD1c⁻ DCs versus resident CD1c⁺ DCs from psoriatic dermis. **A**, Gating strategy used for cell sorting. HLA-DR⁺CD11c⁺CD163⁻ myeloid DCs were sorted into CD1c⁻ (red gate) and CD1c⁺ (blue gate) populations. **B**, Selected upregulated and downregulated inflammatory molecules from the transcriptome of CD1c⁻ DC populations. The full list of differentially expressed genes can be found in Table E2.

visually assess similarities and differences between samples.²² The genomic similarity of these different cell types is represented in a 2-dimensional map (see Fig E1). Although the grouping of similar samples was expected, this analysis showed that there was a clear (right-to-left) progression from *in vitro*-derived macrophages and *in vitro*-derived iDCs to psoriatic CD1c⁻ DCs, psoriatic CD1c⁺ DCs, and *in vitro*-derived mature DCs. Monocytes were located far away from this “line” as a negative control. CD1c⁻ DCs were most closely related to CD1c⁺ DCs followed by iDCs.

The CD1c⁻ DC subset in patients with psoriasis expressed inflammatory genes, including TRAIL, TLR1/2, S100A12, and CD32

The gating strategy to obtain pure CD11c⁺CD163⁻HLA-DR⁺CD1c⁻ (n = 4) and CD11c⁺CD163⁻HLA-DR⁺CD1c⁺ (n = 3) populations is shown in Fig 1, A. Gene array analysis was performed to compare the 2 DC populations by using a fold change of greater than 3 ($P < .03$) and a false discovery rate of less than 0.2. We found that 555 genes were upregulated and 131 genes were downregulated in the CD1c⁻ DC population

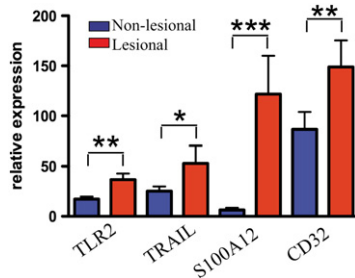


FIG 2. RT-PCR of genes differentially upregulated in CD1c⁺ DCs in non-lesional and lesional psoriatic skin. TLR2, TRAIL, S100A12, and CD32 were upregulated in lesional psoriatic skin (n = 11). Error bars indicate standard errors of the mean. **P* < .05, ***P* < .01, and ****P* < .001.

compared with the CD1c⁺ DC population (see Table E2 in this article's Online Repository at www.jacionline.org). From this list, we selected known inflammatory genes of interest and found that the majority of these genes were upregulated in the CD1c⁺ population (Fig 1, B), supporting prior observations that the CD1c⁺ DC subset is inflammatory in function.² Of particular interest were the inflammatory mediators TRAIL/Tumor necrosis factor ligand superfamily, member 10 (TNFSF10) and S100A12/Extracellular newly identified RAGE-binding protein (ENRAGE) (fold change of 6.1 and 18.1, respectively). Notable receptor genes included TLR1 and TLR2, the Fc fragment of IgG, and low-affinity IIa and IIb receptors (FCγR2a/CD32a and FCγR2b/CD32b; fold change of 9.8, 8.4, 8.7, and 12.8, respectively). Although our single-cell sorting strategy gated out CD163 protein-expressing macrophages, CD163 mRNA was expressed in CD1c⁺ DCs (fold change of 24.3). In addition, CCR2 monocyte chemotactic receptor and the intracellular pattern-recognition receptor nucleotide-binding oligomerization domain protein 2 were expressed in CD1c⁺ myeloid DCs (fold change of 13.7 and 5.6, respectively).

We verified that these genes were potentially important inflammatory mediators in patients with psoriasis by performing RT-PCR for these genes in additional nonlesional and lesional paired biopsy specimens (n = 11 pairs). TLR2, TRAIL, S100A12, and CD32 were significantly upregulated in lesional psoriatic skin compared with nonlesional skin (Fig 2). TLR1 expression was not significantly different in lesional versus nonlesional skin (data not shown).

TRAIL identified the CD11c⁺CD1c⁺ inflammatory DC population

We determined the relative protein expression of TRAIL, TLR1, TLR2, CD68, CD14, and CD209 on CD1c⁺ versus CD1c⁺ dermal DCs by using 8-color FACS analysis (n = 3). Representative FACS plots of single-cell suspensions from psoriatic lesional biopsy specimens are shown in Fig 3. As in the sorting experiments, both CD1c⁺ and CD1c⁺ DC populations were gated on CD11c⁺CD163⁺HLA-DR⁺ cells. We confirmed the gene array expression data that each of these markers was more highly expressed in CD1c⁺ cells compared with CD1c⁺ cells. TRAIL was the most consistent marker for CD1c⁺ inflammatory DCs, which were expressed at a high level on nearly all CD1c⁺ cells. One log difference in level of expression of TRAIL by means of FACS would allow cell sorting to obtain a pure population of

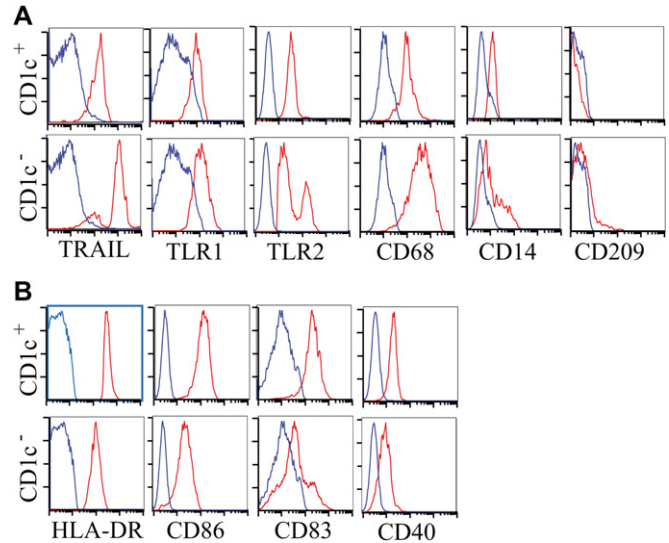


FIG 3. Flow cytometric analysis of psoriatic dermal single-cell suspensions. **A**, CD1c⁺ DCs (bottom row) express higher levels of TRAIL, TLR1, TLR2, CD68, CD14, and CD209 compared with CD1c⁺ DCs (top row). **B**, CD1c⁺ DCs express comparatively higher levels of the DC maturation antigens HLA-DR, CD86, CD83, and CD40. The red histogram represents antigen expression gated on HLA-DR⁺CD11c⁺CD163⁺CD1c⁺ DCs, and the blue histogram is the isotype.

these DCs for further study. TLR2 was expressed at a high level on CD1c⁺ cells but was not highly expressed on CD1c⁺ cells (Fig 3, A). CD1c⁺ DCs expressed higher levels of the DC maturation markers HLA-DR, CD86, CD83, and CD40 compared with CD1c⁺ DCs (Fig 3, B).

We confirmed that TRAIL⁺ cells were localized to the papillary dermis and at the dermal-epidermal junction in lesional psoriatic skin but not in nonlesional skin (Fig 4, A), and TRAIL was expressed by many CD11c⁺ DCs and few CD1c⁺ cells (Fig 4, B). TLR1 (see Fig E2, A, in this article's Online Repository at www.jacionline.org) and TLR2 (see Fig E2, B) also localized to the papillary dermis and dermoepidermal junction in psoriatic lesional skin but not in nonlesional skin, as determined by means of immunohistochemistry. The majority of CD11c⁺ DCs coexpressed TLR1 and TLR2, but no CD1c⁺ cells expressed TLR1 or TLR2. S100A12 was expressed in both lesional and nonlesional keratinocytes and in dermal cells (see Fig E2, C). The majority of S100A12-producing dermal cells expressed CD11c, but very few coexpressed CD1c. CD32 was expressed by papillary dermal cells in both lesional and nonlesional skin (see Fig E2, D). In addition, CD32 was expressed by cells scattered throughout the epidermis and in the reticular dermis of lesional skin. We found that CD32 was expressed by both CD11c⁺ and CD1c⁺ cells.

Characterization of TRAIL⁺ cells and TRAIL receptor-positive cells

TRAIL⁺ cells coexpressed blood-derived antigen CD45, suggesting that TRAIL was only produced by bone marrow-derived leukocytes (Fig 4, C). The majority of TRAIL⁺ cells coexpressed the MHC class II molecule HLA-DR (Fig 4, D), and some TRAIL⁺ cells were also CD3⁺, indicating they were T cells (Fig 4, E). Only occasional CD163⁺ macrophages expressed TRAIL (see Fig E3 in this article's Online Repository at www.jacionline.org).

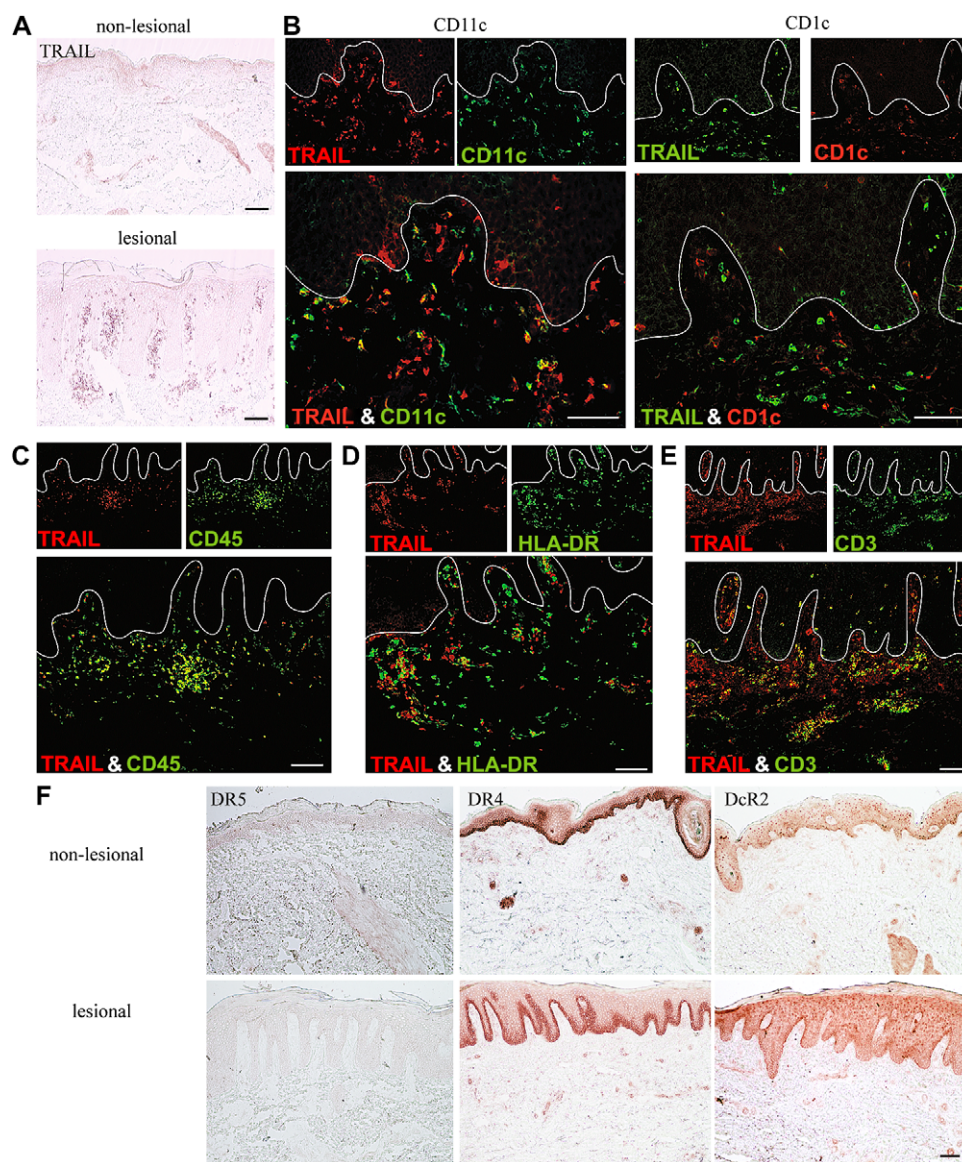


FIG 4. Lesional $CD11c^{+}CD1c^{-}$ DCs expressed TRAIL, and keratinocytes expressed TRAIL receptors. **A**, TRAIL antigen was present in lesional dermis. **B**, The majority of lesional $CD11c^{+}$ cells expressed TRAIL, whereas few cells coexpressed TRAIL and CD1c. **C-E**, Many TRAIL⁺ cells expressed CD45 (Fig 4, C) and HLA-DR (Fig 4, D), and some T cells expressed TRAIL (Fig 4, E). **F**, There was no expression of DR5 but abundant DR4 and some expression of DcR2. Bar = 100 μ m.

[jacionline.org](http://www.jacionline.org)). Thus the majority of TRAIL expression in psoriatic skin localized to $CD11c^{+}CD1c^{-}$ inflammatory DCs.

To determine the potential site of action of TRAIL in psoriatic skin, we evaluated the expression of its activating receptors, death receptor 5 (DR5), death receptor 4 (DR4), and decoy receptor 2 (DcR2; Fig 4, F). Ligand of DR5 and DR4 might more commonly induce apoptosis but also inflammation, whereas DcR2 lacks an apoptosis domain and causes cell inflammation through nuclear factor κ B.¹⁴⁻¹⁶ In both nonlesional and lesional skin, DR5 was not expressed, but DR4 and DcR2 were localized to basal keratinocytes and dermal cells. Few $CD11c^{+}$ cells expressed DR4 (see Fig E4, A, in this article's Online Repository at www.jacionline.org), and there was no overlap between DR4 and either CD3 (see Fig E4, B) or CD163 (see Fig E4, C). In the dermis there was nearly complete overlap between DR4 and the blood vessel

markers vimentin and CD31 and growth receptor insulin-like growth factor 1 receptor b (see Fig E4, D-F).

TRAIL⁺ cells produced IL-23p19 and IL-12/IL-23p40 cytokine subunits, as well as iNOS and TNF

We further characterized the myeloid DC subsets in psoriatic lesions using double-labeled immunofluorescence (Fig 5). The resident myeloid DCs ($CD11c^{+}$) expressed IL-23p19 but not IL-12/23p40 (Fig 5, A), whereas the inflammatory subset identified by CD11c expressed both IL-23 subunits (Fig 5, B).^{4,5} Many IL-12/23p40- and IL-23p19-expressing cells also expressed TRAIL (Fig 5, C), and some TRAIL⁺ cells expressed iNOS and TNF (Fig 5, D). Results are summarized in Table E3 (available in this article's Online Repository at www.jacionline.org).

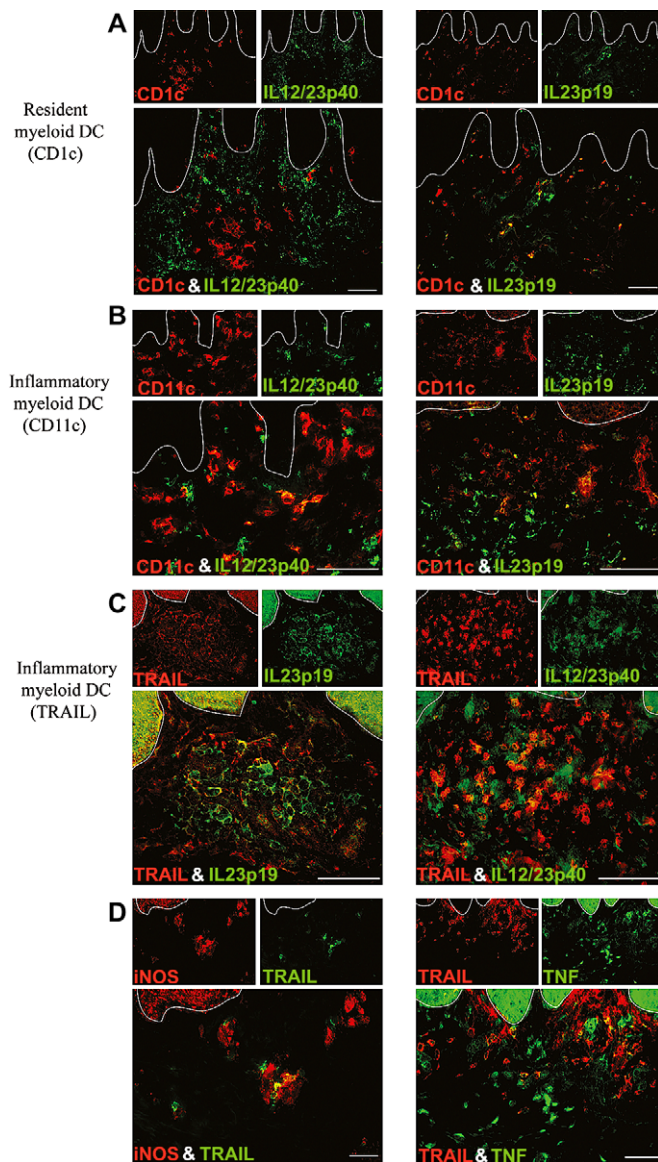


FIG 5. Expression of the T_H17 -polarizing cytokines IL-23p40 and IL-12/IL-23p19 in cutaneous DCs in patients with psoriasis. **A**, $CD1c^+$ resident DCs did not express IL-12/23p40 but did express IL-23p19. **B**, Inflammatory myeloid DCs ($CD11c^+$) expressed both IL-23 subunits. **C** and **D**, $TRAIL^+$ cells coexpressed some IL-12/IL-23p40 and IL-23p19, as well as iNOS and TNF. Bar = 100 μm .

Thus $TRAIL^+$ cells are likely a subset of inflammatory myeloid DCs that contribute to pathogenesis in patients with psoriasis by producing these inflammatory mediators.

TRAIL induced CCL20 in human cultured keratinocytes

Pooled human keratinocytes ($n = 3$) were cultured with recombinant human TRAIL to start to evaluate the potential function of TRAIL in the skin. TRAIL induced dose-dependent CCL20 expression in cultured keratinocytes, although TNF induced 10-fold more CCL20 mRNA expression than 100 ng/mL TRAIL (see Fig E5, A, in this article's Online Repository at www.jacionline.org). A second set of experiments ($n = 3$) was performed to analyze the production of CCL20 protein by

TRAIL. In Fig E5, B, addition of each agent was compared with saline to determine the difference from control. There was some background CCL20 produced (mean, 38 pg/mL), most likely due to endogenous TNF production, because there was a reduction in CCL20 production with the addition of etanercept (to a mean of 22 pg/mL, $P = .1$). There was an increase in the production of CCL20 by TRAIL (56 pg/mL) compared with control values ($P = .3$), but it was greater in magnitude compared with that seen with etanercept alone ($P = .12$). TRAIL appears to induce some TNF because the addition of etanercept decreased the amount of CCL20 produced (43 pg/mL). TNF induced a greater increase in CCL20 levels (179 pg/mL) compared with control values ($P = .13$), and this was almost completely abolished by etanercept (14 pg/mL).

DISCUSSION

In this study, we have identified novel molecular markers of different DC subsets in patients with psoriasis, a common human inflammatory skin disease. These markers were initially identified in the transcriptome of FACS-sorted, dermal single-cell suspensions from inflamed human skin, and expression was confirmed *in situ*. This approach has led to identification of new molecules that are associated with infiltrating leukocytes in patients with psoriasis, and it has expanded our understanding of how $CD11c^+CD1c^-$ DCs might contribute to inflammation in human skin.

We first studied TRAIL as an example of how the list of $CD1c^-$ differentially expressed genes could be used to dissect pathogenic mechanisms of these inflammatory myeloid DCs. TRAIL is best known as an apoptosis-inducing ligand that selectively "kills" tumor cells.¹² In basal cell carcinomas treated with the TLR7/8 agonist imiquimod, TRAIL acted as a cytotoxic molecule.¹¹ During the basal cell carcinoma regression phase, imiquimod-treated, DR4-expressing tumor islets were surrounded by an inflammatory infiltrate containing TRAIL-expressing $CD11c^+$ myeloid DCs, plasmacytoid DCs, and T cells. In vitiligo, TRAIL was proposed to cause apoptosis of melanocytes, resident skin pigment-producing cells. $TRAIL^+CD11c^+$ DCs surrounded depigmented plaques, and both TRAIL and *in vitro*-derived $TRAIL^+$ DCs were cytotoxic to cultured melanocytes.²³

However, recent studies on murine models of allergic asthma have suggested a potential inflammatory role for TRAIL in immune-mediated diseases. In both human asthmatic subjects and an allergen-specific airway hyperreactivity murine model, TRAIL was overexpressed in asthmatic sputum and the bronchial epithelium, respectively. In mice deficient for TRAIL, this allergen-specific airway hyperreactivity was abolished secondary to diminished T-cell trafficking to the lungs.¹⁷ TRAIL and S100A12, both products of inflammatory DCs, potentiate inflammation by upregulating blood vessel leukocyte adhesion molecules, and TRAIL promotes vascular proliferation.²⁴⁻²⁶

There is a third proposed role for TRAIL: that of an anti-inflammatory agent. In patients with atopic dermatitis but not in healthy control subjects, TRAIL was expressed in blood mononuclear cells, T cells, eosinophils, and neutrophils and in cutaneous T cells. Expression of TRAIL in myeloid DCs was not assessed. The investigators proposed an anti-inflammatory function for TRAIL in human skin, demonstrating that TRAIL induced IL-1 receptor antagonist expression in cultured human keratinocytes.¹⁸

Although alternate functions of TRAIL in patients with cutaneous diseases have been proposed, the expression in psoriasis is most consistent with its proinflammatory or cell-damaging effects in other systems.

CCL20, a potent T-cell and DC chemokine, was expressed by bronchial epithelial cells in a TRAIL-dependent manner.¹⁷ Our studies support a similar mechanism of TRAIL-dependent inflammation in psoriatic skin. The TRAIL receptors DR4 and DcR2 were expressed on psoriatic basal keratinocytes, and recombinant human TRAIL induced CCL20 in cultured human keratinocytes. TRAIL might function as an inducer of CCL20 and subsequent T-cell and DC chemotaxis to sites of inflammation, although the biological relevance of the induction of CCL20 by TRAIL remains to be determined.

Thus, TRAIL might contribute to leukocyte trafficking and transmigration through induction of CCL20 in keratinocytes, endothelial cell integrin and selectin upregulation, and insulin-like growth factor 1 receptor b-dependent vascular smooth muscle cell proliferation. In psoriatic skin, there is no evidence for keratinocyte or vessel apoptosis²⁷; however, there is upregulated blood vessel integrin and selectin expression.^{28,29} TRAIL-induced vascular hyperproliferation might contribute to the psoriatic phenotype of supra-abundant ectatic blood vessels coursing through the papillary dermis.³⁰ Therefore, we propose a unifying hypothesis whereby TRAIL production by inflammatory myeloid DCs acts on TRAIL receptors on keratinocytes, vascular smooth muscle cells, and endothelial cells to induce secretion of CCL20, proliferation of blood vessels, and induction of E-selectin and intercellular adhesion molecule 1 expression (see Fig E6 in this article's Online Repository at www.jacionline.org).

Other molecules in the molecular characterization of inflammatory myeloid DCs that are of great interest include TLR1, TLR2, S100A12, and CD32. We confirmed these genes were specific to CD11c⁺ cells and not CD1c⁺ cells in patients with psoriasis by means of immunofluorescence. TLR1/2 molecules are very interesting because they are the receptors for *Listeria monocytogenes*, and infection in mice with this agent induced TNF and iNOS-producing DCs,³¹ which we described in patients with psoriasis and consider a subset of inflammatory myeloid DCs.^{2,32} DCs coexpress the activating (CD32a) and inhibitory (CD32b) isoforms of IgG FcR II (CD32). The balance between these receptors controls DC activation, maturation, and function.³³ Further studies will be required to determine whether and how these molecules function in cell-mediated inflammatory skin diseases.

We have now identified a number of positive surface markers that distinguish "inflammatory" DCs from "resident" CD1c⁺ DCs in human skin. These markers need to be studied on DC subsets that accumulate in different inflammatory conditions, such as atopic dermatitis or Crohn disease, to determine whether they are restricted to specific disease tissues or different types of cell-mediated inflammation (T_H1/T_H17 vs T_H2). Our transcriptome also identified a wide set of molecules in *bona fide* inflammatory DCs that should be compared with molecules induced during *in vitro* manufacture of DCs with various cytokines and ligands. These markers give the potential to more easily sort distinct DC subsets for functional studies. Furthermore, these molecules identify potential therapeutic targets to prevent the development or emigration of pathogenic myeloid DCs into the skin for the prevention or treatment of psoriasis.

We thank the Yale Skin Diseases Research Center core facility for primary pooled human keratinocytes.

Clinical implications: Inflammatory myeloid dermal DCs in patients with psoriasis expressed TRAIL, TLR1, TLR2, S100A12, CD32, and many other inflammatory cytokines and receptors. These molecules could contribute to many different inflammatory pathways, and they form a basis for discriminating 2 key DC populations in the skin.

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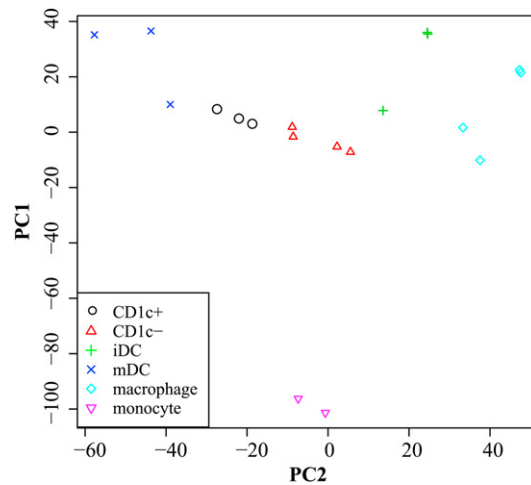


FIG E1. CD1c⁻ DCs were most similar to CD1c⁺ DCs and iDCs. There was a clear (right-to-left) progression in the principal component (PC) analysis from macrophages (blue diamonds) and iDCs (green crosses) to psoriatic CD1c⁻ DCs (red triangles), psoriatic CD1c⁺ DCs (black circles), and mature DCs (blue crosses). Monocytes were located far away from this "line" (pink triangles).

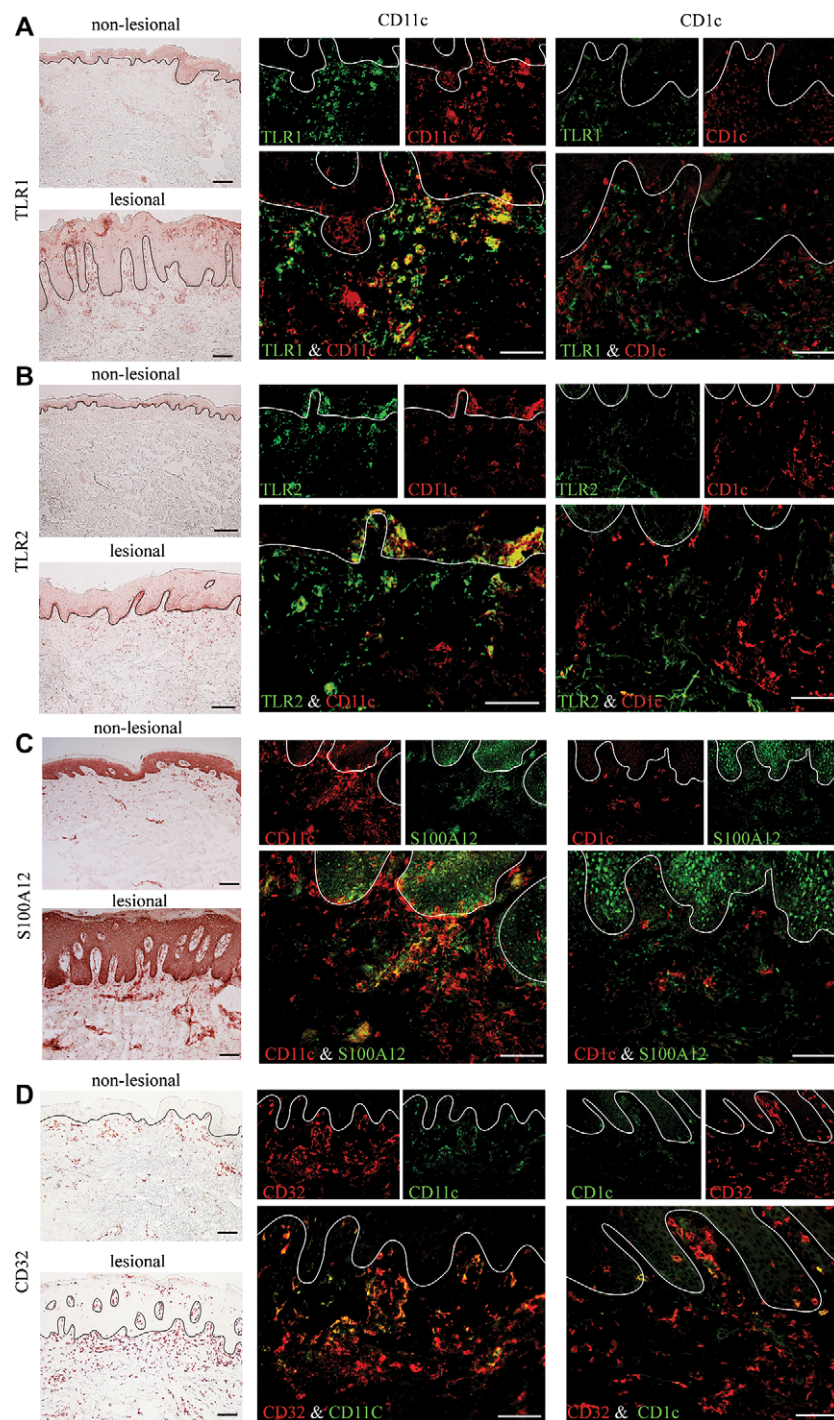


FIG E2. Lesional $CD11c^{+}CD1c^{-}$ DCs expressed TLR1, TLR2, S100A12, and CD32. **A** and **B**, TLR1 (Fig E2, A) and TLR2 (Fig E2, B) were coexpressed by most $CD11c^{+}$ cells but not by $CD1c^{+}$ cells. **C**, Many S100A12 $^{+}$ cells expressed CD11c, but very few coexpressed CD1c. **D**, CD32 was expressed by papillary dermal cells and was expressed by most $CD11c^{+}$ and few $CD1c^{+}$ cells. Bar = 100 μ m.

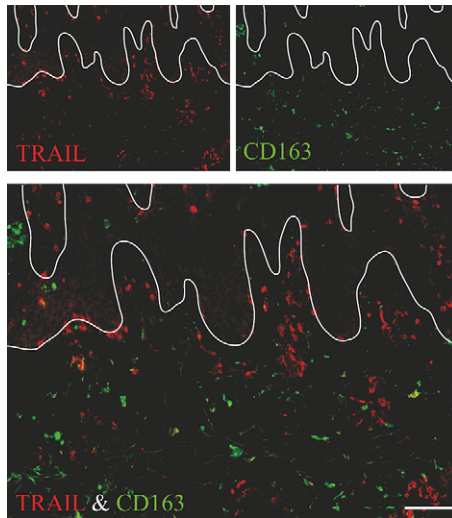


FIG E3. Expression of TRAIL on lesional macrophages. Only occasional CD163⁺ macrophages expressed TRAIL. *Bar* = 100 μ m.

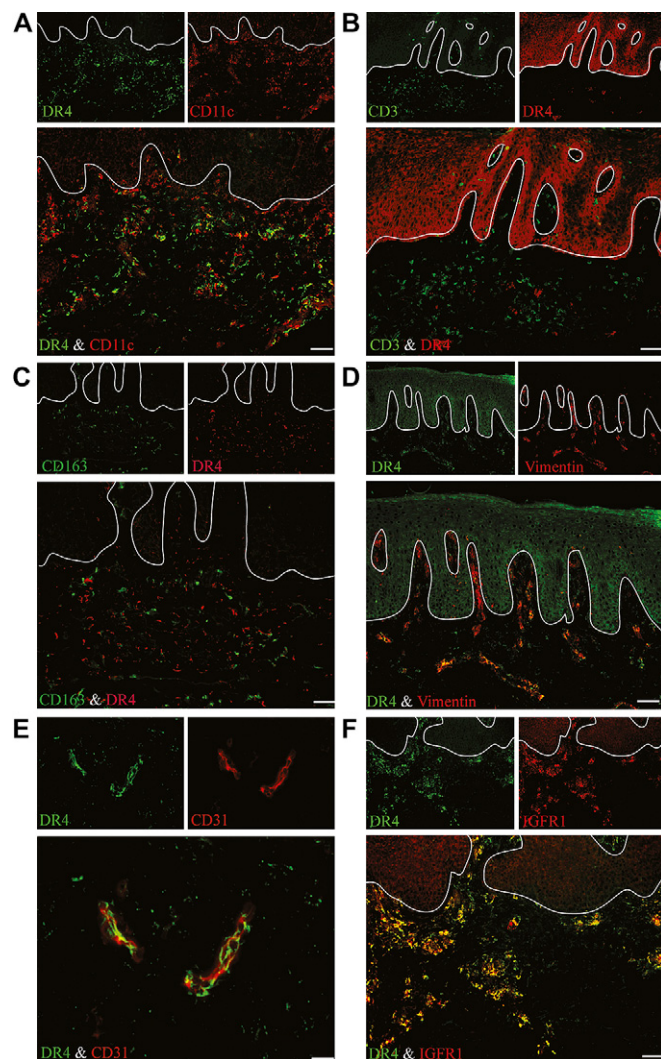


FIG E4. The TRAIL receptor DR4 was expressed on lesional keratinocytes and blood vessels. **A-C**, DR4 was expressed on CD11c⁺ cells (Fig E4, A) but not on CD3⁺ T cells (Fig E4, B) or CD163⁺ macrophages (Fig E4, C). **D-F**, DR4 colocalized with the blood vessel antigens vimentin (Fig E4, D) and CD31 (Fig E4, E) and the growth receptor insulin-like growth factor 1 receptor b (IGFR1) (Fig E4, F). Bar = 100 μ m.

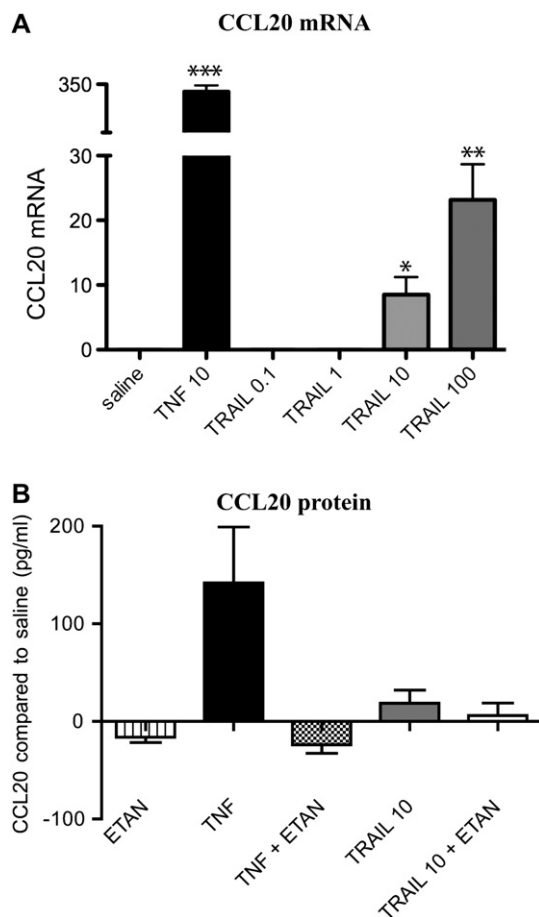


FIG E5. TRAIL induced CCL20 in cultured human keratinocytes. rh-TRAIL or TNF (in nanograms per milliliter) was cultured with pooled human keratinocytes ($n = 3$) for 24 hours, and normalized CCL20 mRNA (**A**) and protein (**B**) expression were measured. CCL20 protein was expressed as change from control value. * $P < .05$, ** $P < .01$, and *** $P < .001$.

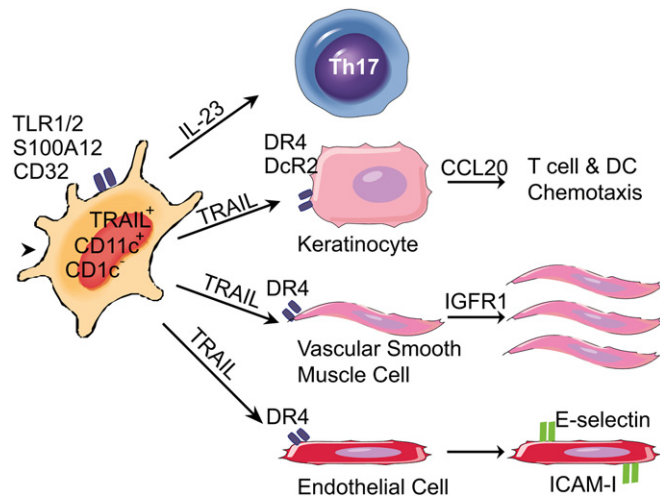


FIG E6. Hypothesis for the role of TRAIL-expressing inflammatory DCs in psoriasis pathogenesis. TRAIL has downstream effects on keratinocytes (CCL20 induction and resultant leukocyte chemotaxis), vascular smooth muscle cells (insulin-like growth factor 1 receptor b induction and subsequent vascular smooth muscle cell proliferation), and endothelial cells (intercellular adhesion molecule 1 [*ICAM-1*] and E-selectin induction and leukocyte transmigration). CD1c⁻TRAIL⁺ inflammatory DCs also express receptors (TLR1/2 and CD32) and inflammatory molecules (S100A12 and IL-23) that potentiate innate and adaptive immunity.

TABLE E1. Reagents and concentrations used for flow cytometry, immunohistochemistry, and immunofluorescence

Name	Vendor	Clone	Isotype	Concentration
Antibodies for flow cytometry and intracellular cytokine detection				
CD11c	BD Biosciences	B-ly6	IgG1	1:100
CD163	Acris Antibodies GmbH	5C6-FAT	IgG1	1:20
HLA-DR	BioLegend	L243	IgG2a	1:50
CD1c	Miltenyi Biotec	AD5-8E7	IgG2a	1:33
TRAIL	R&D Systems	75402.11	IgG1	1:20
TLR1	BioLegend	TLR1.136	IgG1	1:20
TLR2	BioLegend	TL2.1	IgG2a	1:20
CD68	BD Biosciences	Y1/82a	IgG2b	1:20
CD14	BD Biosciences	MoP9	IgG2b	1:20
CD209	BD Biosciences	DCN46	IgG2b	1:20
CD86	BioLegend	IT2.2	IgG2b	1:50
CD83	BD Biosciences	HB15a	IgG2b	1:20
CD40	BD Biosciences	5C3	IgG1	1:20
Antibodies for immunohistochemistry and immunofluorescence				
TLR1	MBL	GD2.F4	IgG1	1:50
TLR2	BioLegend	T2.5	IgG1	1:50
CD11c	BD Biosciences	B-ly6	IgG1	1:100
CD1c	Miltenyi Biotec	AD5-8E7	IgG2a	1:100
TRAIL	R&D Systems	75402.11	IgG1	1:50
S100A12	Abcam	19F5	IgG1	1:50
CD32	BD Biosciences	FLI8.26	IgG2b	1:100
CD45	BD Biosciences	H130	IgG1	1:100
HLA-DR	BD Biosciences	L243	IgG2a	1:100
CD3	BD Biosciences	SK7	IgG1	1:100
CD163	Acris	5C6-FAT	IgG1	1:100
IL-23p19	BioLegend	HLT2736	IgG1	1:50
IL-12/23p40	BioLegend	C11.5	IgG1	1:50
DR4	R&D Systems	69036	IgG1	1:50
Vimentin	Lab Vision	V9	IgG1	1:100
CD31	BD Biosciences	WM59	IgG1	1:100
IGF1Rb	Santa Cruz Biotechnology	C-20	IgG1	1:100
INOS	Santa Cruz	N-20	Affinity purified rabbit	1:20
TNF- α -FITC	BD Biosciences	6401.1111		1:10

FITC, Fluorescein isothiocyanate; *IGF1Rb*, insulin-like growth factor 1 receptor b.

TABLE E3. Summary of coexpression of DC markers and inflammatory mediators in patients with psoriasis by means of 2-color immunofluorescence

Cell marker	Identifies:	IL-12p40	IL-23p19	TNF	iNOS
CD1c	Resident dermal myeloid DCs	ND	Y	Occasional cells*	ND*
CD11c	Inflammatory myeloid DCs	Y†	Y†	Y†	Y†
TRAIL	Inflammatory myeloid DC subset	Y	Y	Y	Y

ND, Not detected; Y, coexpression detected.

*See Zaba et al.^{E1}

†See Zaba et al.^{E1}, Zaba et al.^{E2} and Guttman-Yasky et al.^{E3} New images of CD11c versus IL-23 subunits have been included to compare with TRAIL.

OR Table E2 DEG.xls

Probe	Symbol	Description	FCH	lgFCH	P	fdr	Psor, BDCA+	Psor, BDCA-	Gene	UniGene
215646_s_at	VCAN	versican	45.45	-5.539	0	0.01	4.8	10.339	1462	Hs.643801
211571_s_at	VCAN	versican	31.25	-4.986	0	0.01	4.057	9.043	1462	Hs.643801
205819_at	MARCO	macrophage receptor with collagenous structure	30.30	-4.913	0	0.03	2.697	7.609	8685	Hs.67726
219403_s_at	HPSE	heparanase	27.03	-4.747	0	0	4.61	9.356	10855	Hs.44227
204787_at	VSIG4	V-set and immunoglobulin domain containing 4	25.64	-4.692	0.001	0.04	5.025	9.717	11326	Hs.8904
207075_at	NLRP3	NLR family, pyrin domain containing 3	24.39	-4.602	0	0.04	3.745	8.346	114548	Hs.159483
215049_x_at	CD163	CD163 molecule	24.39	-4.607	0.002	0.06	5.957	10.564	9332	Hs.504641
207674_at	FCAR	Fc fragment of IgA, receptor for	24.39	-4.608	0	0.01	3.316	7.924	2204	Hs.659872
210724_at	EMR3	egf-like module containing, mucin-like, hormone rece	23.81	-4.561	0	0	4.614	9.174	84658	Hs.658712
210772_at	FPRL1	formyl peptide receptor-like 1	23.26	-4.526	0	0.02	3.991	8.517	2358	Hs.99855
219496_at	ANKRD57	ankyrin repeat domain 57	22.73	-4.515	0	0.02	3.028	7.543	65124	Hs.355455
201185_at	HTRA1	HtrA serine peptidase 1	21.28	-4.405	0.002	0.06	3.806	8.212	5654	Hs.501280
205466_s_at	HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	20.83	-4.378	0	0	3.753	8.131	9957	Hs.507348, Hs.
205828_at	MMP3	matrix metalloproteinase 3 (stromelysin 1, progelatina	20.83	-4.38	0.015	0.14	5.284	9.665	4314	Hs.375129
205786_s_at	ITGAM	integrin, alpha M (complement component 3 receptor	20.00	-4.32	0.003	0.07	7.475	11.795	3684	Hs.172631
221748_s_at	TNS1	tensin 1	19.61	-4.294	0	0.03	5.494	9.788	7145	Hs.471381
203645_s_at	CD163	CD163 molecule	18.87	-4.252	0.004	0.08	7.321	11.573	9332	Hs.504641
221666_s_at	PYCARD	PYD and CARD domain containing	18.52	-4.221	0	0.02	5.845	10.066	29108	Hs.499094
205863_at	S100A12	S100 calcium binding protein A12	18.18	-4.194	0	0.03	5.364	9.558	6283	Hs.19413
204619_s_at	VCAN	versican	17.86	-4.155	0	0.01	7.267	11.421	1462	Hs.643801
210992_x_at	FCGR2C	Fc fragment of IgG, low affinity IIc, receptor for (CD32	17.24	-4.12	0.001	0.05	3.998	8.119	9103	Hs.693694
214146_s_at	PPBP	pro-platelet basic protein (chemokine (C-X-C motif) li	16.39	-4.039	0.001	0.05	9.104	13.143	5473	Hs.2164
205119_s_at	FPR1	formyl peptide receptor 1	16.39	-4.046	0.01	0.12	6.66	10.706	2357	Hs.753
218149_s_at	ZNF395	zinc finger protein 395	15.38	-3.938	0.001	0.04	5.082	9.02	55893	Hs.435535, Hs.
206167_s_at	ARHGAP6	Rho GTPase activating protein 6	14.93	-3.904	0	0	3.145	7.048	395	Hs.435291
207224_s_at	SIGLEC7	sialic acid binding Ig-like lectin 7	14.93	-3.905	0	0.02	4.8	8.705	27036	Hs.655393
215813_s_at	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandi	14.71	-3.886	0.001	0.05	4.04	7.926	5742	Hs.201978
218232_at	C1QA	complement component 1, q subcomponent, A chain	14.49	-3.849	0.008	0.11	4.018	7.868	712	Hs.632379
207277_at	CD209	CD209 molecule	14.49	-3.858	0	0.04	4.446	8.304	30835	Hs.278694
219947_at	CLEC4A	C-type lectin domain family 4, member A	14.29	-3.833	0	0.02	8.337	12.169	50856	Hs.504657
205098_at	CCR1	chemokine (C-C motif) receptor 1	14.08	-3.819	0.006	0.1	6.973	10.792	1230	Hs.301921
201798_s_at	FER1L3	fer-1-like 3, myoferlin (C. elegans)	14.08	-3.821	0.001	0.04	4.476	8.297	26509	Hs.655278
212761_at	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	13.89	-3.804	0.002	0.06	5.621	9.424	6934	Hs.593995
205922_at	VNN2	vanin 2	13.70	-3.772	0.002	0.06	7.095	10.867	8875	Hs.293130
206978_at	CCR2	chemokine (C-C motif) receptor 2	13.70	-3.772	0.007	0.11	3.729	7.501	1231	Hs.644637
213113_s_at	SLC43A3	solute carrier family 43, member 3	13.33	-3.731	0	0.02	5.544	9.275	29015	Hs.99962
203922_s_at	CYBB	cytochrome b-245, beta polypeptide (chronic granulor	13.33	-3.733	0	0.02	5.388	9.121	1536	Hs.292356
219386_s_at	SLAMF8	SLAM family member 8	13.33	-3.743	0.004	0.08	5.599	9.342	56833	Hs.438683
221724_s_at	CLEC4A	C-type lectin domain family 4, member A	13.16	-3.713	0	0	3.204	6.917	50856	Hs.504657
207857_at	LILRA2	leukocyte immunoglobulin-like receptor, subfamily A (	13.16	-3.725	0	0.03	4.633	8.359	11027	Hs.655593
204860_s_at	NAIP	NLR family, apoptosis inhibitory protein	12.82	-3.676	0.003	0.07	4.248	7.924	4671	Hs.646951, Hs.

OR Table E2 DEG.xls

Probe	Symbol	Description	FCH	lgFCH	P	fdr	Psor, BDCA+	Psor, BDCA-	Gene	UniGene
210889_s_at	FCGR2B	Fc fragment of IgG, low affinity IIb, receptor (CD32)	12.82	-3.677	0.005	0.09	6.724	10.402	2213	Hs.654395
219890_at	CLEC5A	C-type lectin domain family 5, member A	12.82	-3.677	0.003	0.07	7.308	10.985	23601	Hs.446235
206120_at	CD33	CD33 molecule	12.82	-3.686	0	0.01	3.147	6.833	945	Hs.83731
212192_at	KCTD12	potassium channel tetramerisation domain containing	12.66	-3.654	0.008	0.11	7.928	11.582	115207	Hs.693617
215101_s_at	CXCL5	chemokine (C-X-C motif) ligand 5	12.66	-3.66	0	0.02	8.841	12.501	6374	Hs.89714
219607_s_at	MS4A4A	membrane-spanning 4-domains, subfamily A, membe	12.66	-3.663	0.007	0.1	6.72	10.383	51338	Hs.325960
203939_at	NT5E	5'-nucleotidase, ecto (CD73)	12.66	-3.667	0.001	0.05	4.684	8.351	4907	Hs.153952
210423_s_at	SLC11A1	solute carrier family 11 (proton-coupled divalent metal	12.66	-3.67	0.002	0.07	6.683	10.352	6556	Hs.591607
221210_s_at	NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolini	12.35	-3.622	0.001	0.04	4.741	8.363	80896	Hs.496969
206420_at	IGSF6	immunoglobulin superfamily, member 6	12.35	-3.624	0	0.03	6.048	9.673	10261	Hs.530902
218332_at	BEX1	brain expressed, X-linked 1	12.20	-3.615	0.003	0.07	4.601	8.216	55859	Hs.334370
212298_at	NRP1	neuropilin 1	11.90	-3.573	0	0.03	6.149	9.722	8829	Hs.131704
209933_s_at	CD300A	CD300a molecule	11.90	-3.575	0	0.02	6.988	10.563	11314	Hs.9688
203104_at	CSF1R	colony stimulating factor 1 receptor, formerly McDono	11.76	-3.55	0.009	0.11	6.921	10.47	1436	Hs.654394
207610_s_at	EMR2	egf-like module containing, mucin-like, hormone rece	11.76	-3.553	0	0.01	3.016	6.569	30817	Hs.531619
204150_at	STAB1	stabilin 1	11.76	-3.558	0.007	0.1	4.461	8.019	23166	Hs.301989
203923_s_at	CYBB	cytochrome b-245, beta polypeptide (chronic granulo	11.63	-3.538	0	0.02	5.642	9.18	1536	Hs.292356
202191_s_at	GAS7	growth arrest-specific 7	11.36	-3.5	0	0.03	6.063	9.563	8522	Hs.462214
38037_at	HBEGF	heparin-binding EGF-like growth factor	11.36	-3.504	0.002	0.06	6.982	10.487	1839	Hs.799
209395_at	CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	11.36	-3.51	0.001	0.05	4.088	7.598	1116	Hs.382202
209906_at	C3AR1	complement component 3a receptor 1	11.24	-3.486	0	0.04	8.794	12.28	719	Hs.591148
209160_at	AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hy	11.24	-3.489	0.002	0.06	3.477	6.966	8644	Hs.78183
205978_at	KL	klotho	11.24	-3.491	0	0	3.373	6.865	9365	Hs.524953
217767_at	C3	complement component 3	11.24	-3.492	0.003	0.07	3.507	6.998	718	Hs.529053
211395_x_at	FCGR2C	Fc fragment of IgG, low affinity IIc, receptor for (CD32	11.24	-3.497	0.006	0.1	5.946	9.443	9103	Hs.693694
210510_s_at	NRP1	neuropilin 1	11.11	-3.468	0	0.02	4.721	8.189	8829	Hs.131704
210644_s_at	LAIR1	leukocyte-associated immunoglobulin-like receptor 1	10.99	-3.453	0.001	0.05	6.628	10.081	3903	Hs.572535
201427_s_at	SEPP1	selenoprotein P, plasma, 1	10.87	-3.437	0.007	0.1	7.063	10.499	6414	Hs.275775, Hs.
37145_at	GNLY	granulysin	10.87	-3.444	0.026	0.18	2.629	6.073	10578	Hs.105806
206715_at	TFEC	transcription factor EC	10.87	-3.446	0.002	0.06	5.412	8.858	22797	Hs.125962
208892_s_at	DUSP6	dual specificity phosphatase 6	10.75	-3.42	0.004	0.08	7.401	10.82	1848	Hs.298654
206100_at	CPM	carboxypeptidase M	10.75	-3.43	0.001	0.04	5.926	9.356	1368	Hs.654387
44783_s_at	HEY1	hairy/enhancer-of-split related with YRPW motif 1	10.75	-3.43	0.002	0.06	5.621	9.051	23462	Hs.234434
215051_x_at	AIF1	allograft inflammatory factor 1	10.64	-3.415	0	0.04	8.096	11.511	199	Hs.76364
206028_s_at	MERTK	c-mer proto-oncogene tyrosine kinase	10.64	-3.418	0.003	0.07	3.716	7.134	10461	Hs.306178, Hs.
210152_at	LILRB4	leukocyte immunoglobulin-like receptor, subfamily B (	10.53	-3.399	0.001	0.04	4.845	8.244	11006	Hs.67846
221731_x_at	VCAN	versican	10.53	-3.399	0	0.01	9.749	13.149	1462	Hs.643801
213418_at	HSPA6	heat shock 70kDa protein 6 (HSP70B')	10.42	-3.378	0.012	0.13	5.896	9.274	3310	Hs.654614
217975_at	WBP5	WW domain binding protein 5	10.42	-3.381	0	0.03	6.184	9.564	51186	Hs.533287
218676_s_at	PTCP	phosphatidylcholine transfer protein	10.31	-3.364	0	0.03	5.324	8.688	58488	Hs.285218
205128_x_at	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandi	10.31	-3.371	0.003	0.07	5.958	9.329	5742	Hs.201978

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Probe	Symbol	Description	FCH	lgFCH	P	fdr	Psor, BDCA+	Psor, BDCA-	Gene	UniGene
219505_at	CECR1	cat eye syndrome chromosome region, candidate 1	10.10	-3.332	0.001	0.04	6.233	9.564	51816	Hs.170310
219666_at	MS4A6A	membrane-spanning 4-domains, subfamily A, membe	10.10	-3.333	0.018	0.15	3.52	6.853	64231	Hs.523702
211372_s_at	IL1R2	interleukin 1 receptor, type II	10.00	-3.316	0.013	0.13	6.419	9.735	7850	Hs.25333
210102_at	LOH11CR2A	loss of heterozygosity, 11, chromosomal region 2, ger	10.00	-3.318	0.015	0.14	2.999	6.318	4013	Hs.152944
209555_s_at	CD36	CD36 molecule (thrombospondin receptor)	10.00	-3.32	0.015	0.14	3.912	7.232	948	Hs.120949, Hs.
202838_at	FUCA1	fucosidase, alpha-L- 1, tissue	10.00	-3.325	0.003	0.07	8.734	12.059	2517	Hs.370858
210119_at	KCNJ15	potassium inwardly-rectifying channel, subfamily J, m	9.80	-3.286	0.007	0.1	4.879	8.166	3772	Hs.411299
209875_s_at	SPP1	secreted phosphoprotein 1 (osteopontin, bone sialopr	9.80	-3.294	0.001	0.05	8.335	11.629	6696	Hs.313
210176_at	TLR1	toll-like receptor 1	9.80	-3.294	0.008	0.11	6.401	9.695	7096	Hs.621817, Hs.
202498_s_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter)	9.80	-3.296	0	0.02	5.577	8.873	6515	Hs.419240, Hs.
204620_s_at	VCAN	versican	9.71	-3.282	0	0.02	9.785	13.067	1462	Hs.643801
203971_at	SLC31A1	solute carrier family 31 (copper transporters), membe	9.71	-3.283	0	0.01	5.747	9.03	1317	Hs.532315
209696_at	FBP1	fructose-1,6-bisphosphatase 1	9.71	-3.284	0.019	0.16	5.614	8.898	2203	Hs.494496
215867_x_at	CA12	carbonic anhydrase XII	9.71	-3.286	0.001	0.05	3.994	7.28	771	Hs.210995
201141_at	GPNMB	glycoprotein (transmembrane) nmb	9.52	-3.251	0.003	0.07	7.074	10.325	10457	Hs.190495
38487_at	STAB1	stabilin 1	9.52	-3.255	0.006	0.1	4.557	7.813	23166	Hs.301989
213379_at	COQ2	coenzyme Q2 homolog, prenyltransferase (yeast)	9.43	-3.235	0	0.01	4.86	8.096	27235	Hs.144304
209901_x_at	AIF1	allograft inflammatory factor 1	9.43	-3.245	0	0.02	6.231	9.476	199	Hs.76364
209138_x_at	IGL@	immunoglobulin lambda locus	9.35	-3.221	0.011	0.12	2.439	5.659	3535	Hs.449585
213566_at	RNASE6	ribonuclease, RNase A family, k6	9.35	-3.221	0.011	0.12	7.954	11.175	6039	Hs.23262, Hs.6
219859_at	CLEC4E	C-type lectin domain family 4, member E	9.35	-3.221	0	0	2.899	6.12	26253	Hs.236516
221541_at	CRISPLD2	cysteine-rich secretory protein LCCL domain containi	9.26	-3.204	0.001	0.04	7.41	10.615	83716	Hs.513779
205174_s_at	QPCT	glutaminy-peptide cyclotransferase (glutaminy cyclas	9.26	-3.207	0.001	0.04	7.302	10.509	25797	Hs.79033
200766_at	CTSD	cathepsin D	9.26	-3.208	0.001	0.04	5.332	8.54	1509	Hs.121575, Hs.
213095_x_at	AIF1	allograft inflammatory factor 1	9.26	-3.211	0	0.03	6.927	10.138	199	Hs.76364
205141_at	ANG	angiogenin, ribonuclease, RNase A family, 5	9.17	-3.193	0.008	0.11	5.152	8.345	283	Hs.283749, Hs.
217507_at	SLC11A1	solute carrier family 11 (proton-coupled divalent meta	9.09	-3.182	0.001	0.04	3.255	6.437	6556	Hs.591607
217022_s_at	IGHA1	immunoglobulin heavy constant alpha 1	9.01	-3.168	0.004	0.08	2.484	5.652	3493	Hs.648398
218660_at	DYSF	dysferlin, limb girdle muscular dystrophy 2B (autosom	8.93	-3.155	0	0.02	7.094	10.249	8291	Hs.252180
219161_s_at	CKLF	chemokine-like factor	8.93	-3.155	0.001	0.05	7.546	10.701	51192	Hs.15159
210757_x_at	DAB2	disabled homolog 2, mitogen-responsive phosphopro	8.93	-3.161	0.012	0.13	3.481	6.641	1601	Hs.481980
201109_s_at	THBS1	thrombospondin 1	8.85	-3.144	0	0.03	8.637	11.781	7057	Hs.164226
206278_at	PTAFR	platelet-activating factor receptor	8.85	-3.148	0	0.01	4.154	7.302	5724	Hs.433540
220416_at	ATP8B4	ATPase, Class I, type 8B, member 4	8.77	-3.131	0.001	0.04	4.501	7.633	79895	Hs.511311
206134_at	ADAMDEC1	ADAM-like, decysin 1	8.70	-3.114	0.001	0.04	9.054	12.168	27299	Hs.521459
203650_at	PROCR	protein C receptor, endothelial (EPCR)	8.70	-3.115	0	0.03	5.837	8.952	10544	Hs.647450
203561_at	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	8.70	-3.117	0.002	0.06	7.972	11.089	2212	Hs.352642
205627_at	CDA	cytidine deaminase	8.70	-3.118	0.003	0.07	2.713	5.83	978	Hs.466910
215121_x_at	IGL@	immunoglobulin lambda locus	8.70	-3.118	0.007	0.1	2.334	5.452	3535	Hs.449585
203888_at	THBD	thrombomodulin	8.70	-3.12	0.001	0.05	7.888	11.008	7056	Hs.2030
203946_s_at	ARG2	arginase, type II	8.62	-3.104	0.002	0.06	3.061	6.165	384	Hs.653205

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Probe	Symbol	Description	FCH	lgFCH	P	fdr	Psor, BDCA+	Psor, BDCA-	Gene	UniGene
214677_x_at	IGLJ3	immunoglobulin lambda joining 3	8.62	-3.111	0.014	0.14	4.071	7.181	28831	Hs.449585
219915_s_at	SLC16A10	solute carrier family 16, member 10 (aromatic amino acid	8.55	-3.094	0.001	0.05	5.502	8.596	117247	Hs.591327
219622_at	RAB20	RAB20, member RAS oncogene family	8.47	-3.078	0.003	0.07	7.239	10.317	55647	Hs.508720
203535_at	S100A9	S100 calcium binding protein A9	8.47	-3.079	0.001	0.05	10.097	13.176	6280	Hs.112405
212558_at	SPRY1	sprouty homolog 1, antagonist of FGF signaling (Dros	8.47	-3.081	0.002	0.06	3.873	6.954	10252	Hs.436944
205099_s_at	CCR1	chemokine (C-C motif) receptor 1	8.47	-3.083	0.009	0.12	7.281	10.363	1230	Hs.301921
204924_at	TLR2	toll-like receptor 2	8.40	-3.067	0.001	0.05	9.466	12.533	7097	Hs.519033
219574_at		1-Mar membrane-associated ring finger (C3HC4) 1	8.40	-3.072	0.004	0.08	3.372	6.444	55016	Hs.608487, Hs.
205237_at	FCN1	ficolin (collagen/fibrinogen domain containing) 1	8.40	-3.075	0.002	0.07	7.209	10.284	2219	Hs.440898
222116_s_at	TBC1D16	TBC1 domain family, member 16	8.40	-3.076	0.001	0.04	3.443	6.519	125058	Hs.369819
41469_at	PI3	peptidase inhibitor 3, skin-derived (SKALP)	8.33	-3.061	0.028	0.19	4.492	7.552	5266	Hs.112341
210139_s_at	PMP22	peripheral myelin protein 22	8.26	-3.042	0	0.02	9.02	12.062	5376	Hs.372031
206631_at	PTGER2	prostaglandin E receptor 2 (subtype EP2), 53kDa	8.26	-3.048	0.01	0.12	5.999	9.047	5732	Hs.2090
214452_at	BCAT1	branched chain aminotransferase 1, cytosolic	8.26	-3.05	0	0.01	4.959	8.009	586	Hs.438993
214866_at	PLAUR	plasminogen activator, urokinase receptor	8.20	-3.03	0.011	0.12	7.259	10.289	5329	Hs.466871
205715_at	BST1	bone marrow stromal cell antigen 1	8.20	-3.034	0	0.01	2.465	5.499	683	Hs.169998
219093_at	PID1	phosphotyrosine interaction domain containing 1	8.20	-3.037	0.001	0.04	8.712	11.749	55022	Hs.409352
219938_s_at	PSTPIP2	proline-serine-threonine phosphatase interacting prot	8.20	-3.04	0.001	0.05	4.828	7.868	9050	Hs.567384
222218_s_at	PILRA	paired immunoglobulin-like type 2 receptor alpha	8.13	-3.018	0	0.03	8.022	11.04	29992	Hs.444407
208981_at	PECAM1	platelet/endothelial cell adhesion molecule (CD31 ant	8.13	-3.021	0.005	0.09	7.404	10.425	5175	Hs.514412
219788_at	PILRA	paired immunoglobulin-like type 2 receptor alpha	8.13	-3.025	0.003	0.07	6.236	9.26	29992	Hs.444407
205896_at	SLC22A4	solute carrier family 22 (organic cation transporter), m	8.13	-3.028	0	0.02	3.704	6.731	6583	Hs.310591, Hs.
208933_s_at			8.06	-3.01	0.003	0.07	5.932	8.943		
209348_s_at	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene hc	8.06	-3.014	0.002	0.06	9.146	12.16	4094	Hs.134859
209365_s_at	ECM1	extracellular matrix protein 1	8.00	-3.003	0	0.02	3.853	6.856	1893	Hs.81071
211067_s_at	GAS7	growth arrest-specific 7	8.00	-3.004	0.002	0.06	5.398	8.403	8522	Hs.462214
218831_s_at	FCGRT	Fc fragment of IgG, receptor, transporter, alpha	7.94	-2.984	0.004	0.08	6.782	9.766	2217	Hs.111903
208935_s_at	LGALS8	lectin, galactoside-binding, soluble, 8 (galectin 8)	7.87	-2.974	0.001	0.05	5.143	8.118	3964	Hs.4082, Hs.65
203821_at	HBEGF	heparin-binding EGF-like growth factor	7.81	-2.963	0.002	0.06	8.488	11.451	1839	Hs.799
210164_at	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-ass	7.81	-2.965	0.009	0.11	3.828	6.793	3002	Hs.1051
213624_at	SMPDL3A	sphingomyelin phosphodiesterase, acid-like 3A	7.75	-2.952	0	0.02	5.316	8.268	10924	Hs.486357
202878_s_at	CD93	CD93 molecule	7.69	-2.946	0.001	0.04	9.205	12.152	22918	Hs.97199
213397_x_at	ANG	angiogenin, ribonuclease, RNase A family, 5	7.63	-2.931	0.003	0.07	6.153	9.084	283	Hs.283749, Hs.
203473_at	SLCO2B1	solute carrier organic anion transporter family, memb	7.63	-2.932	0.007	0.1	5.284	8.217	11309	Hs.7884
217914_at	TPCN1	two pore segment channel 1	7.58	-2.92	0	0.03	4.752	7.672	53373	Hs.524763
219385_at	SLAMF8	SLAM family member 8	7.58	-2.925	0.011	0.12	5.062	7.986	56833	Hs.438683
200648_s_at	GLUL	glutamate-ammonia ligase (glutamine synthetase)	7.52	-2.908	0	0.02	8.95	11.858	2752	Hs.518525
202934_at	HK2	hexokinase 2	7.52	-2.913	0	0.02	7.225	10.139	3099	Hs.406266, Hs.
213125_at	OLFML2B	olfactomedin-like 2B	7.46	-2.9	0.013	0.13	4.269	7.169	25903	Hs.507515
205997_at	ADAM28	ADAM metallopeptidase domain 28	7.46	-2.902	0.001	0.05	5.208	8.11	10863	Hs.174030
207957_s_at	PRKCB1	protein kinase C, beta 1	7.46	-2.904	0	0.01	5.65	8.553	5579	Hs.460355

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Probe	Symbol	Description	FCH	lgFCH	P	fdr	Psor, BDCA+	Psor, BDCA-	Gene	UniGene
204900_x_at	SAP30	Sin3A-associated protein, 30kDa	7.46	-2.905	0.003	0.07	6.008	8.913	8819	Hs.591715
206025_s_at	TNFAIP6	tumor necrosis factor, alpha-induced protein 6	7.41	-2.887	0	0.01	7.775	10.661	7130	Hs.437322
204647_at	HOMER3	homer homolog 3 (Drosophila)	7.41	-2.889	0	0.02	5.151	8.04	9454	Hs.410683
201279_s_at	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein	7.41	-2.89	0.011	0.12	4.087	6.977	1601	Hs.481980
206060_s_at	PTPN22	protein tyrosine phosphatase, non-receptor type 22 (L	7.30	-2.863	0.001	0.05	4.354	7.217	26191	Hs.535276
216598_s_at	CCL2	chemokine (C-C motif) ligand 2	7.30	-2.869	0.018	0.15	5.258	8.127	6347	Hs.303649
203504_s_at	ABCA1	ATP-binding cassette, sub-family A (ABC1), member	7.25	-2.857	0	0.02	6.993	9.85	19	Hs.429294
201260_s_at	SYPL1	synaptophysin-like 1	7.25	-2.858	0	0.01	7.203	10.061	6856	Hs.80919
209949_at	NCF2	neutrophil cytosolic factor 2 (65kDa, chronic granulo	7.25	-2.858	0	0.03	8.813	11.671	4688	Hs.587558
201042_at	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-	7.25	-2.861	0.002	0.06	5.782	8.642	7052	Hs.517033
200665_s_at	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	7.25	-2.862	0	0.03	6.169	9.031	6678	Hs.111779
210762_s_at	DLC1	deleted in liver cancer 1	7.19	-2.849	0.016	0.14	2.214	5.063	10395	Hs.134296
206488_s_at	CD36	CD36 molecule (thrombospondin receptor)	7.14	-2.833	0.024	0.17	4.816	7.649	948	Hs.120949, Hs.
218451_at	CDCP1	CUB domain containing protein 1	7.14	-2.834	0.012	0.13	6.606	9.44	64866	Hs.476093
203675_at	NUCB2	nucleobindin 2	7.09	-2.827	0	0.02	5.982	8.809	4925	Hs.654599
204174_at	ALOX5AP	arachidonate 5-lipoxygenase-activating protein	7.09	-2.827	0.001	0.05	7.677	10.504	241	Hs.507658
204438_at	MRC1	mannose receptor, C type 1	7.04	-2.815	0.007	0.1	8.928	11.743	4360	Hs.75182
204774_at	EVI2A	ecotropic viral integration site 2A	7.04	-2.817	0	0.03	9.607	12.423	2123	Hs.591198
209357_at	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich	6.99	-2.802	0.001	0.04	6.197	8.999	10370	Hs.82071
209189_at	FOS	v-fos FBJ murine osteosarcoma viral oncogene hom	6.94	-2.794	0.012	0.13	8.476	11.27	2353	Hs.25647
212831_at	MEGF9	multiple EGF-like-domains 9	6.94	-2.798	0.001	0.04	2.844	5.642	1955	Hs.494977
203760_s_at	SLA	Src-like-adaptor	6.94	-2.8	0.005	0.09	6.987	9.786	6503	Hs.75367
34206_at	CENTD2	centaurin, delta 2	6.90	-2.782	0.002	0.06	5.732	8.514	116985	Hs.503165
205844_at	VNN1	vanin 1	6.90	-2.789	0.01	0.12	5.687	8.476	8876	Hs.12114, Hs.6
219434_at	TREM1	triggering receptor expressed on myeloid cells 1	6.85	-2.771	0.002	0.06	8.584	11.356	54210	Hs.283022
212943_at	KIAA0528	KIAA0528	6.85	-2.773	0	0.01	7.699	10.472	9847	Hs.271014
202877_s_at	CD93	CD93 molecule	6.85	-2.775	0.002	0.06	6.691	9.466	22918	Hs.97199
211924_s_at	PLAUR	plasminogen activator, urokinase receptor	6.85	-2.778	0.004	0.08	8.979	11.757	5329	Hs.466871
203887_s_at	THBD	thrombomodulin	6.80	-2.769	0.002	0.06	9.406	12.175	7056	Hs.2030
204588_s_at	SLC7A7	solute carrier family 7 (cationic amino acid transporter	6.76	-2.753	0.003	0.07	8.442	11.195	9056	Hs.513147
219228_at	ZNF331	zinc finger protein 331	6.76	-2.753	0.001	0.04	5.059	7.812	55422	Hs.185674
211742_s_at	EVI2B	ecotropic viral integration site 2B	6.76	-2.757	0.004	0.08	8.195	10.952	2124	Hs.5509
207038_at	SLC16A6	solute carrier family 16, member 6 (monocarboxylic a	6.76	-2.759	0.002	0.06	3.652	6.411	9120	Hs.42645, Hs.4
203510_at	MET	met proto-oncogene (hepatocyte growth factor recept	6.71	-2.743	0.002	0.06	8.04	10.783	4233	Hs.132966
204232_at	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamm	6.71	-2.743	0.002	0.07	9.707	12.45	2207	Hs.433300
222088_s_at	SLC2A14	solute carrier family 2 (facilitated glucose transporter)	6.71	-2.749	0.003	0.07	7.216	9.965	144195	Hs.655169
221530_s_at	BHLHB3	basic helix-loop-helix domain containing, class B, 3	6.67	-2.733	0.001	0.05	3.343	6.076	79365	Hs.177841
205269_at	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containin	6.62	-2.728	0.009	0.12	7.627	10.355	3937	Hs.304475
201700_at	CCND3	cyclin D3	6.49	-2.702	0.001	0.05	6.872	9.574	896	Hs.534307
206881_s_at	LILRA3	leukocyte immunoglobulin-like receptor, subfamily A (	6.49	-2.704	0.001	0.04	8.603	11.307	11026	Hs.113277
34210_at	CD52	CD52 molecule	6.45	-2.687	0.014	0.13	7.485	10.171	1043	Hs.276770

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Probe	Symbol	Description	FCH	lgFCH	P	fdr	Psor, BDCA+	Psor, BDCA-	Gene	UniGene
210845_s_at	PLAUR	plasminogen activator, urokinase receptor	6.45	-2.69	0.002	0.06	10.246	12.936	5329 Hs.466871	
212345_s_at	CREB3L2	cAMP responsive element binding protein 3-like 2	6.45	-2.693	0.003	0.07	5.26	7.953	64764 Hs.490273	
206995_x_at	SCARF1	scavenger receptor class F, member 1	6.41	-2.679	0.001	0.05	4.695	7.374	8578 Hs.647430	
205684_s_at	DENND4C	DENN/MADD domain containing 4C	6.41	-2.682	0	0.03	5.628	8.31	55667 Hs.249591	
202430_s_at	PLSCR1	phospholipid scramblase 1	6.41	-2.683	0	0.03	8.026	10.709	5359 Hs.130759	
213093_at	PRKCA	protein kinase C, alpha	6.33	-2.658	0	0.04	4.633	7.291	5578 Hs.531704, Hs.	
203507_at	CD68	CD68 molecule	6.33	-2.66	0.001	0.05	6.375	9.035	968 Hs.647419	
200785_s_at	LRP1	low density lipoprotein-related protein 1 (alpha-2-mac	6.29	-2.654	0.008	0.11	4.527	7.181	4035 Hs.162757	
214830_at	SLC38A6	solute carrier family 38, member 6	6.29	-2.656	0.003	0.07	5.066	7.722	145389 Hs.200738	
217983_s_at	RNASET2	ribonuclease T2	6.21	-2.633	0.001	0.04	9.206	11.839	8635 Hs.529989	
202671_s_at	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	6.21	-2.634	0	0.02	6.295	8.929	8566 Hs.284491	
212663_at	FKBP15	FK506 binding protein 15, 133kDa	6.17	-2.625	0.002	0.06	7.1	9.725	23307 Hs.522351	
204396_s_at	GRK5	G protein-coupled receptor kinase 5	6.13	-2.617	0	0.04	5.716	8.333	2869 Hs.524625	
209732_at	CLEC2B	C-type lectin domain family 2, member B	6.10	-2.606	0.004	0.08	7.49	10.096	9976 Hs.85201	
207677_s_at	NCF4	neutrophil cytosolic factor 4, 40kDa	6.10	-2.607	0.001	0.04	7.396	10.003	4689 Hs.474781	
212942_s_at	KIAA1199	KIAA1199	6.10	-2.608	0.012	0.12	7.304	9.912	57214 Hs.459088	
213603_s_at	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family,	6.10	-2.611	0.005	0.09	9.585	12.196	5880 Hs.517601	
202687_s_at	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	6.06	-2.6	0.028	0.19	4.735	7.335	8743 Hs.478275	
208161_s_at	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), me	6.06	-2.604	0.003	0.07	6.818	9.421	8714 Hs.463421	
203549_s_at	LPL	lipoprotein lipase	5.95	-2.576	0.003	0.08	3.846	6.422	4023 Hs.180878	
203963_at	CA12	carbonic anhydrase XII	5.95	-2.576	0.011	0.12	4.952	7.528	771 Hs.210995	
201482_at	QSOX1	quiescin Q6 sulfhydryl oxidase 1	5.92	-2.565	0.001	0.04	7.367	9.932	5768 Hs.518374	
204502_at	SAMHD1	SAM domain and HD domain 1	5.92	-2.567	0.002	0.06	6.3	8.867	25939 Hs.580681	
201779_s_at	RNF13	ring finger protein 13	5.92	-2.568	0	0.01	7.59	10.158	11342 Hs.12333	
202912_at	ADM	adrenomedullin	5.88	-2.554	0.002	0.06	10.365	12.92	133 Hs.441047	
212501_at	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta	5.88	-2.557	0.002	0.06	11.404	13.961	1051 Hs.517106, Hs.	
215043_s_at	SMA5	glucuronidase, beta pseudogene	5.88	-2.559	0.021	0.17	4.41	6.969	11042 Hs.529793, Hs.	
208936_x_at	LGALS8	lectin, galactoside-binding, soluble, 8 (galectin 8)	5.81	-2.537	0.008	0.11	5.722	8.259	3964 Hs.4082, Hs.65	
212744_at	BBS4	Bardet-Biedl syndrome 4	5.81	-2.537	0	0.01	4.545	7.082	585 Hs.208681	
202435_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide	5.81	-2.543	0.003	0.07	8.858	11.401	1545 Hs.154654	
218739_at	ABHD5	abhydrolase domain containing 5	5.81	-2.543	0.001	0.06	4.89	7.433	51099 Hs.19385, Hs.6	
210314_x_at	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	5.78	-2.529	0.008	0.11	7.957	10.486	8741 Hs.54673	
208983_s_at	PECAM1	platelet/endothelial cell adhesion molecule (CD31 ant	5.78	-2.532	0.004	0.08	4.665	7.198	5175 Hs.514412	
211506_s_at	IL8	interleukin 8	5.75	-2.519	0	0.02	10.213	12.732	3576 Hs.624, Hs.449	
203761_at	SLA	Src-like-adaptor	5.75	-2.52	0.001	0.04	7.056	9.577	6503 Hs.75367	
212188_at	KCTD12	potassium channel tetramerisation domain containing	5.75	-2.521	0.009	0.12	8.348	10.868	115207 Hs.693617	
201743_at	CD14	CD14 molecule	5.75	-2.524	0.008	0.11	12.344	14.868	929 Hs.163867	
206214_at	PLA2G7	phospholipase A2, group VII (platelet-activating factor	5.75	-2.526	0.001	0.05	9.862	12.388	7941 Hs.584823	
208891_at	DUSP6	dual specificity phosphatase 6	5.71	-2.512	0.007	0.1	9.478	11.99	1848 Hs.298654	
205270_s_at	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containin	5.71	-2.513	0.003	0.07	5.848	8.361	3937 Hs.304475	
205158_at	RNASE4	ribonuclease, RNase A family, 4	5.71	-2.515	0.022	0.17	3.418	5.933	6038 Hs.283749	

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Probe	Symbol	Description	FCH	lgFCH	P	fdr	Psor, BDCA+	Psor, BDCA-	Gene	UniGene
201506_at	TGFB1	transforming growth factor, beta-induced, 68kDa	5.71	-2.516	0.006	0.1	10.686	13.202	7045 Hs.369397	
218930_s_at	TMEM106B	transmembrane protein 106B	5.68	-2.509	0.001	0.04	5.244	7.753	54664 Hs.396358	
207850_at	CXCL3	chemokine (C-X-C motif) ligand 3	5.65	-2.498	0.001	0.04	11.37	13.867	2921 Hs.89690	
210422_x_at	SLC11A1	solute carrier family 11 (proton-coupled divalent metal	5.62	-2.489	0	0.03	4.919	7.408	6556 Hs.591607	
214560_at	FPRL2	formyl peptide receptor-like 2	5.62	-2.491	0.014	0.13	3.821	6.312	2359 Hs.445466	
209499_x_at	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	5.59	-2.479	0.008	0.11	3.436	5.915	8741 Hs.54673	
202426_s_at	RXRA	retinoid X receptor, alpha	5.59	-2.481	0.001	0.04	5.218	7.7	6256 Hs.590886	
220066_at	NOD2	nucleotide-binding oligomerization domain containing	5.56	-2.476	0	0.03	6.099	8.575	64127 Hs.592072	
213915_at	NKG7	natural killer cell group 7 sequence	5.52	-2.463	0.001	0.04	3.504	5.967	4818 Hs.10306	
211005_at	LAT	linker for activation of T cells	5.52	-2.466	0.001	0.04	6.59	9.056	27040 Hs.632179	
36552_at	DKFZP586P012	hypothetical protein	5.52	-2.466	0.002	0.06	5.072	7.538	26005 Hs.557938, Hs.	
201847_at	LIPA	lipase A, lysosomal acid, cholesterol esterase (Wolman	5.49	-2.458	0.01	0.12	8.232	10.69	3988 Hs.643030	
204007_at	FCGR3B	Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	5.46	-2.451	0.025	0.18	4.19	6.641	2215 Hs.372679	
208146_s_at	CPVL	carboxypeptidase, vitellogenic-like	5.46	-2.451	0.023	0.17	5.123	7.574	54504 Hs.233389, Hs.	
220528_at	VNN3	vanin 3	5.46	-2.452	0.003	0.07	3.05	5.502	55350 Hs.183656	
202497_x_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter)	5.43	-2.439	0.002	0.06	6.909	9.348	6515 Hs.419240, Hs.	
201125_s_at	ITGB5	integrin, beta 5	5.43	-2.441	0.001	0.04	7.511	9.952	3693 Hs.536663	
208438_s_at	FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene	5.41	-2.431	0.001	0.05	7.688	10.119	2268 Hs.1422	
204614_at	SERPINF2	serpin peptidase inhibitor, clade B (ovalbumin), member	5.41	-2.432	0.017	0.15	11.004	13.436	5055 Hs.594481	
209568_s_at	RGL1	retinal guanine nucleotide dissociation stimulator-like 1	5.41	-2.437	0.004	0.08	8.803	11.239	23179 Hs.497148	
202800_at	SLC1A3	solute carrier family 1 (glial high affinity glutamate tran	5.38	-2.427	0.006	0.1	4.614	7.041	6507 Hs.481918	
203695_s_at	DFNA5	deafness, autosomal dominant 5	5.35	-2.418	0.012	0.13	6.908	9.326	1687 Hs.520708	
218559_s_at	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog	5.35	-2.418	0.018	0.15	10.592	13.01	9935 Hs.651210	
204470_at	CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth	5.35	-2.422	0.004	0.08	10.737	13.16	2919 Hs.789	
217202_s_at	GLUL	glutamate-ammonia ligase (glutamine synthetase)	5.32	-2.41	0.001	0.04	7.542	9.952	2752 Hs.518525	
208934_s_at	LGALS8	lectin, galactoside-binding, soluble, 8 (galectin 8)	5.29	-2.4	0.028	0.19	6.002	8.402	3964 Hs.4082, Hs.65	
219952_s_at	MCOLN1	mucolipin 1	5.29	-2.401	0.001	0.05	3.879	6.28	57192 Hs.631858	
204103_at	CCL4	chemokine (C-C motif) ligand 4	5.29	-2.404	0.014	0.13	9.489	11.893	6351 Hs.75703	
206026_s_at	TNFAIP6	tumor necrosis factor, alpha-induced protein 6	5.29	-2.404	0.001	0.05	8.591	10.995	7130 Hs.437322	
212655_at	ZCCHC14	zinc finger, CCHC domain containing 14	5.29	-2.407	0	0.01	3.213	5.621	23174 Hs.156231	
221920_s_at	SLC25A37	solute carrier family 25, member 37	5.26	-2.393	0.003	0.08	5.319	7.712	51312 Hs.122514, Hs.	
220034_at	IRAK3	interleukin-1 receptor-associated kinase 3	5.26	-2.397	0.002	0.06	4.545	6.942	11213 Hs.369265	
202437_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide	5.24	-2.385	0.004	0.08	10.182	12.568	1545 Hs.154654	
216035_x_at	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	5.24	-2.387	0.002	0.06	4.741	7.128	6934 Hs.593995	
201108_s_at	THBS1	thrombospondin 1	5.24	-2.388	0.002	0.06	10.566	12.954	7057 Hs.164226	
213848_at			5.24	-2.388	0.004	0.08	4.887	7.276		
208763_s_at	TSC22D3	TSC22 domain family, member 3	5.21	-2.377	0.003	0.07	6.295	8.672	1831 Hs.522074	
213274_s_at	CTSB	cathepsin B	5.21	-2.378	0.001	0.05	9.207	11.586	1508 Hs.520898	
214164_x_at	CA12	carbonic anhydrase XII	5.18	-2.373	0.005	0.09	5.133	7.506	771 Hs.210995	
205403_at	IL1R2	interleukin 1 receptor, type II	5.18	-2.374	0.015	0.14	9.855	12.229	7850 Hs.25333	
219183_s_at	PSCD4	pleckstrin homology, Sec7 and coiled-coil domains 4	5.18	-2.375	0	0.03	7.343	9.718	27128 Hs.170944	

OR Table E2 DEG.xls

Probe	Symbol	Description	FCH	lgFCH	P	fdr	Psor, BDCA+	Psor, BDCA-	Gene	UniGene
209459_s_at	ABAT	4-aminobutyrate aminotransferase	5.15	-2.363	0.007	0.1	6.019	8.383	18 Hs.336768, Hs.	
202087_s_at	CTSL1	cathepsin L1	5.15	-2.365	0.001	0.04	10.387	12.753	1514 Hs.418123	
202446_s_at	PLSCR1	phospholipid scramblase 1	5.13	-2.355	0	0.02	9.588	11.942	5359 Hs.130759	
212606_at	WDFY3	WD repeat and FYVE domain containing 3	5.13	-2.357	0.001	0.04	3.982	6.338	23001 Hs.480116	
218839_at	HEY1	hairy/enhancer-of-split related with YRPW motif 1	5.10	-2.353	0.013	0.13	2.898	5.251	23462 Hs.234434	
207433_at	IL10	interleukin 10	5.08	-2.342	0.027	0.19	3.727	6.069	3586 Hs.193717	
202917_s_at	S100A8	S100 calcium binding protein A8	5.08	-2.343	0.005	0.09	12.147	14.49	6279 Hs.416073	
205425_at	HIP1	huntingtin interacting protein 1	5.08	-2.344	0.002	0.06	3.805	6.149	3092 Hs.329266, Hs.	
209500_x_at	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	5.05	-2.334	0.009	0.12	7.602	9.936	8741 Hs.54673	
221840_at	PTPRE	protein tyrosine phosphatase, receptor type, E	5.05	-2.337	0.005	0.09	9.227	11.564	5791 Hs.127022	
213275_x_at	CTSB	cathepsin B	5.03	-2.33	0.001	0.04	10.703	13.033	1508 Hs.520898	
214366_s_at	ALOX5	arachidonate 5-lipoxygenase	5.00	-2.319	0.001	0.05	5.266	7.585	240 Hs.89499	
210643_at	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11	4.98	-2.315	0.014	0.14	2.409	4.724	8600 Hs.333791	
58780_s_at	FLJ10357	hypothetical protein FLJ10357	4.98	-2.317	0	0.03	6.397	8.714	55701 Hs.35125	
219451_at	MSRB2	methionine sulfoxide reductase B2	4.95	-2.305	0	0.02	4.123	6.428	22921 Hs.461420	
201780_s_at	RNF13	ring finger protein 13	4.95	-2.306	0	0.01	8.64	10.946	11342 Hs.12333	
202499_s_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter)	4.93	-2.299	0.012	0.13	9.881	12.18	6515 Hs.419240, Hs.	
219471_at	C13orf18	chromosome 13 open reading frame 18	4.90	-2.293	0.011	0.12	4.496	6.789	80183 Hs.98117	
204079_at	TPST2	tyrosylprotein sulfotransferase 2	4.88	-2.283	0.007	0.1	6.186	8.469	8459 Hs.694819	
215078_at	SOD2	superoxide dismutase 2, mitochondrial	4.88	-2.285	0.02	0.16	5.283	7.569	6648 Hs.487046	
216950_s_at	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)	4.88	-2.285	0.013	0.13	2.939	5.224	2209 Hs.77424	
31826_at	FKBP15	FK506 binding protein 15, 133kDa	4.85	-2.278	0	0.03	7.493	9.771	23307 Hs.522351	
217984_at	RNASET2	ribonuclease T2	4.85	-2.28	0.002	0.06	9.841	12.121	8635 Hs.529989	
207104_x_at	LILRB1	leukocyte immunoglobulin-like receptor, subfamily B (	4.85	-2.281	0.002	0.06	6.171	8.452	10859 Hs.655593, Hs.	
209514_s_at	RAB27A	RAB27A, member RAS oncogene family	4.83	-2.272	0	0.01	7.976	10.248	5873 Hs.654978	
204061_at	PRKX	protein kinase, X-linked	4.83	-2.274	0.001	0.04	4.036	6.31	5613 Hs.390788	
211661_x_at	PTAFR	platelet-activating factor receptor	4.83	-2.274	0.001	0.04	4.292	6.565	5724 Hs.433540	
208982_at	PECAM1	platelet/endothelial cell adhesion molecule (CD31 ant	4.81	-2.262	0.002	0.06	10.066	12.328	5175 Hs.514412	
217473_x_at	SLC11A1	solute carrier family 11 (proton-coupled divalent metal	4.81	-2.264	0.001	0.04	4.55	6.815	6556 Hs.591607	
203420_at	FAM8A1	family with sequence similarity 8, member A1	4.81	-2.268	0.004	0.08	5.66	7.928	51439 Hs.95260	
204236_at	FLI1	Friend leukemia virus integration 1	4.78	-2.257	0.003	0.07	7.749	10.006	2313 Hs.504281	
219694_at	FAM105A	family with sequence similarity 105, member A	4.78	-2.261	0	0.02	4.429	6.689	54491 Hs.591751	
212698_s_at	10-Sep	septin 10	4.76	-2.249	0.003	0.07	8.127	10.376	151011 Hs.469615	
201720_s_at	LAPTM5	lysosomal associated multispinning membrane prote	4.76	-2.252	0	0.03	9.022	11.274	7805 Hs.371021	
220122_at	MCTP1	multiple C2 domains, transmembrane 1	4.74	-2.244	0.004	0.08	3.191	5.435	79772 Hs.655087	
218807_at	VAV3	vav 3 guanine nucleotide exchange factor	4.74	-2.247	0.008	0.11	6.808	9.056	10451 Hs.267659	
207071_s_at	ACO1	aconitase 1, soluble	4.72	-2.236	0.001	0.05	4.275	6.512	48 Hs.651276	
214511_x_at	FCGR1B	Fc fragment of IgG, high affinity Ib, receptor (CD64)	4.72	-2.236	0.011	0.12	2.842	5.078	2210 Hs.534956	
202181_at	KIAA0247	KIAA0247	4.72	-2.239	0	0.03	8.228	10.467	9766 Hs.440025	
206504_at	CYP24A1	cytochrome P450, family 24, subfamily A, polypeptide	4.72	-2.241	0.012	0.13	2.493	4.734	1591 Hs.89663	
204225_at	HDAC4	histone deacetylase 4	4.69	-2.229	0.001	0.04	6.351	8.58	9759 Hs.20516, Hs.6	

OR Table E2 DEG.xls

Probe	Symbol	Description	FCH	lgFCH	P	fdr	Psor, BDCA+	Psor, BDCA-	Gene	UniGene
217078_s_at	CD300A	CD300a molecule	4.67	-2.224	0.003	0.07	2.881	5.106	11314 Hs.9688	
212226_s_at	PPAP2B	phosphatidic acid phosphatase type 2B	4.67	-2.225	0.004	0.08	4.133	6.358	8613 Hs.405156, Hs.	
201936_s_at	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	4.65	-2.216	0.001	0.06	4.573	6.789	8672 Hs.467084	
205767_at	EREG	epiregulin	4.65	-2.219	0.003	0.07	10.327	12.546	2069 Hs.115263	
212383_at	ATP6V0A1	ATPase, H+ transporting, lysosomal V0 subunit a1	4.65	-2.221	0	0.04	4.999	7.22	535 Hs.463074	
218856_at	TNFRSF21	tumor necrosis factor receptor superfamily, member 2	4.63	-2.209	0.003	0.07	4.58	6.789	27242 Hs.443577	
210817_s_at	CALCOCO2	calcium binding and coiled-coil domain 2	4.63	-2.211	0	0.02	5.699	7.911	10241 Hs.514920	
201694_s_at	EGR1	early growth response 1	4.63	-2.212	0.011	0.12	7.311	9.523	1958 Hs.326035	
218145_at	TRIB3	tribbles homolog 3 (Drosophila)	4.61	-2.202	0.001	0.05	3.828	6.03	57761 Hs.516826	
221081_s_at	DENND2D	DENN/MADD domain containing 2D	4.61	-2.202	0.003	0.07	5.752	7.954	79961 Hs.557850	
204215_at	C7orf23	chromosome 7 open reading frame 23	4.61	-2.205	0.006	0.09	5.225	7.43	79161 Hs.196129	
205114_s_at	CCL3	chemokine (C-C motif) ligand 3	4.59	-2.199	0.014	0.13	10.713	12.912	6348 Hs.514107	
220023_at	APOB48R	apolipoprotein B48 receptor	4.57	-2.19	0	0.01	3.75	5.941	55911 Hs.200333	
209515_s_at	RAB27A	RAB27A, member RAS oncogene family	4.57	-2.194	0.001	0.05	6.957	9.151	5873 Hs.654978	
204834_at	FGL2	fibrinogen-like 2	4.55	-2.183	0.01	0.12	6.853	9.036	10875 Hs.520989	
203936_s_at	MMP9	matrix metalloproteinase 9 (gelatinase B, 92kDa gelati	4.52	-2.18	0.002	0.06	11.791	13.971	4318 Hs.297413	
212820_at	DMXL2	Dmx-like 2	4.50	-2.17	0	0.01	8.848	11.017	23312 Hs.511386	
207980_s_at	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich	4.48	-2.166	0.014	0.13	4.88	7.046	10370 Hs.82071	
221698_s_at	CLEC7A	C-type lectin domain family 7, member A	4.46	-2.156	0.004	0.08	8.568	10.724	64581 Hs.143929	
202436_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide	4.46	-2.157	0.004	0.08	9.65	11.808	1545 Hs.154654	
201721_s_at	LAPTM5	lysosomal associated multispinning membrane prote	4.44	-2.149	0	0.03	11.96	14.109	7805 Hs.371021	
205147_x_at	NCF4	neutrophil cytosolic factor 4, 40kDa	4.44	-2.151	0.003	0.07	6.281	8.431	4689 Hs.474781	
35974_at	LRMP	lymphoid-restricted membrane protein	4.44	-2.153	0.011	0.12	3.731	5.884	4033 Hs.124922	
218806_s_at	VAV3	vav 3 guanine nucleotide exchange factor	4.44	-2.154	0.002	0.07	3.047	5.201	10451 Hs.267659	
208893_s_at	DUSP6	dual specificity phosphatase 6	4.44	-2.155	0.014	0.13	6.669	8.824	1848 Hs.298654	
209276_s_at	GLRX	glutaredoxin (thioltransferase)	4.44	-2.155	0	0.03	7.171	9.326	2745 Hs.28988	
204748_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandi	4.42	-2.145	0.003	0.07	10.139	12.285	5743 Hs.196384	
201288_at	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	4.42	-2.147	0.012	0.13	10.741	12.888	397 Hs.504877	
201110_s_at	THBS1	thrombospondin 1	4.42	-2.149	0.004	0.08	10.379	12.528	7057 Hs.164226	
218853_s_at	MOSPD1	motile sperm domain containing 1	4.41	-2.136	0.001	0.04	3.75	5.887	56180 Hs.590789	
214370_at	S100A8	S100 calcium binding protein A8	4.41	-2.14	0.005	0.09	5.992	8.132	6279 Hs.416073	
210058_at	MAPK13	mitogen-activated protein kinase 13	4.39	-2.131	0.006	0.09	5.487	7.618	5603 Hs.178695	
205476_at	CCL20	chemokine (C-C motif) ligand 20	4.39	-2.134	0.001	0.04	10.548	12.681	6364 Hs.75498	
208158_s_at	OSBPL1A	oxysterol binding protein-like 1A	4.35	-2.118	0.007	0.1	5.358	7.475	114876 Hs.370725	
218113_at	TMEM2	transmembrane protein 2	4.35	-2.118	0.011	0.12	5.484	7.602	23670 Hs.494146	
206363_at	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene hc	4.35	-2.121	0.028	0.19	7.892	10.012	4094 Hs.134859	
207852_at	CXCL5	chemokine (C-X-C motif) ligand 5	4.35	-2.122	0	0.04	2.971	5.092	6374 Hs.89714	
218773_s_at	MSRB2	methionine sulfoxide reductase B2	4.33	-2.116	0	0.03	6.322	8.438	22921 Hs.461420	
203904_x_at	CD82	CD82 molecule	4.31	-2.107	0.006	0.09	6.807	8.914	3732 Hs.527778	
206020_at	SOCS6	suppressor of cytokine signaling 6	4.29	-2.102	0.002	0.06	4.806	6.908	9306 Hs.44439, Hs.6	
218764_at	PRKCH	protein kinase C, eta	4.29	-2.102	0.001	0.04	8.029	10.131	5583 Hs.333907	

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Probe	Symbol	Description	FCH	lgFCH	P	fdr	Psor, BDCA+	Psor, BDCA-	Gene	UniGene
209566_at	INSIG2	insulin induced gene 2	4.29	-2.104	0	0.03	5.907	8.011	51141 Hs.7089	
203416_at	CD53	CD53 molecule	4.27	-2.093	0.001	0.04	11.051	13.144	963 Hs.443057	
201942_s_at	CPD	carboxypeptidase D	4.26	-2.087	0.001	0.04	4.374	6.46	1362 Hs.446079	
221601_s_at	FAIM3	Fas apoptotic inhibitory molecule 3	4.24	-2.084	0.002	0.06	5.267	7.351	9214 Hs.58831	
213385_at	CHN2	chimerin (chimaerin) 2	4.22	-2.077	0.025	0.18	3.055	5.132	1124 Hs.594763, Hs.	
213629_x_at	MT1JP	metallothionein 1J (pseudogene)	4.22	-2.079	0.004	0.08	7.936	10.016	4498 Hs.513626	
209122_at	ADFP	adipose differentiation-related protein	4.22	-2.08	0.001	0.06	12.254	14.334	123 Hs.3416	
201259_s_at	SYPL1	synaptophysin-like 1	4.20	-2.069	0	0.03	5.73	7.8	6856 Hs.80919	
201272_at	AKR1B1	aldo-keto reductase family 1, member B1 (aldose red	4.18	-2.063	0.002	0.06	9.172	11.234	231 Hs.521212	
219191_s_at	BIN2	bridging integrator 2	4.18	-2.067	0.001	0.04	3.257	5.324	51411 Hs.14770	
210053_at	TAF5	TAF5 RNA polymerase II, TATA box binding protein (T	4.17	-2.058	0.029	0.19	4.703	6.761	6877 Hs.96103	
204249_s_at	LMO2	LIM domain only 2 (rhombotin-like 1)	4.13	-2.044	0	0.03	7.981	10.025	4005 Hs.34560	
202901_x_at	CTSS	cathepsin S	4.13	-2.046	0.001	0.04	8.979	11.025	1520 Hs.181301	
211794_at	FYB	FYN binding protein (FYB-120/130)	4.12	-2.043	0.029	0.19	3.568	5.61	2533 Hs.370503	
201765_s_at	HEXA	hexosaminidase A (alpha polypeptide)	4.08	-2.03	0.004	0.08	5.832	7.862	3073 Hs.604479, Hs.	
217826_s_at	UBE2J1	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog	4.07	-2.021	0.002	0.06	5.296	7.316	51465 Hs.163776	
204401_at	KCNN4	potassium intermediate/small conductance calcium-a	4.07	-2.024	0.014	0.13	3.413	5.438	3783 Hs.10082	
219165_at	PDLIM2	PDZ and LIM domain 2 (mystique)	4.05	-2.018	0.012	0.12	5.518	7.536	64236 Hs.632034	
201393_s_at	IGF2R	insulin-like growth factor 2 receptor	4.03	-2.013	0.001	0.04	7.4	9.413	3482 Hs.487062	
200838_at	CTSB	cathepsin B	4.02	-2.003	0.003	0.07	12.02	14.023	1508 Hs.520898	
221581_s_at	LAT2	linker for activation of T cells family, member 2	4.02	-2.003	0	0.01	7.335	9.338	7462 Hs.647049	
212946_at	RP11-125A7.3	KIAA0564 protein	4.02	-2.004	0.004	0.08	3.064	5.068	23078 Hs.368282	
213056_at	FRMD4B	FERM domain containing 4B	4.00	-2	0.003	0.07	3.991	5.991	23150 Hs.371681	
203124_s_at	SLC11A2	solute carrier family 11 (proton-coupled divalent meta	4.00	-2.001	0.002	0.06	6.684	8.685	4891 Hs.505545	
205267_at	POU2AF1	POU class 2 associating factor 1	4.00	-2.003	0.011	0.12	2.924	4.927	5450 Hs.654525	
212989_at	SGMS1	sphingomyelin synthase 1	3.98	-1.995	0.001	0.04	7.569	9.564	259230 Hs.654698	
221211_s_at	C21orf7	chromosome 21 open reading frame 7	3.98	-1.997	0.01	0.12	2.99	4.987	56911 Hs.222802	
200784_s_at	LRP1	low density lipoprotein-related protein 1 (alpha-2-mac	3.97	-1.986	0.007	0.1	4.279	6.265	4035 Hs.162757	
219553_at	NME7	non-metastatic cells 7, protein expressed in (nucleosi	3.97	-1.99	0.004	0.08	4.43	6.42	29922 Hs.693856	
209300_s_at	NECAP1	NECAP endocytosis associated 1	3.97	-1.991	0.002	0.06	6.03	8.021	25977 Hs.555927	
210184_at	ITGAX	integrin, alpha X (complement component 3 receptor	3.95	-1.981	0.009	0.11	5.768	7.749	3687 Hs.248472	
202902_s_at	CTSS	cathepsin S	3.95	-1.983	0.005	0.09	7.948	9.931	1520 Hs.181301	
206687_s_at	PTPN6	protein tyrosine phosphatase, non-receptor type 6	3.95	-1.984	0.002	0.06	7.09	9.074	5777 Hs.63489	
204436_at	PLEKHQ1	pleckstrin homology domain containing, family Q men	3.95	-1.985	0.001	0.04	6.629	8.614	80301 Hs.207157	
203123_s_at	SLC11A2	solute carrier family 11 (proton-coupled divalent meta	3.94	-1.975	0	0.03	6.926	8.902	4891 Hs.505545	
209774_x_at	CXCL2	chemokine (C-X-C motif) ligand 2	3.94	-1.976	0.001	0.04	11.787	13.763	2920 Hs.590921	
205006_s_at	NMT2	N-myristoyltransferase 2	3.92	-1.969	0.028	0.19	3.171	5.141	9397 Hs.60339	
204861_s_at	NAIP	NLR family, apoptosis inhibitory protein	3.92	-1.97	0.005	0.09	4.513	6.483	4671 Hs.646951, Hs.	
206390_x_at	PF4	platelet factor 4 (chemokine (C-X-C motif) ligand 4)	3.89	-1.961	0.003	0.07	2.65	4.611	5196 Hs.81564	
202990_at	PYGL	phosphorylase, glycogen; liver (Hers disease, glycog	3.88	-1.956	0.002	0.06	8.04	9.996	5836 Hs.282417	
37152_at	PPARD	peroxisome proliferator-activated receptor delta	3.85	-1.943	0.001	0.05	5.821	7.764	5467 Hs.485196	

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Probe	Symbol	Description	FCH	lgFCH	P	fdr	Psor, BDCA+	Psor, BDCA-	Gene	UniGene
218136_s_at	SLC25A37	solute carrier family 25, member 37	3.83	-1.937	0	0.01	3.95	5.887	51312	Hs.122514, Hs.
212830_at	MEGF9	multiple EGF-like-domains 9	3.83	-1.938	0.002	0.06	8.28	10.219	1955	Hs.494977
207016_s_at	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	3.80	-1.928	0.003	0.07	1.882	3.811	8854	Hs.643455
204563_at	SELL	selectin L (lymphocyte adhesion molecule 1)	3.80	-1.929	0.03	0.19	7.204	9.133	6402	Hs.82848
201313_at	ENO2	enolase 2 (gamma, neuronal)	3.79	-1.92	0.019	0.15	5.24	7.16	2026	Hs.511915
204759_at	RCBTB2	regulator of chromosome condensation (RCC1) and E	3.79	-1.924	0.001	0.05	8.98	10.904	1102	Hs.657385
208426_x_at	KIR2DL4	killer cell immunoglobulin-like receptor, two domains,	3.79	-1.924	0.002	0.07	1.966	3.89	3805	Hs.651287, Hs.
211336_x_at	LILRB1	leukocyte immunoglobulin-like receptor, subfamily B (	3.77	-1.914	0.002	0.07	5.978	7.893	10859	Hs.655593, Hs.
205003_at	DOCK4	dedicator of cytokinesis 4	3.77	-1.918	0.001	0.04	8.292	10.21	9732	Hs.654652
213119_at	SLC36A1	solute carrier family 36 (proton/amino acid symporter)	3.76	-1.912	0.001	0.05	7.119	9.031	206358	Hs.269004
204362_at	SKAP2	src kinase associated phosphoprotein 2	3.76	-1.913	0.004	0.08	8.622	10.535	8935	Hs.200770, Hs.
221704_s_at	VPS37B	vacuolar protein sorting 37 homolog B (S. cerevisiae)	3.75	-1.903	0.003	0.07	5.751	7.654	79720	Hs.507162
210951_x_at	RAB27A	RAB27A, member RAS oncogene family	3.73	-1.898	0	0.02	9.014	10.912	5873	Hs.654978
211330_s_at	HFE	hemochromatosis	3.73	-1.899	0.007	0.11	3.036	4.935	3077	Hs.233325
204958_at	PLK3	polo-like kinase 3 (Drosophila)	3.72	-1.893	0.001	0.04	4.319	6.212	1263	Hs.632415
201368_at	ZFP36L2	zinc finger protein 36, C3H type-like 2	3.72	-1.897	0.004	0.08	8.887	10.784	678	Hs.503093, Hs.
213702_x_at	ASAHI	N-acylsphingosine amidohydrolase (acid ceramidase)	3.68	-1.877	0.002	0.06	11.928	13.806	427	Hs.527412
202888_s_at	ANPEP	alanyl (membrane) aminopeptidase (aminopeptidase	3.68	-1.878	0	0.02	9.901	11.779	290	Hs.1239
208944_at	TGFBR2	transforming growth factor, beta receptor II (70/80kDa	3.68	-1.878	0	0.01	7.752	9.63	7048	Hs.82028, Hs.6
210059_s_at	MAPK13	mitogen-activated protein kinase 13	3.66	-1.873	0.006	0.1	6.475	8.348	5603	Hs.178695
204949_at	ICAM3	intercellular adhesion molecule 3	3.65	-1.866	0.012	0.13	7.235	9.101	3385	Hs.654563
202005_at	ST14	suppression of tumorigenicity 14 (colon carcinoma)	3.65	-1.868	0.012	0.13	5.662	7.53	6768	Hs.504315
208650_s_at	CD24	CD24 molecule	3.65	-1.868	0.01	0.12	3.374	5.242	934	Hs.644105, Hs.
209684_at	RIN2	Ras and Rab interactor 2	3.64	-1.861	0.01	0.12	8.628	10.489	54453	Hs.472270
201324_at	EMP1	epithelial membrane protein 1	3.64	-1.862	0.004	0.08	8.494	10.356	2012	Hs.436298
49452_at	ACACB	acetyl-Coenzyme A carboxylase beta	3.64	-1.862	0.002	0.06	2.846	4.708	32	Hs.234898
213805_at	ABHD5	abhydrolase domain containing 5	3.62	-1.856	0.004	0.08	2.917	4.773	51099	Hs.19385, Hs.6
219777_at	GIMAP6	GTPase, IMAP family member 6	3.62	-1.86	0.005	0.09	6.789	8.649	474344	Hs.647105
201739_at	SGK	serum/glucocorticoid regulated kinase	3.60	-1.845	0.027	0.19	7.89	9.734	6446	Hs.510078
212224_at	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	3.60	-1.845	0.024	0.17	2.467	4.312	216	Hs.76392
212905_at	CSTF2T	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64	3.60	-1.845	0	0.02	5.98	7.825	23283	Hs.591358
205568_at	AQP9	aquaporin 9	3.58	-1.841	0.001	0.04	9.694	11.535	366	Hs.104624
201976_s_at	MYO10	myosin X	3.56	-1.83	0.024	0.18	2.696	4.527	4651	Hs.43334, Hs.4
204732_s_at	TRIM23	tripartite motif-containing 23	3.56	-1.83	0.012	0.13	4.003	5.832	373	Hs.792
211368_s_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (inte	3.55	-1.829	0.006	0.09	8.201	10.03	834	Hs.2490
201461_s_at	MAPKAPK2	mitogen-activated protein kinase-activated protein kin	3.53	-1.819	0.023	0.17	3.613	5.432	9261	Hs.643566
204650_s_at	APBB3	amyloid beta (A4) precursor protein-binding, family B,	3.53	-1.821	0.017	0.15	2.745	4.566	10307	Hs.529449
210858_x_at	ATM	ataxia telangiectasia mutated	3.53	-1.821	0.002	0.06	4.786	6.607	472	Hs.367437
44790_s_at	C13orf18	chromosome 13 open reading frame 18	3.52	-1.814	0.017	0.15	6.827	8.641	80183	Hs.98117
219869_s_at	SLC39A8	solute carrier family 39 (zinc transporter), member 8	3.52	-1.817	0.014	0.13	5.555	7.372	64116	Hs.288034
203411_s_at	LMNA	lamin A/C	3.52	-1.818	0.01	0.12	7.007	8.825	4000	Hs.594444, Hs.

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Probe	Symbol	Description	FCH	lgFCH	P	fdr	Psor, BDCA+	Psor, BDCA-	Gene	UniGene
200973_s_at	TSPAN3	tetraspanin 3	3.51	-1.81	0.004	0.08	6.871	8.681	10099	Hs.5062
202193_at	LIMK2	LIM domain kinase 2	3.51	-1.81	0.003	0.07	7.263	9.073	3985	Hs.474596
212154_at	SDC2	syndecan 2	3.51	-1.813	0.008	0.11	8.254	10.067	6383	Hs.1501, Hs.59
212230_at	PPAP2B	phosphatidic acid phosphatase type 2B	3.50	-1.807	0.016	0.14	5.107	6.913	8613	Hs.405156, Hs.
200919_at	PHC2	polyhomeotic homolog 2 (Drosophila)	3.47	-1.794	0.009	0.12	9.262	11.056	1912	Hs.524271
202062_s_at	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	3.47	-1.796	0.001	0.05	3.128	4.923	6400	Hs.181300
205251_at	PER2	period homolog 2 (Drosophila)	3.47	-1.797	0.001	0.04	4.229	6.026	8864	Hs.58756
211495_x_at	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	3.47	-1.797	0.013	0.13	3.731	5.528	8741	Hs.54673
208370_s_at	RCAN1	regulator of calcineurin 1	3.47	-1.798	0.005	0.09	9.091	10.888	1827	Hs.282326
201811_x_at	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	3.46	-1.791	0.001	0.04	9.405	11.196	9467	Hs.257761, Hs.
203209_at	RFC5	replication factor C (activator 1) 5, 36.5kDa	3.46	-1.792	0.002	0.06	4.461	6.253	5985	Hs.506989
211429_s_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiprotein	3.46	-1.792	0	0.03	11.141	12.933	5265	Hs.525557
218043_s_at	AZI2	5-azacytidine induced 2	3.46	-1.792	0	0.03	6.638	8.43	64343	Hs.444724
202155_s_at	NUP214	nucleoporin 214kDa	3.46	-1.793	0.003	0.07	7.389	9.182	8021	Hs.654530
215001_s_at	GLUL	glutamate-ammonia ligase (glutamine synthetase)	3.45	-1.786	0	0.03	12.395	14.181	2752	Hs.518525
216199_s_at	MAP3K4	mitogen-activated protein kinase kinase kinase 4	3.44	-1.78	0.024	0.18	8.202	9.982	4216	Hs.390428
212745_s_at	BBS4	Bardet-Biedl syndrome 4	3.42	-1.775	0	0.03	5.169	6.943	585	Hs.208681
217865_at	RNF130	ring finger protein 130	3.42	-1.776	0.004	0.08	9.088	10.864	55819	Hs.484363
202833_s_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiprotein	3.42	-1.777	0.001	0.04	9.758	11.536	5265	Hs.525557
221058_s_at	CKLF	chemokine-like factor	3.42	-1.778	0.007	0.1	7.423	9.201	51192	Hs.15159
214091_s_at	GPX3	glutathione peroxidase 3 (plasma)	3.41	-1.772	0.026	0.18	5.358	7.13	2878	Hs.386793
221898_at	PDPN	podoplanin	3.41	-1.773	0.023	0.17	8.893	10.667	10630	Hs.468675
206991_s_at	CCR5	chemokine (C-C motif) receptor 5	3.40	-1.764	0.01	0.12	8.621	10.385	1234	Hs.450802, Hs.
202192_s_at	GAS7	growth arrest-specific 7	3.40	-1.766	0.001	0.04	5.86	7.626	8522	Hs.462214
218019_s_at	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	3.40	-1.768	0.003	0.07	6.059	7.827	8566	Hs.284491
211732_x_at	HNMT	histamine N-methyltransferase	3.39	-1.762	0.016	0.14	6.409	8.17	3176	Hs.42151
201941_at	CPD	carboxypeptidase D	3.38	-1.755	0.002	0.06	7.531	9.286	1362	Hs.446079
209460_at	ABAT	4-aminobutyrate aminotransferase	3.38	-1.758	0.011	0.12	5.238	6.996	18	Hs.336768, Hs.
202449_s_at	RXRA	retinoid X receptor, alpha	3.37	-1.752	0.005	0.09	8.125	9.877	6256	Hs.590886
213475_s_at	ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte 1	3.36	-1.746	0.009	0.12	7.356	9.102	3683	Hs.174103
209868_s_at	RBMS1	RNA binding motif, single stranded interacting protein	3.36	-1.748	0.001	0.06	5.987	7.735	5937	Hs.470412
218128_at	NFYB	nuclear transcription factor Y, beta	3.36	-1.749	0.001	0.04	4.974	6.723	4801	Hs.84928
204158_s_at	TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting,	3.34	-1.74	0.004	0.08	9.221	10.962	10312	Hs.495985
213528_at	C1orf156	chromosome 1 open reading frame 156	3.34	-1.742	0.006	0.09	2.686	4.428	92342	Hs.33922
217627_at	ZNF573	zinc finger protein 573	3.34	-1.744	0	0.01	4.55	6.294	126231	Hs.531262
210980_s_at	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase)	3.33	-1.737	0.003	0.07	10.548	12.286	427	Hs.527412
213902_at	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase)	3.33	-1.738	0.009	0.11	8.66	10.398	427	Hs.527412
206548_at	hCG_1776259	hypothetical protein FLJ23556	3.32	-1.73	0.02	0.16	3.519	5.25	79938	Hs.655463
208653_s_at	CD164	CD164 molecule, sialomucin	3.32	-1.73	0.002	0.06	8.485	10.215	8763	Hs.520313
205505_at	GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,	3.32	-1.734	0.004	0.08	3.136	4.871	2650	Hs.521568
202733_at	P4HA2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (pr	3.30	-1.72	0.002	0.07	6.154	7.875	8974	Hs.519568

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Probe	Symbol	Description	FCH	lgFCH	P	fdr	Psor, BDCA+	Psor, BDCA-	Gene	UniGene
214637_at	OSM	oncostatin M	3.30	-1.724	0.008	0.11	2.488	4.213	5008	Hs.248156
203096_s_at	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	3.29	-1.718	0.007	0.1	5.067	6.786	9693	Hs.113912
218404_at	SNX10	sorting nexin 10	3.29	-1.719	0.003	0.07	8.246	9.965	29887	Hs.571296
219980_at	C4orf29	chromosome 4 open reading frame 29	3.29	-1.72	0.011	0.12	4.563	6.283	80167	Hs.445817
212157_at	SDC2	syndecan 2	3.28	-1.711	0.013	0.13	5.346	7.057	6383	Hs.1501, Hs.59
218924_s_at	CTBS	chitinase, di-N-acetyl-	3.28	-1.711	0	0.01	7.113	8.824	1486	Hs.513557
211366_x_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (inte	3.28	-1.713	0.005	0.09	7.449	9.162	834	Hs.2490
209689_at	CCDC93	coiled-coil domain containing 93	3.28	-1.714	0.005	0.09	4.529	6.243	54520	Hs.107845
203245_s_at	FLJ35348	FLJ35348	3.28	-1.715	0.008	0.11	4.017	5.732	266655	Hs.592770, Hs.
203066_at	GALNAC4S-6ST	B cell RAG associated protein	3.27	-1.709	0	0.03	9.696	11.405	51363	Hs.287537
212242_at	TUBA4A	tubulin, alpha 4a	3.27	-1.71	0.003	0.08	9.289	10.999	7277	Hs.75318
209238_at	STX3	syntaxin 3	3.24	-1.692	0.008	0.11	6.405	8.097	6809	Hs.180711
201325_s_at	EMP1	epithelial membrane protein 1	3.24	-1.695	0.013	0.13	5.857	7.552	2012	Hs.436298
204361_s_at	SKAP2	src kinase associated phosphoprotein 2	3.24	-1.695	0.01	0.12	4.122	5.817	8935	Hs.200770, Hs.
203234_at	UPP1	uridine phosphorylase 1	3.23	-1.688	0.001	0.04	9.123	10.811	7378	Hs.488240
211367_s_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (inte	3.23	-1.689	0.007	0.1	6.029	7.718	834	Hs.2490
212459_x_at	SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	3.23	-1.689	0.027	0.19	3.953	5.642	8801	Hs.655250
218217_at	SCPEP1	serine carboxypeptidase 1	3.23	-1.69	0.023	0.17	7.013	8.703	59342	Hs.514950
214835_s_at	SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	3.23	-1.692	0.008	0.11	5.041	6.732	8801	Hs.655250
209719_x_at	SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), memt	3.21	-1.681	0.018	0.15	1.579	3.26	6317	Hs.227948
213236_at	SASH1	SAM and SH3 domain containing 1	3.19	-1.677	0.017	0.15	3.95	5.627	23328	Hs.193133
219232_s_at	EGLN3	egl nine homolog 3 (C. elegans)	3.19	-1.677	0.013	0.13	5.963	7.641	112399	Hs.135507
222294_s_at	RAB27A	RAB27A, member RAS oncogene family	3.18	-1.67	0.002	0.06	7.847	9.517	5873	Hs.654978
202862_at	FAH	fumarylacetoacetate hydrolase (fumarylacetoacetase)	3.18	-1.672	0.019	0.16	5.306	6.978	2184	Hs.73875
213480_at	VAMP4	vesicle-associated membrane protein 4	3.17	-1.665	0.002	0.06	8.533	10.198	8674	Hs.6651
201849_at	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	3.17	-1.667	0.004	0.08	8.85	10.517	664	Hs.144873
219889_at	FRAT1	frequently rearranged in advanced T-cell lymphomas	3.17	-1.669	0.03	0.19	4.611	6.28	10023	Hs.126057
209398_at	HIST1H1C	histone cluster 1, H1c	3.16	-1.66	0.024	0.18	8.107	9.767	3006	Hs.7644
204950_at	CARD8	caspase recruitment domain family, member 8	3.16	-1.663	0.008	0.11	6.771	8.434	22900	Hs.446146, Hs.
205718_at	ITGB7	integrin, beta 7	3.16	-1.663	0.003	0.07	6.476	8.139	3695	Hs.654470
211100_x_at	LILRA2	leukocyte immunoglobulin-like receptor, subfamily A (	3.15	-1.658	0	0.03	2.711	4.369	11027	Hs.655593
202594_at	LEPROTL1	leptin receptor overlapping transcript-like 1	3.15	-1.659	0.009	0.12	6.33	7.988	23484	Hs.146585
205443_at	SNAPC1	small nuclear RNA activating complex, polypeptide 1,	3.13	-1.644	0.001	0.05	6.278	7.922	6617	Hs.179312
221864_at	ORAI3	ORAI calcium release-activated calcium modulator 3	3.13	-1.644	0.007	0.1	7.269	8.913	93129	Hs.460617
211913_s_at	MERTK	c-mer proto-oncogene tyrosine kinase	3.13	-1.646	0.004	0.08	2.556	4.202	10461	Hs.306178, Hs.
214020_x_at	ITGB5	integrin, beta 5	3.12	-1.638	0.01	0.12	7.952	9.59	3693	Hs.536663
214054_at	DOK2	docking protein 2, 56kDa	3.12	-1.641	0.009	0.12	6.441	8.082	9046	Hs.71215
209467_s_at	MKNK1	MAP kinase interacting serine/threonine kinase 1	3.11	-1.634	0.003	0.07	7.694	9.328	8569	Hs.371594
214582_at	PDE3B	phosphodiesterase 3B, cGMP-inhibited	3.11	-1.635	0	0.02	4.769	6.404	5140	Hs.656437
221815_at	ABHD2	abhydrolase domain containing 2	3.11	-1.635	0.015	0.14	6.068	7.702	11057	Hs.122337, Hs.
201940_at	CPD	carboxypeptidase D	3.11	-1.636	0	0.01	8.13	9.767	1362	Hs.446079

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Probe	Symbol	Description	FCH	lgFCH	P	fdr	Psor, BDCA+	Psor, BDCA-	Gene	UniGene
218196_at	OSTM1	osteopetrosis associated transmembrane protein 1	3.11	-1.636	0.006	0.09	8.497	10.133	28962	Hs.226780, Hs.
208130_s_at	TBXAS1	thromboxane A synthase 1 (platelet, cytochrome P450)	3.10	-1.631	0.007	0.1	5.277	6.908	6916	Hs.520757
222146_s_at	TCF4	transcription factor 4	3.10	-1.632	0.004	0.08	6.089	7.721	6925	Hs.644653
203528_at	SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane	3.09	-1.624	0.006	0.1	6.184	7.808	10507	Hs.655281
202353_s_at	PSMD12	proteasome (prosome, macropain) 26S subunit, non-	3.09	-1.626	0.001	0.04	5.267	6.893	5718	Hs.646575
217963_s_at	NGFRAP1	nerve growth factor receptor (TNFRSF16) associated	3.09	-1.628	0.023	0.17	9.319	10.947	27018	Hs.448588
202975_s_at	RHOBTB3	Rho-related BTB domain containing 3	3.08	-1.621	0.005	0.09	2.413	4.034	22836	Hs.445030
209970_x_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin-1)	3.08	-1.621	0.006	0.09	8.647	10.268	834	Hs.2490
213839_at	KIAA0500	KIAA0500 protein	3.08	-1.621	0.026	0.18	6.518	8.139	57237	Hs.593760
207233_s_at	MITF	microphthalmia-associated transcription factor	3.08	-1.622	0.008	0.11	6.336	7.957	4286	Hs.166017, Hs.
220193_at	C1orf113	chromosome 1 open reading frame 113	3.06	-1.611	0.005	0.09	5.031	6.643	79729	Hs.524496
213109_at	TNIK	TRAF2 and NCK interacting kinase	3.06	-1.614	0	0.02	2.641	4.256	23043	Hs.34024
200972_at	TSPAN3	tetraspanin 3	3.05	-1.606	0.003	0.08	8.894	10.5	10099	Hs.5062
203505_at	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	3.05	-1.609	0.002	0.06	9.723	11.331	19	Hs.429294
213103_at	STARD13	StAR-related lipid transfer (START) domain containing 13	3.04	-1.602	0.01	0.12	2.682	4.285	90627	Hs.507704
221569_at	AHL1	Abelson helper integration site 1	3.04	-1.603	0.02	0.16	5.65	7.253	54806	Hs.386684
213199_at	DKFZP586P012K	hypothetical protein	3.04	-1.604	0.003	0.07	5.281	6.885	26005	Hs.557938, Hs.
201028_s_at	CD99	CD99 molecule	3.04	-1.605	0.011	0.12	7.095	8.701	4267	Hs.654354
203402_at	KCNAB2	potassium voltage-gated channel, shaker-related subunit	3.02	-1.594	0.014	0.13	4.788	6.382	8514	Hs.440497
221656_s_at	ARHGEF10L	Rho guanine nucleotide exchange factor (GEF) 10-like	3.02	-1.596	0.009	0.12	5.528	7.124	55160	Hs.443460
206770_s_at	SLC35A3	solute carrier family 35 (UDP-N-acetylglucosamine (U)	3.02	-1.597	0.001	0.04	4.695	6.292	23443	Hs.448979
213497_at	ABTB2	ankyrin repeat and BTB (POZ) domain containing 2	0.33	1.585	0.015	0.14	7.177	5.592	25841	Hs.23361
218907_s_at	LRRC61	leucine rich repeat containing 61	0.33	1.589	0.011	0.12	5.348	3.759	65999	Hs.647119
219584_at	PLA1A	phospholipase A1 member A	0.33	1.593	0.009	0.11	4.693	3.1	51365	Hs.437451
215342_s_at	RABGAP1L	RAB GTPase activating protein 1-like	0.33	1.593	0.027	0.19	6.873	5.279	9910	Hs.585378
220297_at	BTBD7	BTB (POZ) domain containing 7	0.33	1.594	0.006	0.09	5.345	3.751	55727	Hs.525549
208433_s_at	LRP8	low density lipoprotein receptor-related protein 8, apo	0.33	1.598	0.005	0.09	8.213	6.615	7804	Hs.576154
204875_s_at	GMDS	GDP-mannose 4,6-dehydratase	0.33	1.598	0.015	0.14	5.675	4.077	2762	Hs.144496, Hs.
218928_s_at	SLC37A1	solute carrier family 37 (glycerol-3-phosphate transpo	0.33	1.599	0.001	0.05	8.249	6.65	54020	Hs.547009
201391_at	TRAP1	TNF receptor-associated protein 1	0.33	1.603	0.001	0.04	7.819	6.215	10131	Hs.30345
211056_s_at	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo	0.33	1.605	0.013	0.13	7.23	5.625	6715	Hs.552
209369_at	ANXA3	annexin A3	0.33	1.608	0.023	0.17	8.39	6.782	306	Hs.480042
212311_at	KIAA0746	KIAA0746 protein	0.33	1.61	0.02	0.16	4.912	3.301	23231	Hs.479384
204352_at	TRAF5	TNF receptor-associated factor 5	0.33	1.611	0.012	0.13	10.057	8.446	7188	Hs.523930
203506_s_at	MED12	mediator complex subunit 12	0.33	1.612	0.008	0.11	6.218	4.606	9968	Hs.409226
212458_at	SPRED2	sprouty-related, EVH1 domain containing 2	0.33	1.613	0.004	0.08	9.559	7.946	200734	Hs.59332
202771_at	FAM38A	family with sequence similarity 38, member A	0.33	1.614	0.003	0.07	8.465	6.85	9780	Hs.513807
203036_s_at	MTSS1	metastasis suppressor 1	0.33	1.621	0	0.01	7.779	6.158	9788	Hs.336994, Hs.
204992_s_at	PFN2	profilin 2	0.32	1.621	0.019	0.16	5.833	4.211	5217	Hs.91747
211071_s_at	MLLT11	myeloid/lymphoid or mixed-lineage leukemia (trithorax)	0.32	1.627	0.018	0.15	9.521	7.894	10962	Hs.75823
205192_at	MAP3K14	mitogen-activated protein kinase kinase kinase 14	0.32	1.63	0.029	0.19	10.209	8.579	9020	Hs.404183

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Probe	Symbol	Description	FCH	lgFCH	P	fdr	Psor, BDCA+	Psor, BDCA-	Gene	UniGene
201830_s_at	NET1	neuroepithelial cell transforming gene 1	0.32	1.634	0.015	0.14	10.288	8.653	10276	Hs.25155
214306_at	OPA1	optic atrophy 1 (autosomal dominant)	0.32	1.639	0.019	0.16	5.288	3.649	4976	Hs.594504
208806_at	CHD3	chromodomain helicase DNA binding protein 3	0.32	1.641	0.001	0.05	7.312	5.671	1107	Hs.25601
213598_at	KIF2A	kinesin heavy chain member 2A	0.32	1.652	0.023	0.17	9.566	7.914	3796	Hs.558351
221432_s_at	SLC25A28	solute carrier family 25, member 28	0.32	1.651	0	0.02	7.154	5.503	81894	Hs.403790
204977_at	DDX10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	0.32	1.661	0.002	0.07	5.741	4.079	1662	Hs.591931
201607_at	PWP1	PWP1 homolog (S. cerevisiae)	0.32	1.663	0.001	0.05	6.931	5.269	11137	Hs.506652
208453_s_at	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1, solubl	0.31	1.668	0	0.02	7.396	5.728	7511	Hs.390623
208077_at	C9orf38	chromosome 9 open reading frame 38	0.31	1.677	0.018	0.15	5.847	4.17	29044	Hs.676462
219045_at	RHOF	ras homolog gene family, member F (in filopodia)	0.31	1.682	0.011	0.12	9.467	7.786	54509	Hs.524804, Hs.
204791_at	NR2C1	nuclear receptor subfamily 2, group C, member 1	0.31	1.683	0	0.03	8.42	6.737	7181	Hs.108301
212079_s_at	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithora)	0.31	1.684	0.005	0.09	4.725	3.041	4297	Hs.258855, Hs.
205327_s_at	ACVR2A	activin A receptor, type IIA	0.31	1.696	0	0.03	7.518	5.821	92	Hs.470174
221865_at	C9orf91	chromosome 9 open reading frame 91	0.31	1.702	0.014	0.13	9.333	7.631	203197	Hs.522357
202007_at	NID1	nidogen 1	0.31	1.708	0.023	0.17	8.225	6.517	4811	Hs.356624
202668_at	EFNB2	ephrin-B2	0.30	1.718	0.022	0.17	5.067	3.349	1948	Hs.149239
205282_at	LRP8	low density lipoprotein receptor-related protein 8, apo	0.30	1.739	0.017	0.15	7.81	6.071	7804	Hs.576154
203355_s_at	PSD3	pleckstrin and Sec7 domain containing 3	0.30	1.738	0.021	0.16	10.924	9.186	23362	Hs.434255
203337_x_at	ITGB1BP1	integrin beta 1 binding protein 1	0.30	1.742	0.002	0.06	4.872	3.13	9270	Hs.467662
204087_s_at	SLC5A6	solute carrier family 5 (sodium-dependent vitamin trar	0.30	1.748	0.026	0.18	10.141	8.393	8884	Hs.435735
212786_at	CLEC16A	C-type lectin domain family 16, member A	0.30	1.755	0.003	0.07	7.668	5.913	23274	Hs.35490
210888_s_at	ITIH1	inter-alpha (globulin) inhibitor H1	0.29	1.768	0.009	0.12	4.432	2.664	3697	Hs.420257
202734_at	TRIP10	thyroid hormone receptor interactor 10	0.29	1.769	0.001	0.05	10.347	8.578	9322	Hs.515094
220952_s_at	PLEKHA5	pleckstrin homology domain containing, family A mem	0.29	1.77	0.014	0.13	10.372	8.602	54477	Hs.188614
207165_at	HMMR	hyaluronan-mediated motility receptor (RHAMM)	0.29	1.777	0.027	0.19	5.59	3.813	3161	Hs.72550
215784_at	CD1E	CD1e molecule	0.29	1.778	0.015	0.14	4.487	2.709	913	Hs.249217
209212_s_at	KLF5	Kruppel-like factor 5 (intestinal)	0.29	1.78	0.005	0.09	5.118	3.338	688	Hs.508234
217371_s_at	IL15	interleukin 15	0.29	1.786	0.011	0.12	9.367	7.581	3600	Hs.654378
207194_s_at	ICAM4	intercellular adhesion molecule 4 (Landsteiner-Wiene	0.29	1.786	0.002	0.06	6.722	4.935	3386	Hs.631609
37005_at	NBL1	neuroblastoma, suppression of tumorigenicity 1	0.29	1.788	0.001	0.04	5.986	4.198	4681	Hs.654502
219024_at	PLEKHA1	pleckstrin homology domain containing, family A (pho	0.29	1.798	0.022	0.17	7.02	5.222	59338	Hs.643512
217080_s_at	HOMER2	homer homolog 2 (Drosophila)	0.29	1.81	0.008	0.11	7.007	5.197	9455	Hs.578443
211804_s_at	CDK2	cyclin-dependent kinase 2	0.28	1.824	0.006	0.1	4.766	2.942	1017	Hs.19192
218257_s_at	UGCG1	UDP-glucose ceramide glucosyltransferase-like 1	0.28	1.824	0.001	0.04	7.626	5.802	56886	Hs.34180
52975_at	FAM125B	family with sequence similarity 125, member B	0.28	1.829	0.003	0.07	7.257	5.428	89853	Hs.162659
204301_at	KBTBD11	kelch repeat and BTB (POZ) domain containing 11	0.28	1.834	0.012	0.13	4.542	2.709	9920	Hs.5333
212974_at	DENND3	DENN/MADD domain containing 3	0.28	1.835	0.003	0.07	4.833	2.998	22898	Hs.656299
211287_x_at	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity	0.28	1.838	0.001	0.05	7.175	5.337	1438	Hs.520937
218641_at	MGC3032	hypothetical protein MGC3032	0.28	1.844	0.011	0.12	8.242	6.399	65998	Hs.568945
210337_s_at	ACLY	ATP citrate lyase	0.27	1.866	0.021	0.16	7.459	5.593	47	Hs.387567
32625_at	NPR1	natriuretic peptide receptor A/guanylate cyclase A (atr	0.27	1.873	0.019	0.16	8.771	6.898	4881	Hs.490330

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Probe	Symbol	Description	FCH	lgFCH	P	fdr	Psor, BDCA+	Psor, BDCA-	Gene	UniGene
202555_s_at	MYLK	myosin, light chain kinase	0.27	1.883	0.013	0.13	4.521	2.638	4638	Hs.556600
214442_s_at	PIAS2	protein inhibitor of activated STAT, 2	0.27	1.889	0	0.02	6.532	4.644	9063	Hs.658013
200906_s_at	PALLD	palladin, cytoskeletal associated protein	0.27	1.891	0.004	0.08	8.222	6.331	23022	Hs.151220
203158_s_at	GLS	glutaminase	0.27	1.906	0.024	0.18	10.218	8.312	2744	Hs.116448
218638_s_at	SPON2	spondin 2, extracellular matrix protein	0.27	1.912	0	0.02	4.637	2.725	10417	Hs.302963
200897_s_at	PALLD	palladin, cytoskeletal associated protein	0.26	1.916	0.007	0.1	11.366	9.45	23022	Hs.151220
212254_s_at	DST	dystonin	0.26	1.92	0.001	0.04	6.722	4.803	667	Hs.631992, Hs.
218587_s_at	KTELC1	KTEL (Lys-Tyr-Glu-Leu) containing 1	0.26	1.923	0.011	0.12	11.624	9.701	56983	Hs.231750
212960_at	TBC1D9	TBC1 domain family, member 9 (with GRAM domain)	0.26	1.945	0.002	0.06	6.742	4.798	23158	Hs.480819, Hs.
219114_at	C3orf18	chromosome 3 open reading frame 18	0.26	1.947	0	0.02	8.428	6.481	51161	Hs.517860
214632_at	NRP2	neuropilin 2	0.25	1.972	0	0.03	6.453	4.481	8828	Hs.471200
203680_at	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, t	0.25	1.978	0.003	0.08	9.028	7.05	5577	Hs.433068
201667_at	GJA1	gap junction protein, alpha 1, 43kDa	0.25	1.981	0.015	0.14	7.903	5.922	2697	Hs.74471, Hs.6
218826_at	SLC35F2	solute carrier family 35, member F2	0.25	1.992	0.003	0.07	6.229	4.237	54733	Hs.524014
203157_s_at	GLS	glutaminase	0.25	1.996	0.012	0.13	9.098	7.102	2744	Hs.116448
217901_at	DSG2	desmoglein 2	0.25	2	0.012	0.13	10.276	8.276	1829	Hs.412597
207030_s_at	CSRP2	cysteine and glycine-rich protein 2	0.25	2.01	0.006	0.1	10.748	8.738	1466	Hs.530904
219278_at	MAP3K6	mitogen-activated protein kinase kinase kinase 6	0.25	2.012	0.004	0.08	8.328	6.316	9064	Hs.194694
209442_x_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	0.25	2.013	0.014	0.13	7.417	5.404	288	Hs.499725
206249_at	MAP3K13	mitogen-activated protein kinase kinase kinase 13	0.25	2.014	0.01	0.12	6.643	4.629	9175	Hs.656069
204072_s_at	FRY	furry homolog (Drosophila)	0.25	2.022	0.005	0.09	7.014	4.992	10129	Hs.507669, Hs.
209760_at	KIAA0922	KIAA0922	0.24	2.029	0.025	0.18	9.779	7.749	23240	Hs.205572
201242_s_at	ATP1B1	ATPase, Na+/K+ transporting, beta 1 polypeptide	0.24	2.033	0.001	0.05	8.378	6.345	481	Hs.291196
218613_at	PSD3	pleckstrin and Sec7 domain containing 3	0.24	2.054	0.014	0.14	10.137	8.083	23362	Hs.434255
210830_s_at	PON2	paraoxonase 2	0.24	2.069	0.004	0.08	7.621	5.551	5445	Hs.530077
211126_s_at	CSRP2	cysteine and glycine-rich protein 2	0.24	2.084	0.004	0.08	8.022	5.938	1466	Hs.530904
220358_at	SNFT	Jun dimerization protein p21SNFT	0.23	2.09	0.005	0.09	7.678	5.588	55509	Hs.62919
204730_at	RIMS3	regulating synaptic membrane exocytosis 3	0.23	2.096	0.001	0.05	5.752	3.656	9783	Hs.654808
219330_at	VANGL1	vang-like 1 (van gogh, Drosophila)	0.23	2.118	0.001	0.04	5.697	3.578	81839	Hs.515130
203559_s_at	ABP1	amiloride binding protein 1 (amine oxidase (copper-α	0.23	2.12	0.017	0.15	12.952	10.832	26	Hs.647097
215672_s_at	KIAA0828	adenosylhomocysteinase 3	0.23	2.125	0	0.02	4.319	2.195	23382	Hs.600789
209183_s_at	C10orf10	chromosome 10 open reading frame 10	0.23	2.146	0.017	0.15	8.101	5.955	11067	Hs.93675
206771_at	UPK3A	uroplakin 3A	0.22	2.183	0.005	0.09	4.933	2.751	7380	Hs.632787
218574_s_at	LMCD1	LIM and cysteine-rich domains 1	0.21	2.225	0	0.01	6.444	4.219	29995	Hs.475353
205890_s_at	UBD	ubiquitin D	0.21	2.238	0	0.01	11.717	9.479	10537	Hs.44532
219895_at	FAM70A	family with sequence similarity 70, member A	0.21	2.238	0.005	0.09	7.483	5.245	55026	Hs.437563
203354_s_at	PSD3	pleckstrin and Sec7 domain containing 3	0.21	2.24	0.016	0.14	8.662	6.422	23362	Hs.434255
206002_at	GPR64	G protein-coupled receptor 64	0.21	2.267	0.01	0.12	5.284	3.017	10149	Hs.146978
206369_s_at	PIK3CG	phosphoinositide-3-kinase, catalytic, gamma polypepi	0.21	2.268	0	0.03	5.149	2.881	5294	Hs.32942
204412_s_at	NEFH	neurofilament, heavy polypeptide 200kDa	0.21	2.268	0.017	0.15	10.168	7.901	4744	Hs.198760
203724_s_at	RUFY3	RUN and FYVE domain containing 3	0.21	2.272	0.009	0.12	5.402	3.129	22902	Hs.7972

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Probe	Symbol	Description	FCH	lgFCH	P	fdr	Psor, BDCA+	Psor, BDCA-	Gene	UniGene
218266_s_at	FREQ	frequenin homolog (Drosophila)	0.20	2.292	0.006	0.1	4.647	2.355	23413	Hs.694740
211894_x_at	SEZ6L	seizure related 6 homolog (mouse)-like	0.20	2.295	0	0.01	4.428	2.132	23544	Hs.194766
206508_at	CD70	CD70 molecule	0.20	2.296	0	0.01	4.844	2.548	970	Hs.501497
221185_s_at	IQCG	IQ motif containing G	0.20	2.299	0.009	0.11	6.12	3.821	84223	Hs.591675
207978_s_at	NR4A3	nuclear receptor subfamily 4, group A, member 3	0.20	2.339	0.016	0.14	6.631	4.292	8013	Hs.279522
200795_at	SPARCL1	SPARC-like 1 (mast9, hevin)	0.19	2.387	0.015	0.14	4.79	2.403	8404	Hs.62886
206058_at	SLC6A12	solute carrier family 6 (neurotransmitter transporter, b	0.19	2.399	0.013	0.13	7.082	4.683	6539	Hs.437174
211786_at	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	0.19	2.429	0.002	0.06	6.9	4.471	3604	Hs.654459
200907_s_at	PALLD	palladin, cytoskeletal associated protein	0.19	2.43	0.002	0.06	8.402	5.971	23022	Hs.151220
221828_s_at	FAM125B	family with sequence similarity 125, member B	0.19	2.432	0.001	0.04	5.456	3.025	89853	Hs.162659
210073_at	ST8SIA1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltrans	0.18	2.438	0	0.02	7.057	4.619	6489	Hs.408614
203131_at	PDGFRA	platelet-derived growth factor receptor, alpha polypep	0.18	2.472	0.012	0.13	9.056	6.584	5156	Hs.74615
33767_at	NEFH	neurofilament, heavy polypeptide 200kDa	0.18	2.499	0.014	0.14	11.272	8.773	4744	Hs.198760
220636_at	DNAI2	dynein, axonemal, intermediate chain 2	0.17	2.515	0	0.03	5.696	3.181	64446	Hs.147472
218678_at	NES	nestin	0.17	2.521	0.005	0.09	5.051	2.53	10763	Hs.527971
220180_at	CCDC68	coiled-coil domain containing 68	0.17	2.574	0.011	0.12	6.479	3.905	80323	Hs.120790
210652_s_at	C1orf34	chromosome 1 open reading frame 34	0.17	2.577	0.011	0.12	7.876	5.299	22996	Hs.112949
208782_at	FSTL1	folliculin-like 1	0.17	2.594	0	0.03	7.386	4.792	11167	Hs.269512
209582_s_at	CD200	CD200 molecule	0.16	2.6	0.005	0.09	5.848	3.247	4345	Hs.79015
220658_s_at	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	0.15	2.723	0.006	0.09	9.055	6.332	56938	Hs.434269, Hs
212327_at	LIMCH1	LIM and calponin homology domains 1	0.15	2.73	0.022	0.17	8.143	5.413	22998	Hs.335163
206560_s_at	MIA	melanoma inhibitory activity	0.15	2.769	0.003	0.07	7.124	4.355	8190	Hs.646364
204822_at	TTK	TTK protein kinase	0.14	2.865	0.001	0.05	6.563	3.697	7272	Hs.169840
208017_s_at	MCF2	MCF.2 cell line derived transforming sequence	0.14	2.876	0.001	0.04	7.711	4.836	4168	Hs.387262
206714_at	ALOX15B	arachidonate 15-lipoxygenase, type B	0.13	2.953	0.001	0.04	9.848	6.895	247	Hs.111256
217553_at	MGC87042	similar to Six transmembrane epithelial antigen of pro	0.13	2.977	0.004	0.08	8.371	5.394	256227	Hs.512234
207873_x_at	SEZ6L	seizure related 6 homolog (mouse)-like	0.12	3.043	0	0.01	4.981	1.938	23544	Hs.194766
216047_x_at	SEZ6L	seizure related 6 homolog (mouse)-like	0.12	3.044	0	0	5.56	2.516	23544	Hs.194766
214844_s_at	DOK5	docking protein 5	0.06	4.14	0.001	0.05	6.407	2.267	55816	Hs.656582