

Supplemental Material and Methods

Skin samples. Skin punch biopsies (6mm diameter) were obtained from normal volunteers and psoriasis patients under Rockefeller University IRB-approved protocols. Informed consent was obtained and the studies were performed in adherence with the Principles of the Declaration of Helsinki. The lesional tissue for CD163, RFD7, and LAMP2 staining was obtained from a group of patients with moderate-to-severe psoriasis (body surface area >10%) enrolled in a clinical trial (clinicaltrials.gov NCT00115076). There were seven males and three females, and mean age was 41 years. Most patients had been using topical therapy alone, three had used prior systemic agents. All patients had not used topical agents for 2 weeks nor systemics for 4 weeks prior to the biopsy being taken. Paired psoriasis non-lesional and lesional RNA for microarray studies were from baseline biopsies of patients enrolled in another study with the same inclusion and exclusion criteria (clinicaltrials.gov NCT00116181) (Zaba *et al.*, 2009b). The microarray was performed using the same Illumina HT-12 chips that were used for the cultured macrophages. Patient lesional skin biopsies for other immunohistochemistry and immunofluorescence stains were from samples that also met the above inclusion and exclusion criteria. Biopsies were frozen in OCT (Sakura, Tokyo, Japan) and stored at -80 °C for immunohistochemistry and immunofluorescence.

Antibodies. All antibodies used for immunohistochemistry and immunofluorescence are listed in Table S6.

Immunohistochemistry. Normal and psoriasis lesional skin sections (n=5-10) were stained with macrophage markers CD163, RFD7, LAMP2, CD68, Stabilin, and MARCO (dilutions listed in Table S6). Biotin-labeled horse anti-mouse and biotin-labeled goat anti-rabbit antibodies

(Vector Laboratories) were used to detect the mouse monoclonal and rabbit polyclonal antibodies, respectively. The staining signal was amplified with avidin-biotin complex (Vector Laboratories) and developed using chromogen 3-amino-9-ethylcarbazole (Sigma-Aldrich). The number of positive cells per mm epidermis surface length was counted manually using computer-assisted image analysis (NIH Image 6.1;<http://rsb.info.nih.gov/nih-image>). The cell counts were also calculated per area of the dermis (Figure S6). Cell counts were analyzed by Mann Whitney U test and significance was accepted as $p < 0.05$.

Immunofluorescence. Frozen skin sections from psoriasis patients (n=5) were fixed with acetone and blocked in 10% normal goat serum (Vector Laboratories) for 30 minutes. Primary antibodies CD163 and CD11c were incubated overnight at 4°C and amplified with the appropriate secondary antibody (goat anti-mouse IgG1 conjugated to Alexa Fluor 488 or 568) for 30 minutes. For colocalization with CD163 or CD11c, sections were then co-stained overnight with a second antibody, as listed in Table S6, and amplified with the appropriate secondary antibody (Table S6) for 30 minutes.

Images were acquired using the appropriate filters of a Zeiss Axioplan 2 widefield fluorescence microscope with a Plan Neofluar 20 x 0.7 numerical aperture lens and a Hamamatsu Orca ER-cooled charge-coupled device camera, controlled by METAVUE software (MDS Analytical Technologies, Downington, PA). Alternatively, images were acquired using appropriate filters of an upright confocal microscope Zeiss Axioplan 2 (LSM 510) with C-Apochromat 40x/1.2 W objective using Argon/Krypton laser-488nm and 568nm. Images in each figure are presented both as single color stains (green and red) located above the merged image, so that localization of two markers on similar or different cells can be appreciated. Cells that coexpress the two markers in a similar location are yellow in color. A white line denotes the

dermoepidermal junction. Dermal collagen fibers gave green autofluorescence, and antibodies conjugated with a fluorochrome often gave background epidermal fluorescence. Size bar = 100 μm

Macrophage cultures. Peripheral blood mononuclear cells from normal blood donor buffy coats (New York Blood Center) (n=7) were purified by gradient centrifugation with Ficoll-Paque Plus (Pharmacia, Piscataway, NJ, U.S.A.), and collected at the interface. Monocytes were isolated by plastic adherence. Macrophages were generated by culturing monocytes for 7 days in RPMI (Invitrogen) supplemented with human M-CSF (50ng/ml) plus 1% HSA. Macrophage phenotype was confirmed by flow cytometry as CD163⁺, CD68⁺, HLA-DR⁺, CD86⁺, CD11c^{lo}, CD83⁻ (data not shown). Macrophage polarization was determined by removing the culture medium and culturing cells for an additional 24 hours in RPMI supplemented with 20 ng/ml IFN- γ (for M1 polarization), 25ng/ml IL-4 (for M2 polarization), 20ng/ml TNF- α , 1 ug/ml LPS, and 1 ug/ml LPS plus 20ng/ml IFN- γ . Cells were harvested in RLT buffer and stored in -80°C for RNA extraction.

Reverse transcriptase-polymerase chain reaction. RNA was extracted from cultured macrophages using the RNeasy Mini KIT (Qiagen, Valencia, CA, U.S.A.). Reverse transcriptase (RT)-polymerase chain reaction (PCR) was performed using EZ PCR core reagents, primers and probes (Applied Biosystems, Foster City, CA, U.S.A.) as previously published (Chamian *et al.*, 2005). Sequences of primers and probes used in this study are as follows: IL23p19 (Assay ID Hs00372324_m1), IL23p40 Forward: ACATCTACCGAAGTCCAATGCA Reverse: GGAATTGTAATAGCGATCCTGAGC Probe:6-FAM TGCACGCAGACATTCCCGCCT-TAMRA (Gene Bank Accession Number AF180563), IL12p35 (Assay ID Hs00168405_m1), and CCL20 (Assay ID Hs00171125_m1). The results

were normalized to HARP housekeeping gene and analyzed with Applied Biosystems PRISM 7700. RT-PCR data was analyzed using a repeated measures ANOVA and Dunnett's Multiple Comparison Test was used to compare with control. The p values were designated as $p < 0.05$ (*), $p < 0.01$ (**) and $p < 0.001$ (***).

Gene Array. RNA extracted from cultured macrophages (biological replicates $n=7$) and psoriasis non-lesional and lesional biopsies ($n=5$ pairs) was amplified and labeled (Message Amp Premier RNA Amplification Kit, Ambion Inc., TX). A total of 750ng of biotinylated cRNA was hybridized to Illumina Human HT-12 Bead Chip (Illumina, Inc. San Diego, CA, USA). Data was read and preprocessed using the *lumi* package available at R/Bioconductor (<http://www.bioconductor.org/>). Quantile normalization was used to normalize all microarray chips. Probes with standard deviation greater than 0.1 or present in more than 4 samples were kept for further analysis (a probe was called present if detection p-value was smaller than 0.1). To compare gene expression of *in vitro* cytokine treated macrophages versus control, and lesional versus non-lesional samples of psoriasis tissues, a moderated paired t-test available in *limma* package from R/Bioconductor was used. P values were adjusted for multiple hypotheses using the Benjamini–Hochberg procedure, which controls the false discovery rate (FDR). Genes were considered significant if they had a fold change (FCH) greater than 2, and FDR less than 0.01. The log-2 fold change for cytokine treated macrophages were clustered using a hierarchical cluster with Pearson correlation coefficient and presented in a heatmap. Gene Set Enrichment Analysis (GSEA) approach (Subramanian *et al.*, 2005; Zaba *et al.*, 2009a) was used to correlate the response profile of the macrophage pathways in psoriasis lesional versus non-lesional skin.

The data discussed in this publication have been deposited in NCBI's Gene Expression Omnibus and are accessible through GEO Series accession number GSE18686.

References

Chamian F, Lowes MA, Lin SL, Lee E, Kikuchi T, Gilleaudeau P, *et al.* (2005). Alefacept reduces infiltrating T cells, activated dendritic cells, and inflammatory genes in psoriasis vulgaris. *Proc Natl Acad Sci U S A* 102:2075-2080.

Subramanian A, Tamayo P, Mootha VK, Mukherjee S, Ebert BL, Gillette MA, *et al.* (2005). Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. *Proc Natl Acad Sci U S A* 102:15545-15550.

Zaba LC, Fuentes-Duculan J, Eungdamrong NJ, Abello MV, Novitskaya I, Pierson KC, *et al.* (2009a). Psoriasis Is Characterized by Accumulation of Immunostimulatory and Th1/Th17 Cell-Polarizing Myeloid Dendritic Cells. *J Invest Dermatol* 129:79-88.

Zaba LC, Suarez-Farinas M, Fuentes-Duculan J, Nograles KE, Guttman-Yassky E, Cardinale I, *et al.* (2009b). Effective treatment of psoriasis with etanercept is linked to suppression of IL-17 signaling, not immediate response TNF genes. *J Allergy Clin Immunol* 124:1022-1010 e1021-1395.

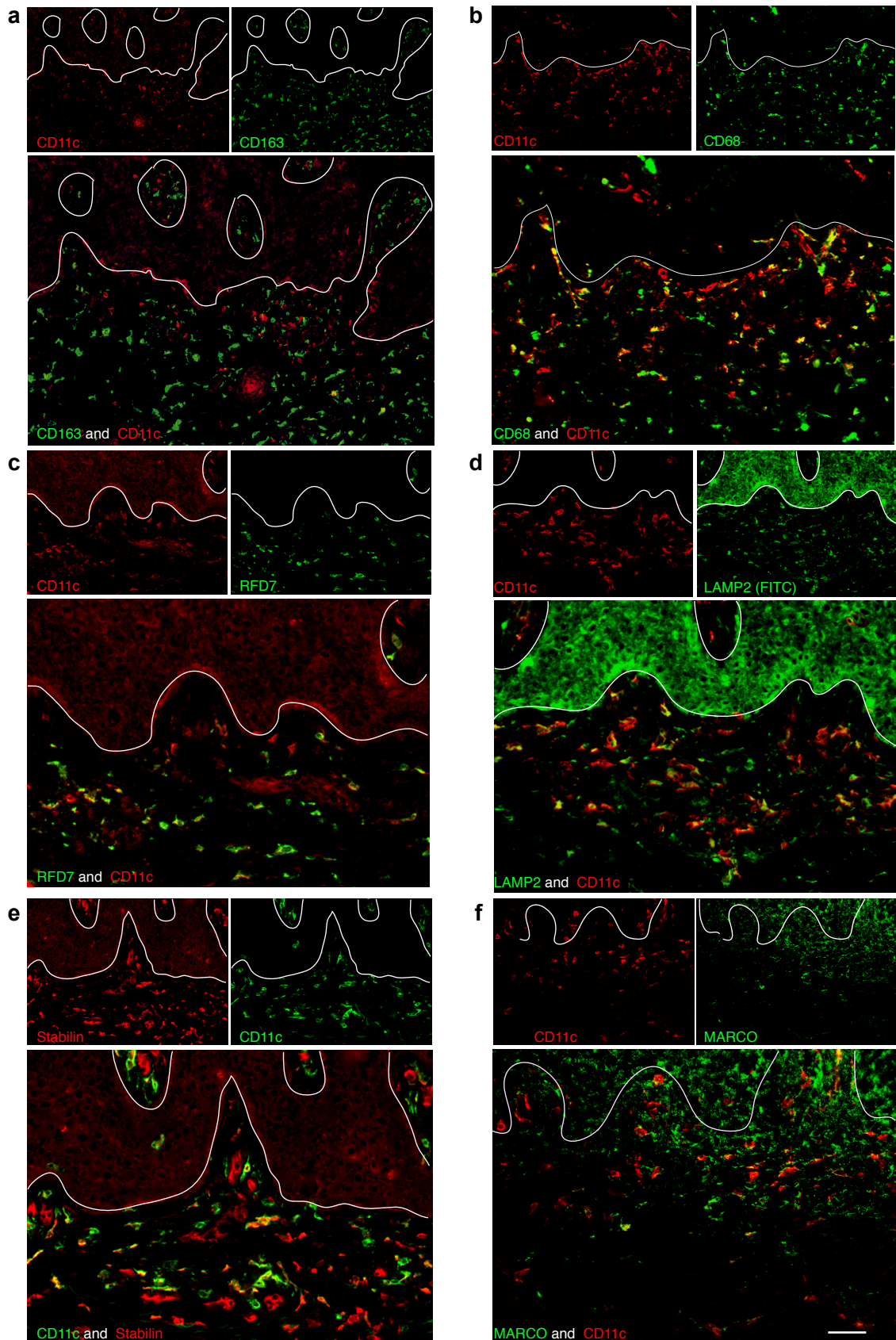


Figure S1. CD11c coexpression with macrophage markers in psoriasis lesions. a) CD11c was coexpressed on a few CD163⁺ cells. There was greater co-expression of CD11c with (b) CD68, (c) RFD7, (d) LAMP2, (e) Stabilin, and (f) MARCO. Bar =100 μ m

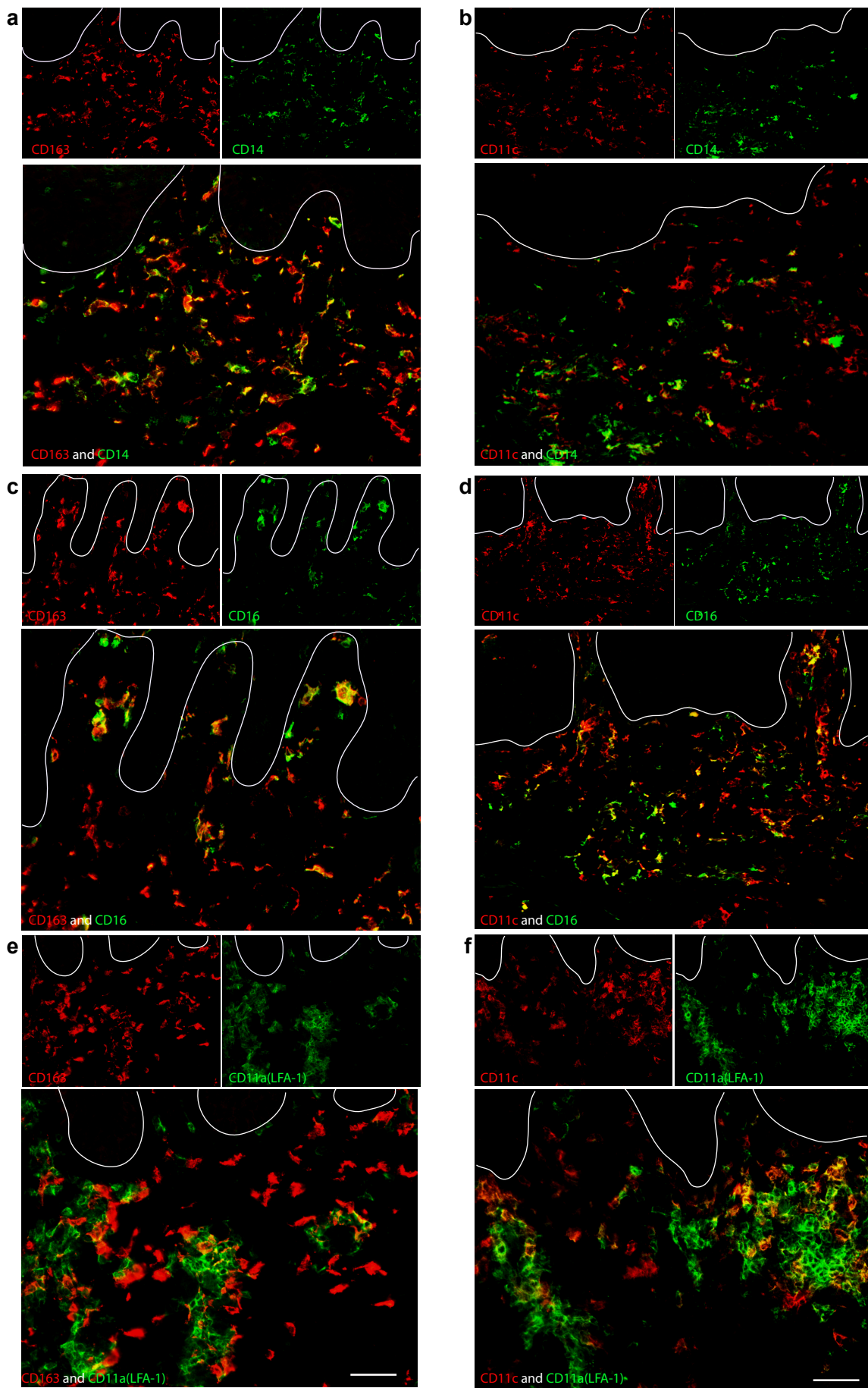


Figure S2. CD163⁺ macrophages also expressed CD14, CD16 and LFA-1 in psoriasis lesional skin. (a, b) CD163 showed greater coexpression of CD14 than CD11c⁺ DCs. CD16 (c, d) and LFA-1 (e, f) were present on both CD163⁺ macrophages and CD11c⁺ DCs. Bar =100 μ m

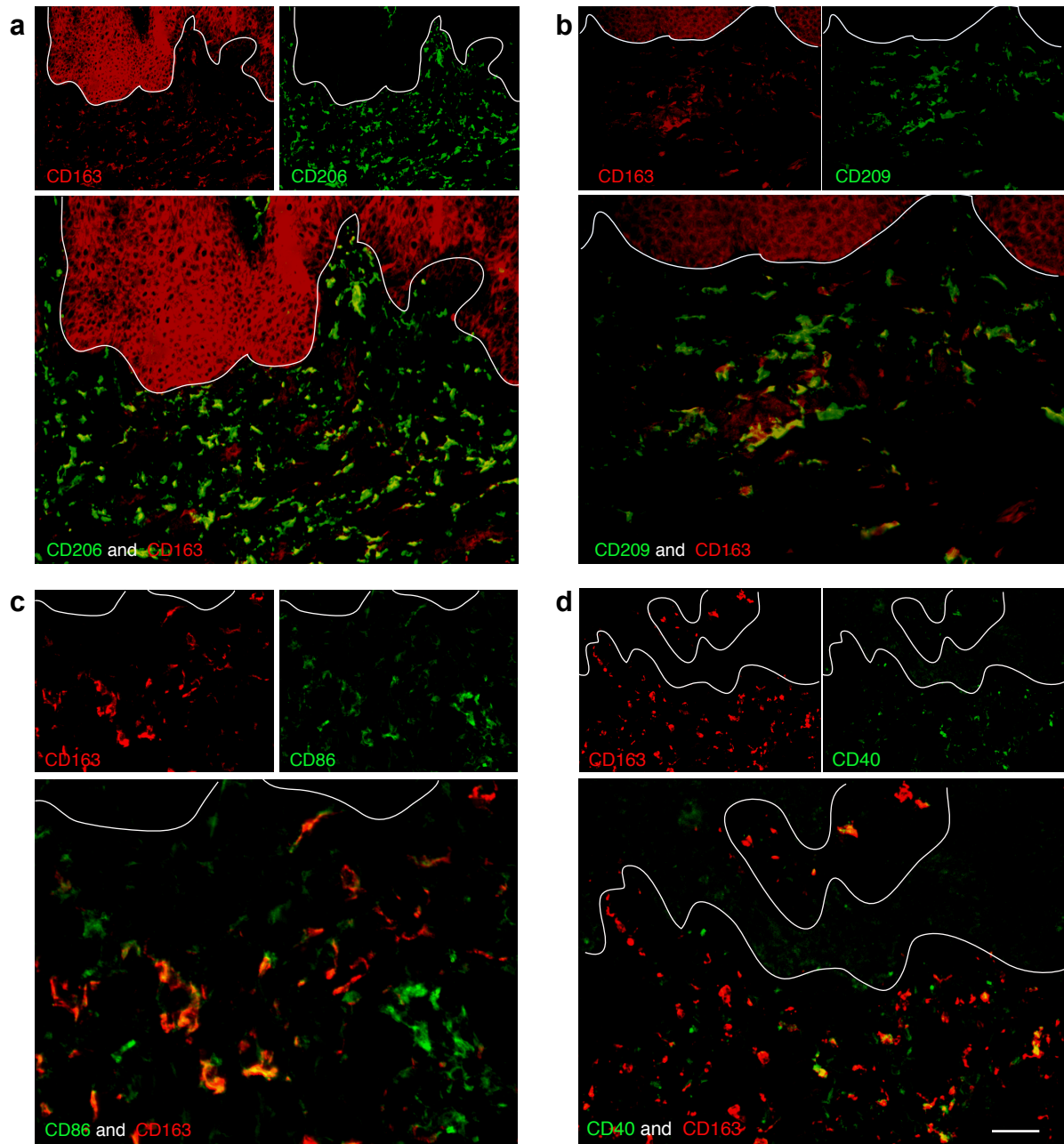


Figure S3. CD163⁺ macrophages also expressed C-lectins and co-stimulatory molecules in psoriasis lesional skin. (a) Almost all CD163⁺ cells co-expressed CD206, and (b) the majority coexpressed CD209. Less than half of the CD163⁺ cells co-expressed the co-stimulatory molecules (c) CD86 and (d) CD40. Bar =100 μ m

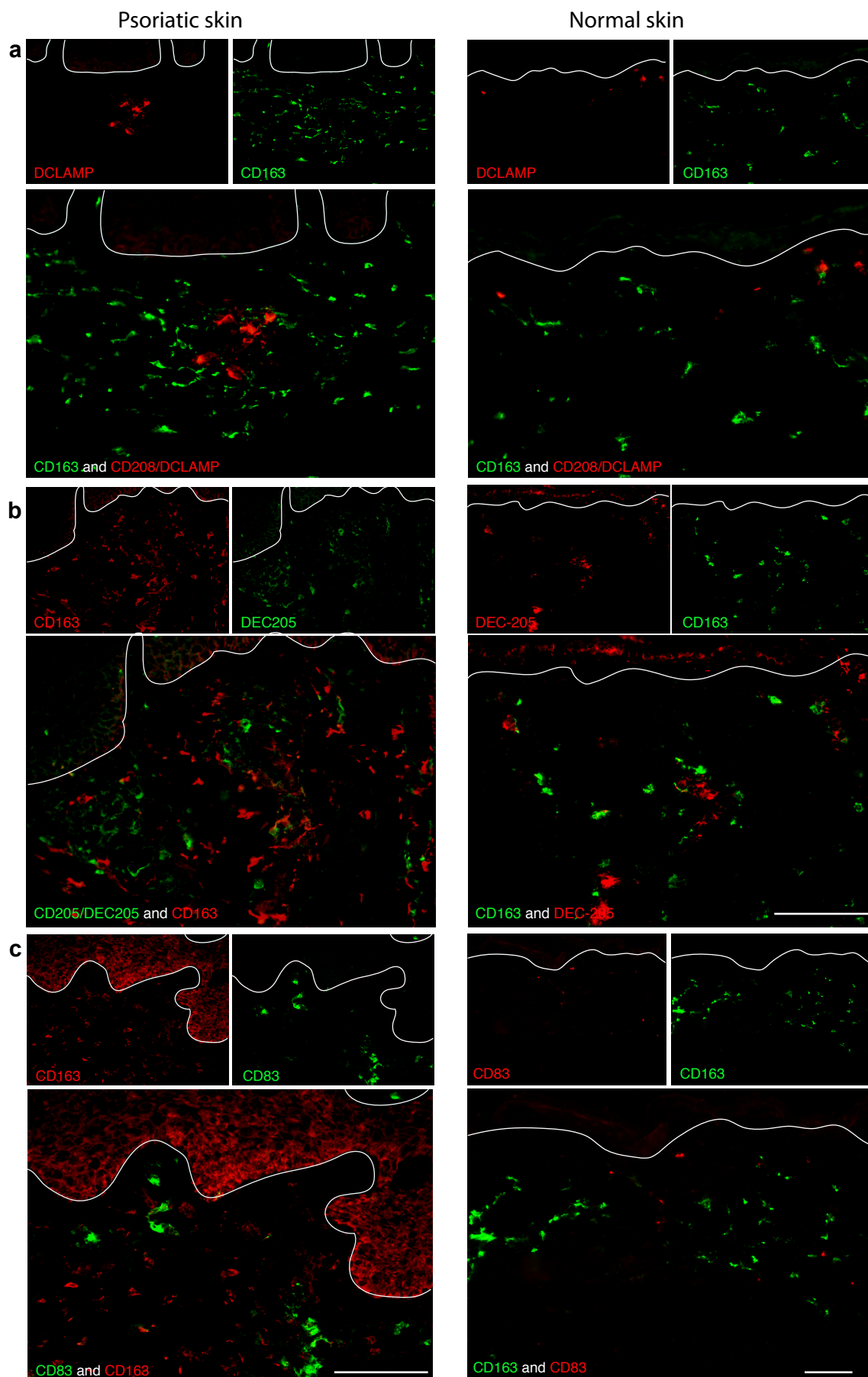


Figure S4. Macrophages in psoriasis lesions and normal skin did not express mature DC markers. CD 163⁺ macrophages did not co-express well-recognized DC maturation markers (a) CD208/DC-LAMP, (b)CD205/DEC-205, and (c) CD83. Bar =100 μ m

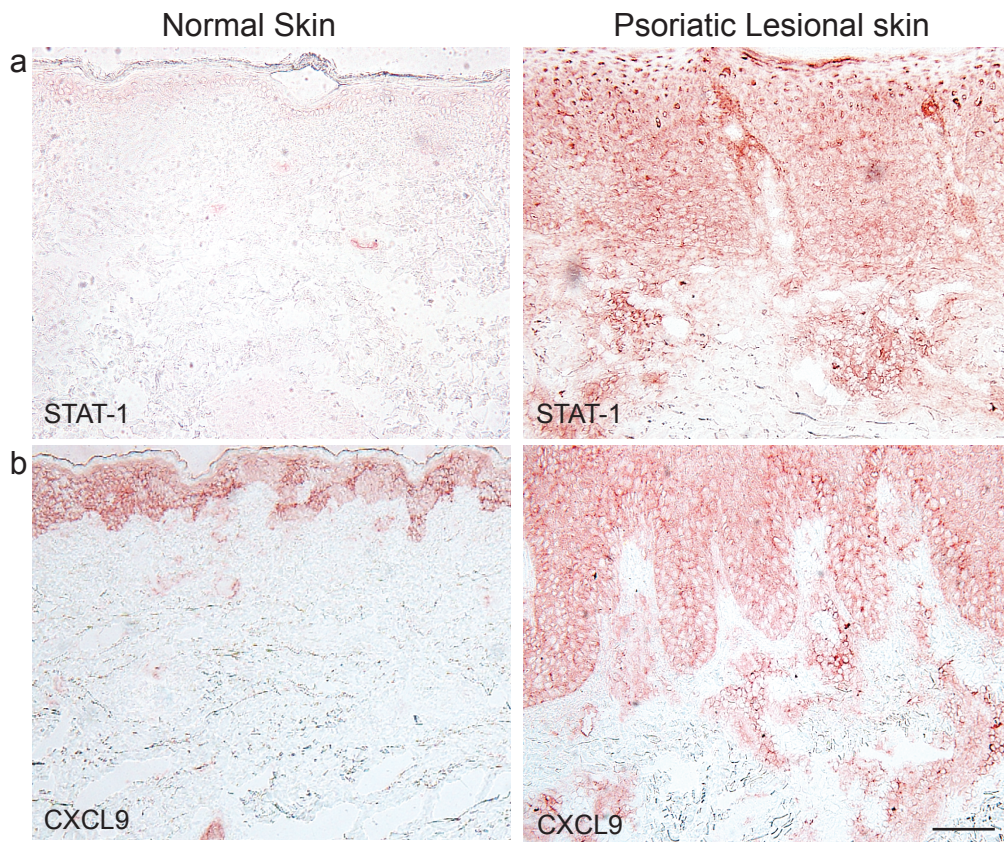
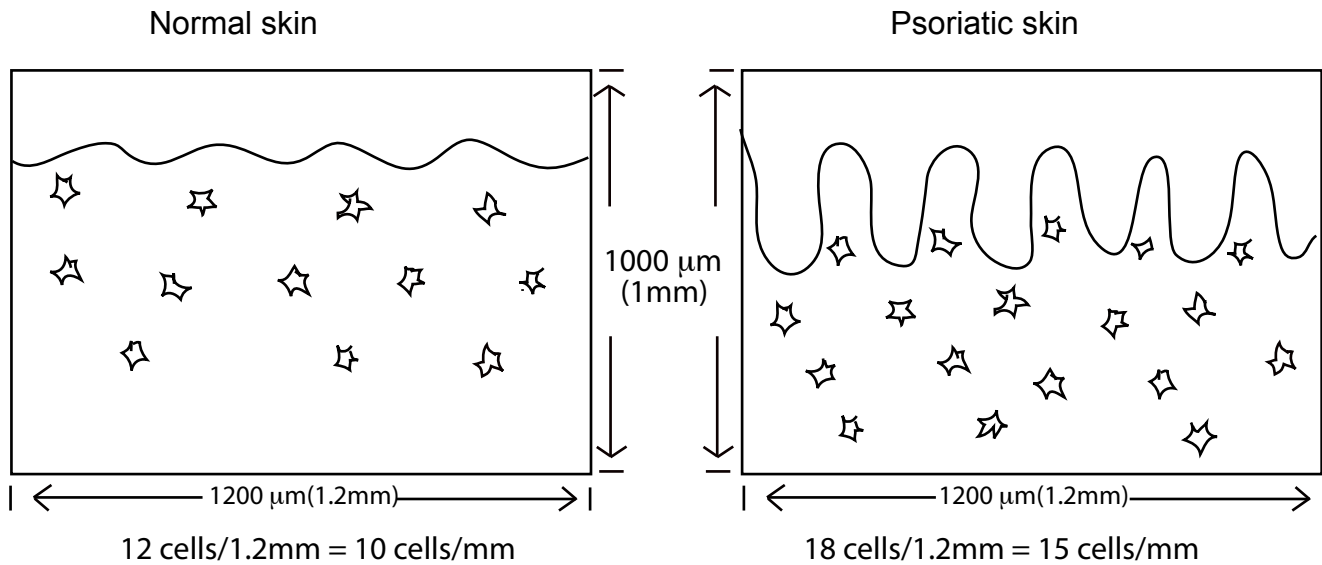
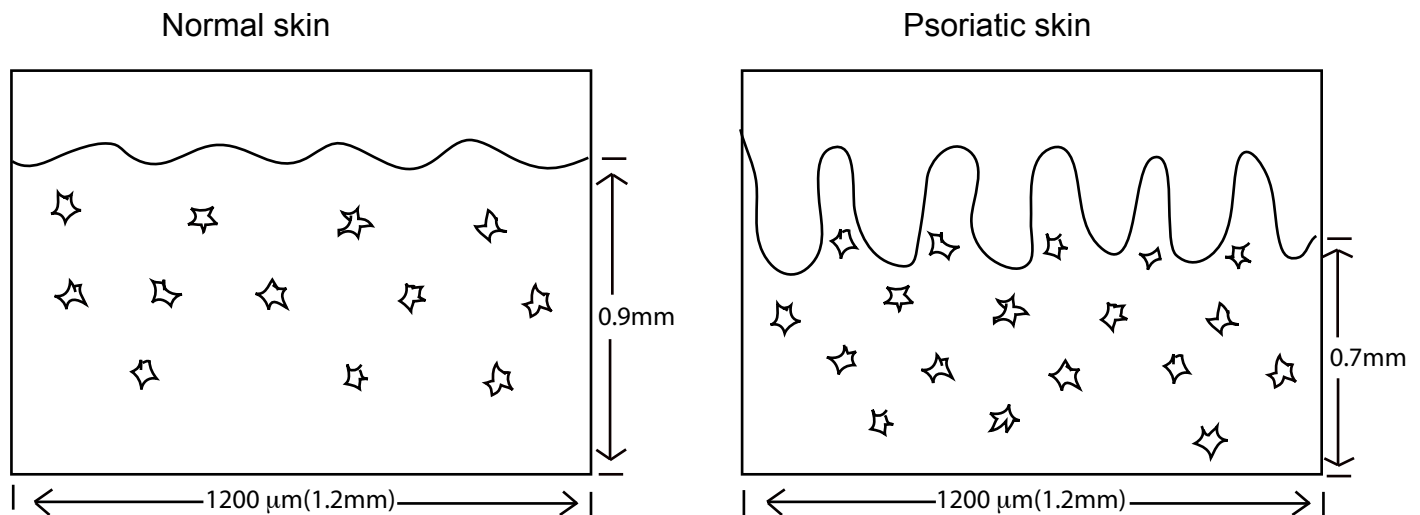


Figure S5. IFN- γ induced genes STAT-1 and CXCL9 immunohistochemistry in normal skin and psoriasis lesions. (a) STAT-1 expression was increased in psoriasis compared to normal skin. (b) CXCL9 showed low level expression in normal skin, and was increased in psoriasis. Bar =100 μ m

Method A - Analysis field defined by epidermis surface length



Method B - Analysis field defined by cell density per square area (mm^2) of dermis



*e.g. area of dermis = $0.9\text{mm} \times 1.2\text{mm} = 1.08 \text{mm}^2$

$$12 \text{ cells}/1.08\text{mm}^2 = 11 \text{ cells}/\text{mm}^2$$

area of dermis = $0.7\text{mm} \times 1.2\text{mm} = 0.84 \text{mm}^2$

$$18 \text{ cells}/0.84\text{mm}^2 = 21 \text{ cells}/\text{mm}^2$$

Figure S6. Methods for counting cells. The diagrams illustrate two methods used for counting cells. In **Method A**, a representative image is captured, which is a field measuring $1000\mu\text{m}$ (1mm) \times $1200\mu\text{m}$ (1.2mm). The cells are counted manually using computer-assisted image analysis (NIH Image 6.1; <http://rsb.info.nih.gov/nih-image>), and the number quantified per epidermis surface length. Examples for normal skin and psoriasis are shown. This method was used to obtain cell counts for Figure 1. In **Method B**, the same number of cells are counted, but cell number is calculated per area of dermis. Examples of the area of dermis are shown, but the image J program is used to calculate the actual area. This method was used to obtain cell counts for Table S1.

Table S1. Macrophage markers used in this study

Macrophage Marker	Description/ Function	Cell counts / square area
CD163 Hemoglobin Scavenger Receptor	Exclusive expression in monocyte-macrophage system ; Immunologic function is homeostatic, participates in adhesion to endothelial cells, tolerance induction and tissue regeneration (Moestrup, 2004; Onofre, 2009)	<p>CD163</p>
RFD7	Recognizes mature tissue macrophages ; Responsible for TNF- α production in alveolar macrophages (Taams, 1999; Pantelidis, 2001)	<p>RFD7</p>
CD68 Macrosialin	Highly expressed by human monocytes and tissue macrophages ; Expresses both IL-12 and IL-23 (Ochoa, 2008; Yawalkar, 2009)	<p>CD68</p>
LAMP2 (Lysosomal-Associated Membrane Protein 2) LAMPB LGP110	Protects the lysosomal membrane from proteolytic enzymes within lysosomes ; Acts as a receptor for proteins to be imported into lysosomes (Eskelinen, 2006)	<p>LAMP2</p>
Stabilin-1 MS-1 Antigen FEEL1	Expressed in sinusoidal endothelial cells and macrophages ; Endocytic and sorting receptor, internalization of acLDL (Kzhyshkowska, 2004; Hansen, 2005)	<p>Stabilin</p>
MARCO (Macrophage Receptor with Collagenous structure) Scavenger Receptor Class A, Member 2 (SCARA 2)	Transmembrane protein of the Class A scavenger receptor family ; Scavenging of bacteria, inhaled particles and airborne pathogens (Sankala, 2002; Arredouani, 2005)	<p>MARCO</p>

* p < 0.05, ** p < 0.01, *** p < 0.001

Table S2.xls

Psoriasis_LSVsNL_p01fch2_Macrophages

1 upregulated, -1 is down-regulated

PROBE_ID	SYMBOL	DEFINITION	CHROMOSOME	Ps LS-NL	Ps LS-NL_P	PS LS-NL_FDR	IFNg -C	IL4 -C	TNFA-C	LPS -C	LPSandIFNg -C	IFNg -C_P	IL4 -C_P	TNFA-C_P	LPS -C_P	LPSandIFNg -C_P	IFNg -C_FDR	IL4 -C_FDR	TNFA-C_FDR	LPS -C_FDR	LPSandIFNg -C_FDR	IFNg	IL4	TNFA	LPS	LPSandIFNg	
29	ILMN_167781	ABCC3	ATP-binding ca	17	-1.022	0.000	0.000	-0.42	0.29	0.16	-0.17	-0.80	0.19	0.36	0.61	0.58	0.01	0.29	0.81	0.93	0.86	0.03	0	0	0	0	0
81	ILMN_176385	ACACB	acetyl-Coenzym	12	-1.432	0.000	0.000	-0.17	-0.01	-0.09	-0.33	-0.16	0.22	0.96	0.52	0.02	0.26	0.33	1.00	0.90	0.30	0.35	0	0	0	0	0
109	ILMN_171554	ACOT1	acyl-CoA thioe	14	-1.041	0.000	0.000	-0.08	-0.26	-0.02	-0.06	0.05	0.55	0.06	0.89	0.69	0.73	0.66	0.40	0.98	0.90	0.80	0	0	0	0	0
120	ILMN_168570	ACOX2	acyl-Coenzym	3	-1.384	0.000	0.000	-1.36	-0.42	-0.39	-0.47	-1.63	0.00	0.24	0.27	0.18	0.00	0.00	0.71	0.77	0.59	0.00	-1	0	0	0	-1
125	ILMN_207859	ACP5	acid phosphat	19	1.054	0.000	0.000	-1.92	0.04	-0.56	-0.83	-2.39	0.00	0.91	0.14	0.03	0.00	0.00	0.99	0.65	0.33	0.00	-1	0	0	0	-1
128	ILMN_175832	ACPP	acid phosphat	3	1.362	0.000	0.000	-0.23	-0.04	-0.27	0.03	-0.10	0.22	0.82	0.15	0.86	0.58	0.33	0.98	0.67	0.96	0.67	0	0	0	0	0
187	ILMN_210310	ADAMDEC1	ADAM-like, dex	8	1.540	0.000	0.000	0.49	-0.72	0.47	0.48	0.78	0.01	0.00	0.01	0.01	0.72	0.02	0.01	0.26	0.22	0.00	0	0	0	0	0
237	ILMN_169559	ADRB2	adrenergic, bel	5	-1.373	0.000	0.000	0.31	-0.34	-0.20	0.11	0.72	0.29	0.23	0.48	0.70	0.01	0.40	0.70	0.89	0.91	0.03	0	0	0	0	0
275	ILMN_179487	AGPAT9	1-acylglycerol	4	1.183	0.000	0.000	-1.67	-0.52	-0.38	-0.73	-2.29	0.00	0.21	0.35	0.08	0.00	0.00	0.67	0.82	0.46	0.00	-1	0	0	0	-1
337	ILMN_171312	AKR1C3	aldo-keto redu	10	-1.068	0.000	0.000	-0.98	-1.54	0.24	-0.48	-1.52	0.01	0.00	0.53	0.21	0.00	0.03	0.01	0.91	0.62	0.00	0	-1	0	0	-1
351	ILMN_167087	ALCAM	activated leukc	3	-1.235	0.000	0.000	-0.30	-0.34	0.25	0.15	-0.34	0.32	0.26	0.41	0.61	0.25	0.43	0.73	0.85	0.67	0.34	0	0	0	0	0
360	ILMN_179482	ALDH3A2	aldehyde dehy	17	-1.047	0.000	0.000	-1.16	-0.55	-0.15	-0.44	-1.42	0.00	0.00	0.39	0.02	0.00	0.00	0.06	0.84	0.28	0.00	-1	0	0	0	-1
361	ILMN_240164	ALDH3A2	aldehyde dehy	17	-1.006	0.000	0.000	-1.09	-0.46	-0.04	-0.48	-1.26	0.00	0.01	0.80	0.01	0.00	0.00	0.15	0.97	0.22	0.00	-1	0	0	0	-1
403	ILMN_239314	ALOX15B	arachidonate 1	17	-1.437	0.000	0.000	0.94	0.89	1.05	0.38	0.76	0.00	0.00	0.00	0.12	0.00	0.00	0.02	0.02	0.52	0.01	0	0	1	0	0
422	ILMN_177937	AMMECR1	Alport syndrom X	1	1.223	0.000	0.000	0.05	0.01	-0.01	0.04	0.11	0.58	0.95	0.92	0.71	0.24	0.69	1.00	0.99	0.91	0.33	0	0	0	0	0
431	ILMN_180130	AMY2A	amylase, alpha	1	-1.086	0.000	0.000	-0.59	-0.21	0.17	-0.08	-0.65	0.00	0.18	0.28	0.60	0.00	0.00	0.64	0.78	0.87	0.00	0	0	0	0	0
446	ILMN_176072	ANG	angiogenin, rib	14	-1.394	0.000	0.000	-0.03	-0.78	-0.71	-0.57	0.00	0.93	0.02	0.03	0.07	0.99	0.96	0.19	0.38	0.45	1.00	0	0	0	0	0
472	ILMN_221582	ANKRD20A1	ankyrin repeat	9	-1.331	0.000	0.000	-0.65	-0.80	-0.49	-0.28	-0.87	0.02	0.01	0.08	0.30	0.00	0.05	0.10	0.54	0.70	0.01	0	0	0	0	0
474	ILMN_179984	ANKRD22	ankyrin repeat	10	1.021	0.000	0.000	3.76	-0.02	0.58	0.79	4.24	0.00	0.97	0.25	0.12	0.00	0.00	1.00	0.75	0.53	0.00	1	0	0	0	1
594	ILMN_178900	APOC1	apolipoprotein	19	-1.714	0.000	0.000	-1.43	-0.58	-0.28	-0.82	-1.56	0.00	0.13	0.46	0.04	0.00	0.00	0.56	0.88	0.35	0.00	-1	0	0	0	-1
597	ILMN_178017	APOD	apolipoprotein	3	-1.468	0.000	0.000	0.05	0.06	-0.02	-0.04	0.19	0.75	0.70	0.92	0.81	0.25	0.82	0.95	0.99	0.95	0.34	0	0	0	0	0
598	ILMN_174093	APOE	apolipoprotein	19	-1.237	0.000	0.000	-0.62	-0.56	-0.03	-0.41	-0.61	0.06	0.09	0.94	0.20	0.07	0.51	0.47	0.99	0.61	0.11	0	0	0	0	0
618	ILMN_171506	AQP9	aquaporin 9 (A	15	-1.434	0.034	0.000	0.88	0.73	0.17	0.44	1.13	0.00	0.00	0.49	0.07	0.00	0.00	0.08	0.89	0.45	0.00	0	0	0	0	1
668	ILMN_213280	ARHGGEF10	Rho guanine ni	8	-1.108	0.000	0.000	0.15	0.08	0.09	-0.01	0.03	0.30	0.59	0.50	0.92	0.83	0.41	0.91	0.90	0.98	0.87	0	0	0	0	0
710	ILMN_212002	ARL5B	ADP-ribosylat	10	1.298	0.000	0.000	0.63	0.02	0.28	0.16	0.89	0.00	0.92	0.13	0.39	0.00	0.01	0.99	0.65	0.75	0.00	0	0	0	0	0
717	ILMN_176981	ARL6IP5	ADP-ribosylat	3	-1.006	0.000	0.000	0.09	-0.04	0.24	0.21	0.14	0.21	0.59	0.00	0.00	0.05	0.32	0.91	0.10	0.17	0.09	0	0	0	0	0
869	ILMN_165807	ATP1B1	ATPase, Na+/K	1	1.211	0.001	0.000	-0.35	0.34	-0.08	-0.22	-0.60	0.29	0.30	0.80	0.50	0.07	0.41	0.77	0.97	0.82	0.12	0	0	0	0	0
871	ILMN_173029	ATP1B1	ATPase, Na+/K	1	1.014	0.001	0.000	-0.28	0.35	-0.05	-0.14	-0.51	0.36	0.25	0.87	0.65	0.10	0.48	0.72	0.98	0.89	0.16	0	0	0	0	0
879	ILMN_181566	ATP2A2	ATPase, Ca++	12	1.105	0.000	0.000	0.16	0.03	0.04	0.16	0.39	0.15	0.78	0.75	0.14	0.00	0.24	0.97	0.96	0.55	0.00	0	0	0	0	0
976	ILMN_168095	AURKA	aurora kinase	20	1.173	0.000	0.000	-0.07	0.16	0.07	0.01	0.00	0.54	0.18	0.56	0.96	0.99	0.64	0.64	0.91	0.99	1.00	0	0	0	0	0
977	ILMN_235743	AURKA	aurora kinase	20	1.114	0.000	0.000	-0.06	0.15	0.08	-0.02	0.02	0.58	0.18	0.49	0.89	0.85	0.68	0.64	0.89	0.97	0.89	0	0	0	0	0
979	ILMN_168421	AURKB	aurora kinase l	17	1.198	0.000	0.000	-0.19	-0.57	-0.01	-0.43	-0.39	0.34	0.01	0.97	0.03	0.05	0.46	0.09	1.00	0.35	0.09	0	0	0	0	0
985	ILMN_170187	AXL	AXL receptor t	19	-1.134	0.000	0.000	1.29	0.06	-0.06	0.39	1.39	0.00	0.83	0.80	0.13	0.00	0.00	0.98	0.97	0.53	0.00	1	0	0	0	1
986	ILMN_236452	AXL	AXL receptor t	19	-1.004	0.000	0.000	1.19	0.04	0.16	0.43	1.52	0.00	0.87	0.52	0.09	0.00	0.00	0.98	0.90	0.48	0.00	1	0	0	0	1
1031	ILMN_169141	BAMBI	BMP and activi	10	-1.021	0.000	0.000	0.32	-0.12	0.60	0.32	0.25	0.22	0.64	0.03	0.23	0.33	0.32	0.93	0.38	0.64	0.43	0	0	0	0	0
1062	ILMN_176761	BBS2	Bardet-Biedl s	16	-1.006	0.000	0.000	0.11	-0.13	0.02	-0.10	0.18	0.34	0.24	0.84	0.37	0.11	0.45	0.71	0.98	0.74	0.18	0	0	0	0	0
1074	ILMN_176363	BCAR3	breast cancer	1	-1.167	0.000	0.000	-0.66	0.89	0.01	-0.25	-1.00	0.02	0.00	0.98	0.34	0.00	0.04	0.04	1.00	0.72	0.00	0	0	0	0	-1
1092	ILMN_224695	BCL2	B-cell CLL/lym	18	-1.005	0.000	0.000	-0.13	-0.36	0.08	-0.11	-0.08	0.34	0.01	0.56	0.41	0.53	0.45	0.12	0.92	0.77	0.62	0	0	0	0	0
1240	ILMN_170506	BTBD11	BTB (POZ) don	12	1.091	0.000	0.000	0.90	-0.26	0.22	0.30	0.93	0.00	0.22	0.32	0.17	0.00	0.00	0.69	0.80	0.58	0.00	0	0	0	0	0
1283	ILMN_176755	C10orf10	chromosome 1	10	-1.278	0.000	0.000	-0.39	-0.41	0.11	0.00	-0.24	0.02	0.02	0.50	0.99	0.14	0.05	0.19	0.89	1.00	0.21	0	0	0	0	0
1306	ILMN_171020	C10orf6	chromosome 1	10	-1.405	0.000	0.000	-0.68	0.11	-0.21	-0.29	-0.97	0.00	0.49	0.18	0.06	0.00	0.00	0.88	0.70	0.42	0.00	0	0	0	0	0
1378	ILMN_165849	C13orf15	chromosome 1	13	-1.146	0.000	0.000	-1.37	-0.23	0.24	-0.32	-2.07	0.01	0.65	0.62	0.52	0.00	0.02	0.93	0.94	0.83	0.00	-1	0	0	0	-1
1459	ILMN_180541	C15orf48	chromosome 1	15	1.391	0.000	0.000	1.12	-0.25	0.95	0.87	1.29	0.00	0.19	0.00	0.00	0.00	0.00	0.65	0.01	0.01	0.00	1	0	0	0	1
1460	ILMN_165469	C15orf48	chromosome 1	15	1.255	0.000	0.000	1.88	-0.22	1.12	1.23	2.34	0.00	0.51	0.00	0.00	0.00	0.00	0.88	0.12	0.07	0.00	1	0	0	1	1
1586	ILMN_167481	C1orf115	chromosome 1	1	-1.118	0.000	0.000	-0.13	0.29	0.13	-0.25	-0.08	0.49	0.13	0.48	0.18	0.65	0.61	0.55	0.88	0.59	0.73	0	0	0	0	0
1686	ILMN_228338	C20orf24	chromosome 2	20	1.324	0.000	0.000	-0.15	-0.02	-0.04	0.10	-0.08	0.31	0.88	0.80	0.50	0.50	0.43	0.99	0.97	0.81	0.67	0	0	0	0	0
1694	ILMN_172816	C20orf45	chromosome 2	20	1.138	0.000	0.000	0.34	0.09	0.12	0.11	0.44	0.00	0.43	0.27	0.30	0.00	0.01	0.84	0.77	0.69	0.00	0	0	0	0	0
1853	ILMN_214884	C6orf166	chromosome 6	6	1.186	0.000	0.000	0.38	0.10	0.07	0.00	0.34	0.00	0.37	0.55	0.98	0.00	0.01	0.81	0.91	1.00	0.01	0	0	0	0	0
1897	ILMN_167260	C7orf41	chromosome 7	7	-1.263	0.000	0.000	-																			

Table S2.xls

2216	ILMN_177296	CCL8	chemokine (C-	17	1.181	0.002	0.000	4.19	0.63	0.43	2.52	4.79	0.00	0.43	0.59	0.00	0.00	0.85	0.92	0.14	0.00	1	0	0	0	1	
2220	ILMN_178612	CCNA2	cyclin A2 (CCN	4	1.146	0.000	0.000	-0.21	-0.56	0.16	-0.36	-0.28	0.28	0.00	0.40	0.07	0.15	0.40	0.09	0.85	0.44	0.22	0	0	0	0	
2224	ILMN_180193	CCNB2	cyclin B2 (CCN	15	1.348	0.000	0.000	-0.77	-0.39	-0.05	-0.50	-1.00	0.00	0.07	0.81	0.02	0.00	0.00	0.42	0.97	0.30	0.00	0	0	0	-1	
2236	ILMN_237442	CCNE1	cyclin E1 (CCN	19	1.646	0.000	0.000	-0.32	0.13	0.07	-0.24	-0.42	0.01	0.31	0.58	0.06	0.00	0.03	0.77	0.92	0.41	0.00	0	0	0	0	
2264	ILMN_168937	CCRN4L	CCR4 carbon c	4	1.376	0.000	0.000	0.59	0.96	0.11	0.20	0.92	0.03	0.00	0.69	0.46	0.00	0.06	0.02	0.95	0.79	0.00	0	0	0	0	
2316	ILMN_234122	CD34	CD34 molecule	1	-1.322	0.000	0.000	0.43	0.04	0.17	0.27	0.51	0.00	0.75	0.16	0.03	0.00	0.00	0.96	0.68	0.34	0.00	0	0	0	0	
2317	ILMN_173279	CD34	CD34 antigen (1	-1.431	0.000	0.000	0.28	-0.12	0.09	0.21	0.43	0.05	0.39	0.53	0.14	0.00	0.09	0.82	0.91	0.54	0.01	0	0	0	0	
2318	ILMN_178486	CD36	CD36 molecule	7	1.118	0.015	0.000	-1.40	-0.07	-0.44	-0.45	-1.65	0.00	0.81	0.17	0.16	0.00	0.00	0.97	0.70	0.57	0.00	-1	0	0	-1	
2359	ILMN_178058	CD83	CD83 molecule	6	1.130	0.000	0.000	0.17	0.38	0.41	0.19	0.31	0.47	0.12	0.09	0.43	0.19	0.58	0.54	0.56	0.78	0.27	0	0	0	0	
2382	ILMN_174791	CDC2	cell division cy	10	1.344	0.000	0.000	-0.31	-0.61	0.14	-0.36	-0.34	0.17	0.01	0.54	0.11	0.13	0.26	0.13	0.91	0.51	0.20	0	0	0	0	
2383	ILMN_166339	CDC20	cell division cy	1	1.615	0.000	0.000	-0.52	-0.54	0.05	-0.48	-0.74	0.05	0.04	0.86	0.07	0.01	0.10	0.33	0.98	0.44	0.01	0	0	0	0	
2408	ILMN_167023	CDC45L	CDC45 cell divi	22	1.098	0.000	0.000	-0.40	-0.56	0.21	-0.29	-0.47	0.09	0.02	0.36	0.22	0.05	0.16	0.21	0.83	0.63	0.09	0	0	0	0	
2412	ILMN_168345	CDCA5	cell division cy	11	1.291	0.000	0.000	-0.49	-0.80	-0.02	-0.45	-0.75	0.03	0.00	0.91	0.05	0.00	0.07	0.03	0.99	0.40	0.01	0	0	0	0	
2431	ILMN_173092	CDK5R1	cyclin-depende	17	1.588	0.000	0.000	-0.32	-0.25	-0.10	-0.08	-0.40	0.00	0.01	0.29	0.39	0.00	0.01	0.16	0.79	0.76	0.00	0	0	0	0	
2492	ILMN_176300	CENTA2	centaurin, alph	17	1.625	0.000	0.000	0.39	-0.19	-0.22	-0.04	0.32	0.02	0.24	0.17	0.78	0.05	0.04	0.71	0.69	0.94	0.08	0	0	0	0	
2513	ILMN_174701	CEP55	centrosomal or	10	1.113	0.000	0.000	-0.21	-0.39	0.07	-0.25	-0.39	0.29	0.06	0.73	0.21	0.06	0.41	0.38	0.96	0.62	0.10	0	0	0	0	
2523	ILMN_235994	CES1	carboxylestera	16	-1.129	0.001	0.000	0.07	-0.99	0.10	-0.16	0.01	0.89	0.04	0.83	0.74	0.99	0.92	0.31	0.98	0.92	0.99	0	0	0	0	
2530	ILMN_177428	CFB	complement fa	6	1.383	0.000	0.000	5.15	0.53	1.25	2.46	5.97	0.00	0.38	0.04	0.00	0.00	0.00	0.82	0.44	0.03	0.00	1	0	0	1	
2533	ILMN_181091	CFH	complement fa	1	-1.208	0.000	0.000	0.59	-0.04	-0.01	-0.03	0.60	0.01	0.86	0.96	0.90	0.01	0.02	0.98	1.00	0.98	0.02	0	0	0	0	
2534	ILMN_241219	CFH	complement fa	1	-1.332	0.000	0.000	0.41	0.00	0.06	0.00	0.41	0.03	0.98	0.74	0.99	0.03	0.06	1.00	0.96	1.00	0.05	0	0	0	0	
2535	ILMN_165780	CFH	complement fa	1	-1.419	0.000	0.000	0.18	0.06	0.02	0.02	0.32	0.13	0.58	0.88	0.84	0.01	0.22	0.91	0.98	0.96	0.02	0	0	0	0	
2543	ILMN_173022	CGNL1	cingulin-like 1	15	-1.499	0.000	0.000	1.22	-0.18	0.14	0.19	1.52	0.00	0.46	0.56	0.43	0.00	0.00	0.86	0.92	0.78	0.00	1	0	0	1	
2575	ILMN_232627	CHI3L2	chitinase 3-like	1	2.297	0.000	0.000	1.65	0.07	0.01	0.52	2.05	0.00	0.86	0.98	0.19	0.00	0.00	0.98	1.00	0.59	0.00	1	0	0	1	
2641	ILMN_179089	CKAP4	cytoskeleton-a	12	1.058	0.000	0.000	1.52	-0.34	0.34	0.48	1.82	0.00	0.19	0.98	0.16	0.00	0.34	0.00	0.65	0.70	0.43	0.00	1	0	0	1
2648	ILMN_207229	CKS2	CDC28 protein	9	1.176	0.000	0.000	-0.25	-0.03	0.08	-0.09	-0.46	0.13	0.83	0.61	0.56	0.01	0.21	0.98	0.93	0.85	0.01	0	0	0	0	
2649	ILMN_175632	CKS2	CDC28 protein	9	1.460	0.000	0.000	-0.16	-0.05	0.06	0.04	-0.27	0.33	0.76	0.70	0.82	0.09	0.44	0.96	0.95	0.95	0.15	0	0	0	0	
2655	ILMN_166083	CLCN3	chloride chann	4	1.067	0.000	0.000	-0.33	-0.06	-0.12	-0.10	-0.42	0.00	0.59	0.26	0.33	0.00	0.01	0.91	0.76	0.72	0.00	0	0	0	0	
2666	ILMN_172533	CLDN23	claudin 23 (CL	8	-1.730	0.000	0.000	0.59	0.29	-0.06	0.37	0.77	0.00	0.15	0.76	0.07	0.00	0.01	0.60	0.96	0.44	0.00	0	0	0	0	
2728	ILMN_170989	CLPX	CipX caseinoly	15	1.052	0.000	0.000	0.05	0.09	0.02	0.03	0.12	0.48	0.25	0.77	0.67	0.13	0.59	0.72	0.96	0.90	0.19	0	0	0	0	
2743	ILMN_170408	CMAH	cytidine monor	6	-1.193	0.000	0.000	0.40	0.12	0.03	-0.09	0.52	0.00	0.26	0.80	0.37	0.00	0.00	0.73	0.97	0.74	0.00	0	0	0	0	
2774	ILMN_165572	CNNM4	cyclin M4 (CNN	2	1.034	0.000	0.000	0.19	-0.01	0.10	0.11	0.12	0.12	0.94	0.38	0.37	0.32	0.20	0.99	0.84	0.74	0.42	0	0	0	0	
2798	ILMN_171188	COBL	cordon-bleu hc	7	-1.222	0.000	0.000	0.18	0.42	0.35	0.44	0.38	0.35	0.03	0.07	0.03	0.05	0.47	0.28	0.52	0.32	0.09	0	0	0	0	
2822	ILMN_167405	COL8A2	collagen, type	1	-1.061	0.000	0.000	-0.96	-0.41	0.53	-0.19	-1.13	0.01	0.23	0.12	0.58	0.00	0.02	0.69	0.63	0.86	0.00	0	0	0	-1	
2887	ILMN_166241	COX7A1	cytochrome c c	19	-1.328	0.000	0.000	-0.07	0.13	0.05	-0.10	-0.10	0.52	0.23	0.62	0.35	0.39	0.63	0.70	0.94	0.73	0.49	0	0	0	0	
2928	ILMN_169017	CRABP2	cellular retinoi	1	1.856	0.000	0.000	-1.63	0.17	-0.07	-0.33	-2.11	0.01	0.77	0.91	0.56	0.00	0.02	0.96	0.99	0.85	0.00	-1	0	0	-1	
2931	ILMN_173799	CRAT	carnitine acety	9	-1.380	0.000	0.000	0.20	-0.28	0.04	0.08	0.25	0.13	0.04	0.79	0.57	0.06	0.22	0.31	0.97	0.85	0.11	0	0	0	0	
2950	ILMN_165692	CRIP1	cysteine-rich p	14	-1.581	0.000	0.000	-0.72	0.13	-0.17	0.04	-0.65	0.08	0.75	0.66	0.92	0.11	0.14	0.96	0.94	0.98	0.17	0	0	0	0	
2977	ILMN_179618	CRY2	cryptochrome .	11	-1.370	0.000	0.000	0.27	0.02	0.10	0.01	0.31	0.01	0.84	0.32	0.92	0.00	0.03	0.98	0.80	0.98	0.01	0	0	0	0	
3002	ILMN_237645	CSF2RA	colony stimulat	11	1.113	0.000	0.000	0.08	0.09	0.25	-0.02	0.17	0.69	0.67	0.22	0.93	0.41	0.77	0.94	0.74	0.98	0.51	0	0	0	0	
3032	ILMN_181192	CSRP1	cysteine and g	1	-1.200	0.000	0.000	-0.52	-0.27	-0.06	-0.20	-0.54	0.00	0.06	0.68	0.15	0.00	0.00	0.38	0.95	0.56	0.00	0	0	0	0	
3036	ILMN_169866	CST6	cystatin E/M (C	11	-1.133	0.000	0.000	-0.54	-0.05	-0.11	-0.09	-0.41	0.00	0.76	0.54	0.60	0.02	0.01	0.96	0.91	0.86	0.05	0	0	0	0	
3037	ILMN_169773	CST6	PREDICTED: cystatin	-1.126	0.001	0.000	-0.34	-0.02	-0.09	-0.14	-0.31	0.03	0.87	0.56	0.36	0.04	0.07	0.98	0.91	0.73	0.08	0	0	0	0	0	
3040	ILMN_166988	CSTA	cystatin A (ste	3	1.821	0.000	0.000	-0.08	-0.36	0.09	-0.06	0.03	0.60	0.03	0.55	0.68	0.84	0.70	0.24	0.91	0.90	0.88	0	0	0	0	
3041	ILMN_176179	CSTB	cystatin B (ste	21	1.151	0.000	0.000	-0.53	0.00	-0.12	-0.16	-0.73	0.00	0.98	0.30	0.17	0.00	0.00	1.00	0.79	0.58	0.00	0	0	0	0	
3071	ILMN_168810	CTNBP1P1	catenin, beta ii	1	-1.262	0.000	0.000	-0.70	-0.16	-0.16	0.01	-0.79	0.00	0.46	0.47	0.97	0.00	0.01	0.86	0.88	0.99	0.00	0	0	0	0	
3086	ILMN_224246	CTSC	cathepsin C (C	11	1.188	0.000	0.000	-0.46	0.98	-0.32	-0.25	-0.25	0.11	0.00	0.26	0.38	0.38	0.18	0.03	0.76	0.75	0.48	0	0	0	0	
3087	ILMN_169634	CTSC	cathepsin C (C	11	1.299	0.000	0.000	-0.50	1.06	-0.41	-0.29	-0.27	0.09	0.00	0.17	0.33	0.35	0.15	0.02	0.69	0.71	0.45	0	1	0	0	
3100	ILMN_166626	CTS2	cathepsin Z (C	20	-1.060	0.000	0.000	-0.42	0.04	-0.22	-0.19	-0.41	0.01	0.79	0.17	0.24	0.01	0.03	0.97	0.69	0.64	0.03	0	0	0	0	
3127	ILMN_179175	CXCL10	chemokine (C-	4	1.559	0.000	0.000	6.34	0.04	0.49	1.82	7.22	0.00	0.96	0.48	0.01	0.00	0.00	1.00	0.89	0.25	0.00	1	0	0	1	
3136	ILMN_174535	CXCL9	chemokine (C-	4	1.467	0.001	0.000	6.94	0.50	0.51	1.30	6.95	0.00	0.35	0.35	0.02	0.00	0.00	0.80	0.82	0.30	0.00	1	0	0	1	
3174	ILMN_171230	CYBRD1	cytochrome b i	2	-1.215	0.000	0.000	-1.46	-0.09	-0.53	-0.72	-1.61	0.00	0.75	0.06	0.01	0.00	0.00	0.96	0.49	0.26	0.00	-1	0	0	-1	
3175																											

Table S2.xls

3905	ILMN_170974	ENDOGL1	endonuclease (3	1.051	0.000	0.000	3.21	-0.75	1.12	2.01	3.45	0.00	0.06	0.01	0.00	0.00	0.00	0.39	0.23	0.00	0.00	1	0	0	1	1
3935	ILMN_167579	EPDR1	ependymin rel	7	-1.279	0.000	0.000	-0.48	0.55	-0.25	-0.43	-0.55	0.01	0.01	0.18	0.02	0.00	0.03	0.09	0.70	0.32	0.01	0	0	0	0	0
3949	ILMN_238854	EPST11	epithelial stron	13	2.419	0.000	0.000	3.66	-0.01	-0.31	1.75	4.01	0.00	0.97	0.37	0.00	0.00	0.00	1.00	0.83	0.00	0.00	1	0	0	1	1
3982	ILMN_174496	ER01L	ER01-like (S, c	14	1.348	0.000	0.000	0.49	0.20	0.20	0.26	0.63	0.00	0.16	0.16	0.07	0.00	0.00	0.61	0.68	0.45	0.00	0	0	0	0	0
4066	ILMN_167176	F12	coagulation fac	5	1.051	0.000	0.000	-0.39	0.07	0.11	-0.05	-0.43	0.00	0.58	0.39	0.70	0.00	0.01	0.91	0.84	0.91	0.00	0	0	0	0	0
4069	ILMN_212957	F3	coagulation fac	1	-1.489	0.000	0.000	-0.48	-0.10	0.79	0.10	-0.81	0.17	0.78	0.03	0.78	0.02	0.26	0.96	0.38	0.93	0.05	0	0	0	0	0
4075	ILMN_177300	FABP4	fatty acid bindi	8	-1.909	0.000	0.000	-1.05	1.53	-0.72	-0.75	-1.22	0.04	0.00	0.16	0.14	0.02	0.09	0.08	0.68	0.55	0.04	-1	1	0	0	-1
4076	ILMN_214676	FABP5	fatty acid bindi	8	2.021	0.000	0.000	-1.54	0.45	-0.58	-0.44	-1.60	0.00	0.17	0.08	0.18	0.00	0.00	0.63	0.55	0.59	0.00	-1	0	0	0	-1
4077	ILMN_169630	FABP5	fatty acid bindi	8	2.927	0.000	0.000	-1.27	0.59	-0.55	-0.31	-1.32	0.00	0.06	0.08	0.32	0.00	0.00	0.40	0.55	0.71	0.00	-1	0	0	0	-1
4079	ILMN_167013	FADS1	fatty acid desa	11	-2.329	0.000	0.000	-0.34	0.21	0.17	0.11	-0.25	0.11	0.33	0.42	0.61	0.24	0.20	0.79	0.86	0.87	0.33	0	0	0	0	0
4080	ILMN_207506	FADS2	fatty acid desa	11	-1.083	0.000	0.000	-0.14	-0.02	-0.01	-0.03	0.01	0.38	0.88	0.93	0.85	0.93	0.49	0.99	0.99	0.96	0.95	0	0	0	0	0
4105	ILMN_175867	FAM107B	family with sec	10	-1.019	0.000	0.000	-0.16	-0.62	0.23	0.06	-0.47	0.42	0.00	0.23	0.75	0.02	0.54	0.05	0.74	0.93	0.04	0	0	0	0	0
4152	ILMN_238795	FAM134B	family with sec	5	-1.242	0.000	0.000	-0.24	-1.07	0.01	-0.04	-0.22	0.15	0.00	0.95	0.82	0.19	0.24	0.00	0.99	0.95	0.27	0	-1	0	0	0
4156	ILMN_240125	FAM13A1	family with sec	4	-1.063	0.000	0.000	-0.29	-0.08	-0.40	-0.22	-0.28	0.11	0.65	0.03	0.23	0.12	0.19	0.94	0.40	0.64	0.19	0	0	0	0	0
4157	ILMN_175251	FAM13A1	family with sec	4	-1.084	0.000	0.000	-0.39	-0.20	-0.47	-0.31	-0.51	0.05	0.32	0.02	0.12	0.01	0.10	0.78	0.36	0.53	0.03	0	0	0	0	0
4194	ILMN_170601	FAM43A	family with sec	3	1.885	0.000	0.000	-0.32	-0.37	-0.23	-0.16	-0.40	0.01	0.00	0.05	0.17	0.00	0.02	0.05	0.47	0.58	0.00	0	0	0	0	0
4269	ILMN_172879	FBP1	fructose-1,6-bi	9	-1.079	0.000	0.000	-1.69	-0.36	0.09	-0.90	-1.99	0.00	0.41	0.84	0.04	0.00	0.00	0.84	0.98	0.38	0.00	-1	0	0	0	-1
4309	ILMN_174711	FBXO46	PREDICTED: F	19	1.045	0.000	0.000	0.10	-0.03	-0.03	-0.02	0.09	0.30	0.73	0.78	0.88	0.36	0.41	0.95	0.97	0.97	0.46	0	0	0	0	0
4312	ILMN_170145	FBXO6	F-box protein (1	1.270	0.000	0.000	1.71	0.33	0.16	0.87	2.06	0.00	0.16	0.49	0.00	0.00	0.00	0.60	0.89	0.06	0.00	1	0	0	0	1
4368	ILMN_169529	FERMT2	fermitin family	14	-1.347	0.000	0.000	0.64	-0.09	0.29	0.40	0.85	0.00	0.61	0.09	0.02	0.00	0.00	0.92	0.57	0.31	0.00	0	0	0	0	0
4378	ILMN_177268	FGD3	FYVE, RhoGEF	9	1.054	0.000	0.000	0.75	-0.50	0.07	0.03	0.79	0.00	0.02	0.73	0.88	0.00	0.00	0.19	0.96	0.97	0.00	0	0	0	0	0
4380	ILMN_210414	FGD5	FYVE, RhoGEF	3	-1.202	0.000	0.000	-1.08	-0.01	-0.13	-0.55	-1.21	0.00	0.97	0.60	0.03	0.00	0.00	1.00	0.93	0.35	0.00	-1	0	0	0	-1
4392	ILMN_180584	FHL1	four and a half X	1	-1.801	0.000	0.000	-0.35	0.08	-0.16	-0.24	-0.52	0.09	0.69	0.43	0.24	0.01	0.16	0.94	0.86	0.65	0.03	0	0	0	0	0
4467	ILMN_167703	FLJ21986	hypothetical pr	7	-1.193	0.000	0.000	0.06	-0.56	0.51	0.00	-0.05	0.72	0.00	0.00	1.00	0.79	0.80	0.05	0.20	1.00	0.84	0	0	0	0	0
4472	ILMN_170728	FLJ22662	hypothetical pr	12	1.604	0.000	0.000	-0.59	-0.01	0.00	-0.11	-0.54	0.00	0.97	0.99	0.48	0.00	0.00	1.00	1.00	0.80	0.00	0	0	0	0	0
4510	ILMN_220487	FLVCR2	feline leukemic	14	1.262	0.000	0.000	-0.64	0.27	-0.12	0.00	-0.57	0.00	0.12	0.48	0.99	0.00	0.00	0.54	0.89	1.00	0.01	0	0	0	0	0
4570	ILMN_170008	FST	folllistatin (FST	5	-1.614	0.000	0.000	-0.02	0.42	0.08	0.06	-0.03	0.87	0.00	0.44	0.55	0.75	0.91	0.01	0.87	0.84	0.81	0	0	0	0	0
4626	ILMN_174336	FZD4	frizzled homolc	11	-1.441	0.000	0.000	0.32	-0.25	0.59	0.15	0.37	0.06	0.14	0.00	0.35	0.03	0.11	0.58	0.09	0.73	0.06	0	0	0	0	0
4644	ILMN_215128	GABARAPL1	GABA(A) recep	12	-1.074	0.000	0.000	-0.03	0.03	0.05	0.16	0.08	0.76	0.75	0.59	0.10	0.40	0.83	0.96	0.92	0.50	0.50	0	0	0	0	0
4655	ILMN_168201	GAL	galanin prepro	11	-3.853	0.000	0.000	-0.48	0.27	0.44	0.53	-0.32	0.40	0.64	0.44	0.36	0.57	0.52	0.93	0.87	0.74	0.66	0	0	0	0	0
4706	ILMN_175512	GBA	glucosidase, be	1	1.196	0.000	0.000	-0.18	0.03	-0.15	-0.08	-0.07	0.05	0.72	0.11	0.40	0.45	0.09	0.95	0.59	0.76	0.55	0	0	0	0	0
4714	ILMN_214878	GBP1	guanylate bind	1	1.622	0.000	0.000	3.77	0.11	1.23	1.45	3.94	0.00	0.72	0.00	0.00	0.00	0.00	0.95	0.05	0.01	0.00	1	0	1	1	1
4715	ILMN_170111	GBP1	guanylate bind	1	1.629	0.000	0.000	3.97	0.17	1.24	1.59	4.28	0.00	0.62	0.00	0.00	0.00	0.00	0.92	0.08	0.01	0.00	1	0	1	1	1
4719	ILMN_211456	GBP5	guanylate bind	1	1.442	0.000	0.000	5.04	-0.04	0.48	1.37	5.21	0.00	0.91	0.17	0.00	0.00	0.00	0.99	0.70	0.04	0.00	1	0	0	1	1
4773	ILMN_219591	GGH	gamma-glutar	8	1.067	0.000	0.000	-0.09	-0.35	0.22	0.05	0.01	0.53	0.02	0.14	0.74	0.97	0.64	0.23	0.65	0.92	0.98	0	0	0	0	0
4774	ILMN_168175	GGH	gamma-glutar	8	1.148	0.000	0.000	0.00	-0.48	0.54	0.14	0.18	1.00	0.00	0.00	0.37	0.26	1.00	0.09	0.12	0.74	0.35	0	0	0	0	0
4792	ILMN_175427	GINS3	GINS complex	16	1.102	0.000	0.000	0.16	-0.10	0.15	0.08	0.10	0.06	0.23	0.08	0.33	0.24	0.12	0.70	0.53	0.71	0.33	0	0	0	0	0
4801	ILMN_176938	GJB2	gap junction p	13	2.520	0.000	0.000	0.75	-1.05	0.87	0.69	1.03	0.04	0.01	0.02	0.06	0.01	0.09	0.10	0.34	0.42	0.02	0	-1	0	0	1
4804	ILMN_172547	GK	glycerol kinase X	1	1.696	0.000	0.000	1.00	0.05	0.17	0.23	1.22	0.00	0.84	0.49	0.34	0.00	0.00	0.98	0.89	0.72	0.00	1	0	0	0	1
4805	ILMN_239329	GK	glycerol kinase X	1	1.757	0.000	0.000	0.97	0.16	0.24	0.33	1.16	0.00	0.54	0.35	0.20	0.00	0.00	0.89	0.82	0.61	0.00	0	0	0	0	1
4838	ILMN_222104	GM2A	GM2 gangliosic	5	1.845	0.000	0.000	-0.24	0.07	0.19	0.03	-0.26	0.14	0.66	0.25	0.87	0.11	0.22	0.94	0.75	0.97	0.17	0	0	0	0	0
4850	ILMN_241292	GMPPB	GDP-mannose	3	1.027	0.000	0.000	0.20	-0.04	0.01	-0.03	0.24	0.10	0.74	0.96	0.77	0.04	0.17	0.96	1.00	0.93	0.08	0	0	0	0	0
4860	ILMN_177396	GNA15	guanine nuclec	19	1.234	0.000	0.000	0.69	-0.07	0.17	0.18	0.86	0.00	0.76	0.46	0.45	0.00	0.01	0.96	0.88	0.79	0.00	0	0	0	0	0
4921	ILMN_217885	GPAM	glycerol-3-pho	10	-1.398	0.000	0.000	-0.55	-0.09	-0.09	-0.02	-0.62	0.00	0.47	0.51	0.87	0.00	0.00	0.87	0.90	0.97	0.00	0	0	0	0	0
4922	ILMN_175821	GPAM	glycerol-3-pho	10	-1.246	0.001	0.000	-0.53	-0.09	-0.10	-0.11	-0.62	0.00	0.37	0.33	0.31	0.00	0.00	0.81	0.81	0.70	0.00	0	0	0	0	0
4934	ILMN_205197	GPC3	glypican 3 (GP X	1	-1.146	0.000	0.000	0.03	-0.11	0.05	0.01	0.00	0.83	0.37	0.69	0.96	0.99	0.88	0.81	0.95	0.99	0.99	0	0	0	0	0
4974	ILMN_167114	GPR68	G protein-coup	14	1.899	0.000	0.000	-0.41	-0.60	0.41	0.14	-0.71	0.21	0.07	0.22	0.67	0.04	0.32	0.44	0.73	0.90	0.07	0	0	0	0	0
5032	ILMN_180104	GSN	gelsolin (amylc	9	-1.093	0.000	0.000	-0.98	0.10	0.32	-0.23	-1.18	0.00	0.74	0.29	0.43	0.00	0.01	0.96	0.78	0.78	0.00	0	0	0	0	-1
5044	ILMN_173618	GSTM3	glutathione S-t	1	-1.154	0.001	0.000	-0.45	-0.29	0.06	-0.15	-0.59	0.00	0.02	0.65	0.24	0.00	0.00	0.24	0.94	0.64	0.00	0	0	0	0	0
5105	ILMN_166803	GYPC	glycophorin C (2	-1.097	0.000	0.000	1.90	-0.36	0.92	0.64	2.17	0.00	0.13	0.00	0.01	0.00	0.00	0.56	0.05	0.22	0.00					

Table S2.xls

5772	ILMN_1910908	RST24587 Athersys	RA	2.033	0.000	0.000	1.41	-0.14	0.20	0.30	1.74	0.00	0.58	0.45	0.25	0.00	0.00	0.91	0.87	0.65	0.00	1	0	0	0	1	
5791	ILMN_238950	HSD11B1	hydroxysteroid	1	-1.847	0.000	0.000	1.68	0.88	0.95	1.41	2.26	0.00	0.09	0.07	0.01	0.00	0.01	0.48	0.51	0.22	0.00	1	0	0	0	1
5818	ILMN_215391	HSPA2	heat shock 70k	14	-1.251	0.000	0.000	0.39	-0.01	0.14	0.19	0.50	0.00	0.93	0.25	0.11	0.00	0.01	0.99	0.75	0.52	0.00	0	0	0	0	0
5828	ILMN_220083	HSPB7	heat shock 27k	1	-1.313	0.000	0.000	-0.19	-0.21	0.12	0.26	-0.15	0.28	0.23	0.49	0.14	0.37	0.39	0.70	0.89	0.54	0.47	0	0	0	0	0
5881	ILMN_171363	ICHTHYIN	ichthyin protei	5	1.194	0.000	0.000	0.42	-0.22	0.98	0.54	0.69	0.22	0.53	0.01	0.12	0.05	0.32	0.89	0.21	0.53	0.09	0	0	0	0	0
5908	ILMN_171093	IFI16	interferon, qan	1	1.171	0.000	0.000	0.61	-0.24	-0.37	0.15	0.88	0.00	0.22	0.06	0.44	0.00	0.01	0.69	0.49	0.79	0.00	0	0	0	0	0
5909	ILMN_205878	IFI27	interferon, alp	14	1.866	0.000	0.000	6.58	0.24	-0.06	3.47	7.55	0.00	0.72	0.93	0.00	0.00	0.00	0.95	0.99	0.00	0.00	1	0	0	1	1
5912	ILMN_176006	IFI44L	interferon-indu	1	2.002	0.000	0.000	3.14	-0.21	-0.23	1.83	3.66	0.00	0.48	0.44	0.00	0.00	0.00	0.87	0.87	0.00	0.00	1	0	0	1	1
5913	ILMN_172391	IFI44L	interferon-indu	1	2.253	0.000	0.000	5.29	-0.06	0.01	3.45	6.15	0.00	0.89	0.98	0.00	0.00	0.00	0.99	1.00	0.00	0.00	1	0	0	1	1
5914	ILMN_234779	IFI6	interferon, alp	1	3.647	0.000	0.000	3.19	-0.11	0.08	2.34	4.04	0.00	0.78	0.84	0.00	0.00	0.00	0.96	0.98	0.00	0.00	1	0	0	1	1
5915	ILMN_168738	IFI6	interferon, alp	1	2.005	0.000	0.000	1.91	-0.06	0.06	1.45	2.51	0.00	0.82	0.83	0.00	0.00	0.00	0.97	0.98	0.00	0.00	1	0	0	1	1
5916	ILMN_178137	IFIH1	interferon indu	2	1.495	0.000	0.000	2.18	0.08	0.13	0.95	2.78	0.00	0.79	0.66	0.00	0.00	0.00	0.97	0.94	0.12	0.00	1	0	0	0	1
5917	ILMN_170769	IFIT1	interferon-indu	10	2.152	0.000	0.000	4.93	-0.15	-0.20	2.89	6.05	0.00	0.78	0.71	0.00	0.00	0.00	0.96	0.95	0.00	0.00	1	0	0	1	1
5921	ILMN_170178	IFIT3	interferon-indu	10	1.676	0.000	0.000	4.64	-0.14	0.06	2.65	5.45	0.00	0.77	0.90	0.00	0.00	0.00	0.96	0.99	0.00	0.00	1	0	0	1	1
5950	ILMN_166936	IGFBP6	insulin-like gro	12	-1.811	0.000	0.000	1.07	-0.17	0.00	0.21	1.44	0.03	0.73	1.00	0.68	0.01	0.07	0.96	1.00	0.90	0.01	1	0	0	0	1
5995	ILMN_179957	IL19	interleukin 19	1	2.180	0.001	0.000	1.11	0.05	0.07	0.22	0.59	0.00	0.89	0.84	0.57	0.12	0.02	0.99	0.98	0.85	0.19	1	0	0	0	0
5995	ILMN_168259	IL19	interleukin 19	1	1.673	0.002	0.000	0.80	0.00	0.13	0.11	0.54	0.00	1.00	0.63	0.69	0.05	0.01	1.00	0.94	0.90	0.09	0	0	0	0	0
5998	ILMN_177550	IL1B	interleukin 1, t	2	1.886	0.010	0.000	3.27	-1.38	2.06	2.10	3.91	0.00	0.03	0.00	0.00	0.00	0.00	0.28	0.13	0.11	0.00	1	0	0	0	1
5999	ILMN_180490	IL1F5	interleukin 1 fe	2	2.397	0.000	0.000	0.37	-0.31	-0.03	0.15	0.40	0.14	0.20	0.91	0.55	0.11	0.22	0.67	0.99	0.84	0.17	0	0	0	0	0
6000	ILMN_169771	IL1F7	interleukin 1 fe	2	-2.255	0.000	0.000	2.33	0.10	-0.12	0.30	2.61	0.00	0.77	0.71	0.36	0.00	0.00	0.96	0.96	0.74	0.00	1	0	0	0	1
6001	ILMN_215871	IL1F9	interleukin 1 fe	2	3.203	0.000	0.000	2.69	-0.08	0.28	0.54	2.52	0.00	0.85	0.52	0.22	0.00	0.00	0.98	0.90	0.63	0.00	1	0	0	0	1
6007	ILMN_177487	IL1RN	interleukin 1 rr	2	1.203	0.000	0.000	1.11	1.00	0.60	0.86	1.44	0.00	0.01	0.11	0.22	0.00	0.01	0.13	0.59	0.31	0.00	1	0	0	0	1
6024	ILMN_165218	IL4R	interleukin 4 rr	16	1.513	0.000	0.000	0.31	0.09	0.29	0.22	0.48	0.04	0.53	0.06	0.14	0.00	0.09	0.89	0.50	0.55	0.01	0	0	0	0	0
6029	ILMN_234257	IL7R	interleukin 7 rr	5	1.174	0.000	0.000	1.94	0.02	1.08	1.60	2.68	0.00	0.98	0.05	0.00	0.00	0.00	1.00	0.47	0.19	0.00	1	0	0	0	1
6030	ILMN_169134	IL7R	PREDICTED: interleuk	4	1.405	0.001	0.000	2.15	0.18	1.36	1.89	3.26	0.00	0.75	0.02	0.00	0.00	0.00	0.96	0.37	0.14	0.00	1	0	0	0	1
6031	ILMN_218437	IL8	interleukin 8 (I	4	4.261	0.001	0.000	0.97	-0.14	0.97	0.98	1.12	0.01	0.69	0.01	0.01	0.02	0.94	0.22	0.19	0.01	0	0	0	0	1	
6032	ILMN_166673	IL8	interleukin 8 (I	4	3.416	0.003	0.000	1.48	-0.09	1.24	1.15	1.69	0.00	0.81	0.00	0.00	0.00	0.00	0.97	0.13	0.17	0.00	1	0	0	0	1
6072	ILMN_179347	INSIG1	insulin induced	7	-1.331	0.000	0.000	-0.37	-0.16	0.36	0.17	-0.27	0.11	0.48	0.12	0.46	0.25	0.19	0.87	0.63	0.79	0.34	0	0	0	0	0
6110	ILMN_174596	IRAK2	interleukin-1 rr	3	1.762	0.000	0.000	0.54	-0.64	0.80	0.38	0.70	0.02	0.01	0.00	0.11	0.00	0.05	0.12	0.10	0.51	0.01	0	0	0	0	0
6111	ILMN_166169	IRAK3	interleukin-1 rr	12	1.053	0.000	0.000	0.85	-0.40	0.37	0.24	0.85	0.00	0.07	0.09	0.27	0.00	0.00	0.42	0.57	0.67	0.00	0	0	0	0	0
6122	ILMN_234906	IRF7	interferon reagu	11	1.814	0.000	0.000	3.06	-0.02	-0.02	1.70	3.72	0.00	0.94	0.95	0.00	0.00	0.00	0.99	1.00	0.00	0.00	1	0	0	1	1
6123	ILMN_179818	IRF7	interferon reagu	11	2.224	0.000	0.000	3.36	0.01	0.00	1.87	3.93	0.00	0.99	0.99	0.00	0.00	0.00	1.00	1.00	0.00	0.00	1	0	0	1	1
6124	ILMN_166659	IRF8	interferon reagu	16	1.082	0.000	0.000	-0.24	0.10	0.15	-0.23	-0.42	0.11	0.50	0.31	0.13	0.01	0.19	0.88	0.80	0.53	0.02	0	0	0	0	0
6134	ILMN_205401	ISG15	ISG15 ubiquititi	1	2.733	0.000	0.000	4.65	0.02	-0.04	2.70	5.56	0.00	0.98	0.94	0.00	0.00	0.00	1.00	0.99	0.00	0.00	1	0	0	1	1
6135	ILMN_165991	ISG20	interferon stim	15	1.524	0.000	0.000	5.87	0.01	0.20	2.16	6.99	0.00	0.99	0.76	0.00	0.00	0.00	1.00	0.96	0.14	0.00	1	0	0	0	1
6189	ILMN_173610	ITPR2	inositol 1,4,5-t	12	-1.089	0.000	0.000	0.00	0.00	0.35	0.02	-0.06	0.99	0.98	0.04	0.93	0.71	0.99	1.00	0.45	0.98	0.78	0	0	0	0	0
6238	ILMN_174496	KCNAB1	potassium volt	3	-1.081	0.000	0.000	-0.67	-0.06	0.21	-0.65	-1.10	0.07	0.86	0.57	0.08	0.00	0.13	0.98	0.92	0.46	0.01	0	0	0	0	-1
6292	ILMN_228599	KIAA0101	KIAA0101 (KIA	15	1.579	0.000	0.000	-0.75	-0.97	-0.02	-0.59	-0.97	0.02	0.00	0.95	0.06	0.00	0.04	0.06	0.99	0.41	0.01	0	0	0	0	0
6318	ILMN_181062	KIAA0367	KIAA0367 (KIA	9	-1.064	0.000	0.000	0.00	-0.17	-0.32	-0.15	-0.12	0.98	0.36	0.08	0.42	0.49	0.99	0.81	0.55	0.77	0.59	0	0	0	0	0
6434	ILMN_169556	KIF20A	kinesin family	5	1.236	0.000	0.000	-0.23	-0.28	0.17	-0.17	-0.30	0.15	0.07	0.28	0.27	0.06	0.24	0.43	0.78	0.67	0.10	0	0	0	0	0
6455	ILMN_173593	KLF2	Kruppel-like fa	19	-1.017	0.000	0.000	-0.50	0.84	-0.30	-0.36	-0.86	0.07	0.00	0.26	0.18	0.00	0.13	0.06	0.76	0.59	0.01	0	0	0	0	0
6461	ILMN_177852	KLF9	Kruppel-like fa	9	-1.247	0.000	0.000	0.83	0.42	0.89	0.69	1.01	0.00	0.10	0.00	0.01	0.00	0.01	0.51	0.10	0.23	0.00	0	0	0	0	1
6489	ILMN_207965	KLRB1	killer cell lectin	12	1.244	0.012	0.000	-0.12	0.11	0.02	0.18	0.07	0.57	0.59	0.91	0.40	0.74	0.68	0.91	0.99	0.76	0.80	0	0	0	0	0
6522	ILMN_174651	KYNU	kynureninase (2	3.626	0.000	0.000	0.80	-0.56	0.69	0.60	1.09	0.00	0.00	0.00	0.00	0.00	0.05	0.05	0.09	0.00	0	0	0	0	1	
6523	ILMN_173751	KYNU	kynureninase (2	2.175	0.000	0.000	1.12	-0.54	0.79	0.73	1.49	0.00	0.01	0.00	0.00	0.00	0.00	0.13	0.05	0.07	0.00	1	0	0	0	1
6551	ILMN_217081	LAMP3	lysosomal-assc	3	1.356	0.000	0.000	3.44	1.28	0.89	1.83	4.71	0.00	0.06	0.19	0.01	0.00	0.00	0.39	0.71	0.22	0.00	1	0	0	0	1
6577	ILMN_176766	LASS6	LAG1 homolog	2	-1.117	0.000	0.000	-0.16	0.17	-0.25	-0.11	-0.27	0.30	0.28	0.11	0.48	0.09	0.42	0.74	0.59	0.80	0.14	0	0	0	0	0
6610	ILMN_223495	LEPR	leptin receptor	1	-2.078	0.000	0.000	-0.19	-0.16	-0.07	0.06	-0.18	0.09	0.15	0.54	0.57	0.12	0.16	0.59	0.91	0.86	0.18	0	0	0	0	0
6621	ILMN_180378	LGALS3	lectin, galactos	14	-1.165	0.000	0.000	-1.31	0.20	-0.47	-0.48	-1.69	0.00	0.50	0.12	0.11	0.00	0.00	0.88	0.63	0.52	0.00	-1	0	0	0	-1
6622	ILMN_165968	LGALS3BP	lectin, galactos	17	1.174	0.000	0.000	2.19	0.30	0.28	1.16	2.77	0.00	0.26	0.29	0.00	0.00	0.00									

Table S2.xls

7572	ILMN_166521	LTBP4	latent transfor	19	-1.006	0.000	0.000	0.16	-0.13	-0.04	0.05	0.16	0.13	0.19	0.70	0.64	0.12	0.21	0.66	0.95	0.89	0.19	0	0	0	0	0
7593	ILMN_178115	LYN	v-yes-1 Yamac	8	1.277	0.000	0.000	0.82	-0.52	0.07	0.29	0.91	0.00	0.02	0.77	0.21	0.00	0.00	0.24	0.96	0.62	0.00	0	0	0	0	0
7607	ILMN_181520	LYZ	lysozyme (ren	12	1.575	0.001	0.000	-0.11	-0.33	-0.03	-0.16	-0.13	0.56	0.08	0.89	0.38	0.49	0.66	0.44	0.98	0.75	0.58	0	0	0	0	0
7619	ILMN_177756	MAD2L1	MAD2 mitotic	4	1.193	0.000	0.000	-0.41	-0.37	0.11	-0.32	-0.53	0.06	0.08	0.60	0.13	0.02	0.12	0.46	0.93	0.54	0.03	0	0	0	0	0
7630	ILMN_166157	MAFA	v-maf musculo	8	1.505	0.000	0.000	1.76	0.05	0.18	1.34	2.27	0.00	0.83	0.40	0.00	0.00	0.00	0.98	0.85	0.00	0.00	1	0	0	1	1
7886	ILMN_212290	MELK	maternal embr	9	1.553	0.000	0.000	0.33	-0.57	0.06	-0.27	0.47	0.09	0.01	0.77	0.18	0.02	0.17	0.10	0.96	0.58	0.04	0	0	0	0	0
7923	ILMN_173341	MFPAP5	microfibrillar a	12	-1.506	0.000	0.000	-0.57	-0.27	-0.12	-0.24	-0.50	0.00	0.05	0.37	0.08	0.00	0.00	0.36	0.83	0.45	0.00	0	0	0	0	0
7947	ILMN_175074	MGC102966	PREDICTED: si	17	3.315	0.000	0.000	-0.01	0.01	0.09	-0.02	0.00	0.90	0.91	0.32	0.84	0.96	0.93	0.99	0.80	0.96	0.97	0	0	0	0	0
7974	ILMN_177612	MGC42367	similar to 201C	2	-1.246	0.000	0.000	-0.52	-0.32	-0.46	-0.32	-0.42	0.03	0.18	0.05	0.18	0.08	0.07	0.63	0.47	0.58	0.12	0	0	0	0	0
7990	ILMN_178195	MGST1	microsomal gl	12	-1.403	0.001	0.000	0.62	-0.28	0.21	0.44	0.96	0.03	0.30	0.43	0.11	0.00	0.06	0.76	0.86	0.51	0.00	0	0	0	0	0
7992	ILMN_235516	MGST1	microsomal gl	12	-2.061	0.000	0.000	0.45	-0.36	0.29	0.38	0.65	0.07	0.14	0.23	0.12	0.01	0.13	0.58	0.74	0.53	0.02	0	0	0	0	0
8002	ILMN_181513	MICALL1	MICAL-like 1 (I	22	1.272	0.000	0.000	0.50	0.32	0.35	0.42	0.71	0.00	0.04	0.03	0.01	0.00	0.01	0.32	0.37	0.22	0.00	0	0	0	0	0
8052	ILMN_220291	MLSTD1	male sterility d	12	-2.102	0.000	0.000	0.45	1.48	0.16	-0.09	0.48	0.00	0.00	0.28	0.55	0.00	0.01	0.00	0.78	0.84	0.01	0	1	0	0	0
8064	ILMN_207375	MMP12	matrix metallo	11	1.249	0.006	0.000	-0.43	1.59	0.05	0.53	0.23	0.53	0.02	0.94	0.44	0.74	0.64	0.24	0.99	0.78	0.80	0	0	0	0	0
8071	ILMN_168540	MMP7	matrix metallo	11	-1.352	0.005	0.000	0.70	-0.20	0.50	0.98	1.32	0.13	0.66	0.28	0.04	0.01	0.22	0.94	0.77	0.36	0.01	0	0	0	0	1
8072	ILMN_219207	MMP7	matrix metallo	11	-1.444	0.002	0.000	0.71	-0.13	0.66	1.02	1.44	0.12	0.77	0.14	0.03	0.00	0.20	0.96	0.66	0.33	0.01	0	0	0	0	1
8073	ILMN_179631	MMP9	matrix metallo	20	1.179	0.000	0.000	-0.15	-0.12	0.15	0.00	-0.20	0.21	0.32	0.21	1.00	0.10	0.32	0.78	0.72	1.00	0.15	0	0	0	0	0
8087	ILMN_224798	MOCS1	molybdenum c	6	1.465	0.000	0.000	-0.01	0.07	0.23	0.10	-0.11	0.94	0.49	0.02	0.30	0.24	0.96	0.88	0.33	0.70	0.33	0	0	0	0	0
8110	ILMN_178136	MPHOSPH6	M-phase phosf	16	1.496	0.000	0.000	-0.32	0.07	-0.04	-0.08	-0.26	0.02	0.60	0.78	0.58	0.07	0.06	0.92	0.97	0.86	0.11	0	0	0	0	0
8118	ILMN_177651	MPPE1	metallophosph	18	-1.257	0.000	0.000	-0.30	-0.15	-0.15	-0.12	-0.42	0.01	0.16	0.16	0.26	0.00	0.02	0.60	0.68	0.67	0.00	0	0	0	0	0
8123	ILMN_175293	MPZL2	myelin protein	11	1.158	0.000	0.000	-0.35	-0.23	-0.23	-0.44	-0.41	0.04	0.17	0.17	0.01	0.01	0.08	0.62	0.70	0.23	0.03	0	0	0	0	0
8284	ILMN_168666	MT2A	metallothioneir	16	1.267	0.000	0.000	3.24	-0.97	1.35	2.20	3.56	0.00	0.02	0.00	0.00	0.00	0.00	0.23	0.13	0.00	0.00	1	0	0	1	1
8315	ILMN_176929	MTRR11	myotubularin r	1	-1.085	0.000	0.000	0.67	-0.22	0.01	0.07	0.70	0.00	0.11	0.96	0.63	0.00	0.00	0.52	1.00	0.88	0.00	0	0	0	0	0
8349	ILMN_237191	MUC1	mucin 1, cell si	1	-1.665	0.000	0.000	1.33	0.13	0.08	0.40	1.54	0.00	0.65	0.79	0.15	0.00	0.00	0.93	0.97	0.56	0.00	1	0	0	0	1
8350	ILMN_175699	MUC1	mucin 1, cell si	1	-2.241	0.000	0.000	1.69	0.07	0.00	0.47	1.91	0.00	0.84	1.00	0.17	0.00	0.00	0.98	1.00	0.58	0.00	1	0	0	0	1
8352	ILMN_181097	MUC1L	mucin-like 1 (I	12	-1.304	0.000	0.000	2.31	0.17	0.11	0.21	2.48	0.00	0.61	0.74	0.53	0.00	0.00	0.92	0.96	0.83	0.00	1	0	0	0	1
8365	ILMN_166235	MX1	mxvovirus (infl	21	2.417	0.000	0.000	4.25	-0.24	-0.19	2.84	4.80	0.00	0.57	0.65	0.00	0.00	0.00	0.90	0.94	0.00	0.00	1	0	0	1	1
8366	ILMN_223192	MX2	mxvovirus (infl	21	1.728	0.000	0.000	3.85	-0.01	-0.34	2.15	4.68	0.00	0.98	0.44	0.00	0.00	0.00	1.00	0.87	0.00	0.00	1	0	0	1	1
8367	ILMN_221467	MXD1	MAX dimerizati	2	1.101	0.000	0.000	0.37	0.07	-0.01	-0.03	0.44	0.08	0.75	0.98	0.87	0.04	0.14	0.96	1.00	0.97	0.07	0	0	0	0	0
8370	ILMN_235057	MYADM	myeloid-associ	19	-1.067	0.000	0.000	-1.17	-0.44	-0.04	-0.25	-1.23	0.00	0.13	0.88	0.39	0.00	0.00	0.56	0.98	0.75	0.00	-1	0	0	0	-1
8371	ILMN_230884	MYADM	myeloid-associ	19	-1.497	0.000	0.000	-1.52	-0.50	-0.04	-0.59	-1.79	0.00	0.16	0.91	0.10	0.00	0.00	0.61	0.99	0.49	0.00	-1	0	0	0	-1
8379	ILMN_173852	MYD88	myeloid differe	3	1.011	0.000	0.000	0.67	-0.56	-0.07	0.25	0.92	0.00	0.00	0.65	0.11	0.00	0.00	0.03	0.94	0.52	0.00	0	0	0	0	0
8382	ILMN_166008	MYH11	myosin, heavy	16	-1.478	0.000	0.000	3.41	-0.06	0.92	1.40	3.99	0.00	0.92	0.12	0.02	0.00	0.00	0.99	0.61	0.30	0.00	1	0	0	0	1
8392	ILMN_167506	MYL9	myosin, light c	20	-1.818	0.000	0.000	-0.11	0.36	0.10	0.18	-0.16	0.65	0.14	0.68	0.46	0.52	0.74	0.57	0.95	0.79	0.61	0	0	0	0	0
8407	ILMN_169822	MYOSA	myosin VA (he	15	1.135	0.000	0.000	-0.03	-0.01	-0.02	-0.06	-0.05	0.79	0.92	0.88	0.60	0.70	0.85	0.99	0.98	0.87	0.77	0	0	0	0	0
8411	ILMN_168034	MYOM1	myomesin 1, I	18	-1.356	0.000	0.000	-0.13	0.24	-0.07	-0.11	-0.16	0.35	0.09	0.62	0.41	0.24	0.46	0.47	0.94	0.77	0.33	0	0	0	0	0
8444	ILMN_165387	NAMPT	nicotinamide p	7	1.783	0.000	0.000	1.50	-0.54	0.23	0.61	1.71	0.00	0.14	0.52	0.09	0.00	0.50	0.57	0.90	0.48	0.00	1	0	0	0	1
8459	ILMN_210941	NAPSB	napsin B aspar	19	1.103	0.000	0.000	0.86	0.14	-0.05	0.18	1.05	0.00	0.60	0.85	0.50	0.00	0.01	0.92	0.98	0.81	0.00	0	0	0	0	1
8484	ILMN_178959	NBL1	neuroblastoma	1	-1.178	0.000	0.000	-0.35	0.06	0.26	-0.04	-0.29	0.06	0.74	0.17	0.84	0.13	0.12	0.96	0.69	0.96	0.19	0	0	0	0	0
8502	ILMN_175144	NCAPG	non-SMC cond	4	1.217	0.000	0.000	-0.29	-0.44	0.11	-0.36	-0.43	0.18	0.05	0.59	0.09	0.05	0.28	0.34	0.93	0.49	0.08	0	0	0	0	0
8609	ILMN_173814	NES	nestin (NES), r	1	1.029	0.002	0.000	-0.43	-0.29	0.23	0.19	-0.69	0.12	0.30	0.40	0.50	0.01	0.20	0.76	0.85	0.81	0.03	0	0	0	0	0
8611	ILMN_176084	NETO2	neuropilin (NRI	16	1.103	0.000	0.000	-0.19	0.34	0.21	0.17	-0.12	0.23	0.03	0.17	0.28	0.46	0.34	0.28	0.70	0.68	0.56	0	0	0	0	0
8630	ILMN_204976	NFE2L3	nuclear factor	7	1.043	0.000	0.000	1.84	0.40	0.85	0.85	2.23	0.00	0.16	0.00	0.00	0.00	0.00	0.60	0.17	0.16	0.00	1	0	0	0	1
8711	ILMN_172376	NLRX1	NLR family me	11	1.339	0.000	0.000	-0.31	-0.08	-0.17	-0.33	-0.45	0.01	0.49	0.13	0.00	0.00	0.02	0.88	0.64	0.16	0.00	0	0	0	0	0
8712	ILMN_169875	NLRX1	NLR family me	11	1.203	0.000	0.000	-0.15	0.06	-0.05	-0.11	-0.19	0.04	0.44	0.52	0.12	0.01	0.08	0.85	0.90	0.53	0.02	0	0	0	0	0
8745	ILMN_176259	NOD2	nucleotide-binc	16	1.441	0.000	0.000	1.29	-0.40	-0.19	-0.23	1.45	0.00	0.30	0.62	0.55	0.00	0.01	0.77	0.94	0.84	0.00	1	0	0	0	1
8780	ILMN_178718	NOV	nephroblastom	8	-1.328	0.000	0.000	-0.65	-0.27	-0.42	-0.49	-0.81	0.00	0.08	0.01	0.00	0.00	0.45	0.25	0.13	0.00	0	0	0	0	0	
8782	ILMN_217217	NP	nucleoside pho	14	1.841	0.000	0.000	0.09	0.12	0.07	0.18	0.11	0.67	0.59	0.75	0.41	0.62	0.76	0.91	0.96	0.77	0.70	0	0	0	0	0
8798	ILMN_211025	NPM3	nucleophosmin	10	1.047	0.000	0.000	-1.08	0.09	-0.08	-0.40	-1.40	0.00	0.53	0.59	0.01	0.00	0.00	0.89	0.92	0.21	0.00	-1	0	0	0	-1
8864	ILMN_176973	NT5C3	5'-nucleotidase	7	1.078	0.000	0.000	2.54	0.10	-0.03	0.76	3.58	0.00	0.82	0.95	0.09	0.00	0.00	0.97	0.99	0.48	0.00					

Table S2.xls

9389	ILMN_167354	PGM2	phosphoglucon	4	1.171	0.000	0.000	-0.45	0.10	0.14	-0.06	-0.30	0.00	0.51	0.34	0.70	0.04	0.01	0.88	0.82	0.91	0.08	0	0	0	0	0
9393	ILMN_178138	PGM5	phosphoglucon	9	-1.585	0.000	0.000	-0.53	-0.26	-0.40	-0.37	-0.55	0.00	0.09	0.01	0.02	0.00	0.00	0.48	0.27	0.28	0.00	0	0	0	0	0
9394	ILMN_170959	PGM5	phosphoglucon	9	-1.638	0.000	0.000	-0.52	-0.25	-0.34	-0.46	-0.61	0.00	0.14	0.05	0.01	0.00	0.01	0.58	0.46	0.22	0.00	0	0	0	0	0
9461	ILMN_177307	PHYH	phytanoyl-CoA	10	-1.210	0.000	0.000	-1.01	0.10	0.37	-0.52	-1.23	0.00	0.48	0.02	0.00	0.00	0.00	0.87	0.31	0.08	0.00	-1	0	0	0	-1
9557	ILMN_233902	PKD1	polycystic kidn	16	-1.093	0.000	0.000	-0.03	-0.01	0.09	0.04	-0.06	0.80	0.91	0.47	0.76	0.63	0.85	0.99	0.88	0.93	0.72	0	0	0	0	0
9578	ILMN_169762	PLA2G4B	phospholipase	15	1.361	0.000	0.000	1.37	-0.11	0.20	0.22	1.50	0.00	0.67	0.46	0.41	0.00	0.00	0.94	0.88	0.77	0.00	1	0	0	0	1
9588	ILMN_165605	PLAU	plasminogen a	10	1.020	0.000	0.000	-1.33	-0.34	-0.20	-0.80	-1.75	0.00	0.26	0.52	0.01	0.00	0.00	0.73	0.90	0.25	0.00	-1	0	0	0	-1
9594	ILMN_176939	PLCD1	phospholipase	3	1.063	0.000	0.000	-0.08	-0.13	0.51	0.24	0.01	0.51	0.31	0.00	0.06	0.96	0.62	0.77	0.04	0.41	0.97	0	0	0	0	0
9597	ILMN_206156	PLCH2	phospholipase	1	-1.372	0.000	0.000	-0.06	0.09	-0.10	-0.10	-0.07	0.52	0.31	0.26	0.28	0.42	0.63	0.78	0.76	0.68	0.52	0	0	0	0	0
9600	ILMN_174745	PLCXD1	phosphatidylin X	1	1.208	0.000	0.000	-1.21	0.01	-0.41	-0.61	-1.58	0.00	0.97	0.13	0.02	0.00	0.00	1.00	0.63	0.31	0.00	-1	0	0	0	-1
9607	ILMN_179576	PLEK	pleckstrin (PLE	2	1.249	0.011	0.000	0.38	0.19	0.41	0.11	0.27	0.04	0.29	0.02	0.53	0.13	0.08	0.75	0.36	0.83	0.20	0	0	0	0	0
9685	ILMN_166258	PNPLA7	patatin-like ph	9	-1.549	0.000	0.000	-0.88	0.01	-0.29	-0.57	-1.34	0.00	0.98	0.27	0.03	0.00	0.01	1.00	0.77	0.34	0.00	0	0	0	0	-1
9779	ILMN_167428	PPAD	peroxisome pri	6	1.279	0.000	0.000	-0.46	-0.41	0.06	0.05	-0.34	0.00	0.01	0.67	0.72	0.02	0.01	0.11	0.95	0.91	0.04	0	0	0	0	0
9781	ILMN_180022	PPARG	peroxisome pri	3	-1.423	0.000	0.000	-2.35	1.46	-0.51	-0.84	-3.01	0.00	0.00	0.18	0.03	0.00	0.00	0.01	0.70	0.33	0.00	-1	1	0	0	-1
9836	ILMN_176196	PPP1R14A	protein phosph	19	-1.390	0.000	0.000	-0.43	0.74	-0.01	-0.16	-0.37	0.00	0.00	0.96	0.17	0.00	0.00	1.00	0.58	0.01	0.00	0	0	0	0	0
9859	ILMN_166073	PPP2R2B	protein phosph	5	-1.015	0.000	0.000	-0.13	-0.10	0.00	-0.11	-0.15	0.11	0.26	0.97	0.19	0.09	0.20	0.73	1.00	0.59	0.14	0	0	0	0	0
9902	ILMN_165507	PRDM1	PR domain con	6	1.481	0.000	0.000	0.99	-0.13	0.60	0.69	1.24	0.00	0.66	0.04	0.02	0.00	0.00	0.94	0.44	0.30	0.00	0	0	0	0	1
9928	ILMN_178750	PRIC285	peroxisomal pr	20	1.884	0.000	0.000	4.49	0.07	0.10	2.14	5.15	0.00	0.88	0.82	0.00	0.00	0.00	0.99	0.98	0.01	0.00	1	0	0	1	1
9950	ILMN_180690	PRKCB1	protein kinase	16	-1.028	0.000	0.000	-0.85	-0.40	-0.30	-0.49	-1.26	0.00	0.09	0.19	0.04	0.00	0.00	0.47	0.71	0.36	0.00	0	0	0	0	-1
10019	ILMN_166180	PRRG4	proline rich Gl	11	1.083	0.000	0.000	0.68	0.18	-0.17	0.14	0.78	0.00	0.23	0.25	0.36	0.00	0.00	0.70	0.75	0.74	0.00	0	0	0	0	0
10098	ILMN_178661	PSME2	proteasome (p	14	1.084	0.000	0.000	1.69	0.18	0.76	1.09	1.98	0.00	0.25	0.00	0.00	0.00	0.00	0.72	0.01	0.00	0.00	1	0	0	1	1
10194	ILMN_175755	PTRF	polymerase I a	17	-1.010	0.000	0.000	0.85	0.83	0.08	0.19	0.80	0.02	0.02	0.81	0.59	0.03	0.05	0.24	0.98	0.86	0.06	0	0	0	0	0
10199	ILMN_175319	PTTG1	pituitary tumor	5	1.468	0.000	0.000	0.30	-0.31	0.29	0.21	0.38	0.04	0.04	0.05	0.16	0.01	0.09	0.30	0.47	0.57	0.03	0	0	0	0	0
10200	ILMN_204277	PTTG1	pituitary tumor	5	1.150	0.000	0.000	0.41	-0.44	0.37	0.11	0.39	0.00	0.00	0.01	0.40	0.01	0.01	0.05	0.25	0.76	0.01	0	0	0	0	0
10204	ILMN_204902	PTTG3	pituitary tumor	8	1.441	0.000	0.000	0.35	-0.32	0.38	0.24	0.40	0.01	0.01	0.00	0.05	0.00	0.02	0.16	0.17	0.40	0.01	0	0	0	0	0
10253	ILMN_241128	QSOX1	quiescin Q6 su	1	1.081	0.000	0.000	0.94	1.38	0.60	0.40	1.04	0.00	0.00	0.00	0.05	0.00	0.00	0.17	0.39	0.00	0	1	0	0	0	1
10295	ILMN_166069	RAB31	RAB31, membr	18	1.003	0.000	0.000	0.03	0.24	-0.04	-0.12	-0.12	0.77	0.04	0.76	0.29	0.29	0.84	0.32	0.96	0.69	0.38	0	0	0	0	0
10302	ILMN_213497	RAB38	RAB38, membr	11	1.162	0.000	0.000	-0.99	0.51	-0.55	-0.45	-1.09	0.00	0.03	0.72	0.04	0.00	0.00	0.24	0.32	0.38	0.00	0	0	0	0	-1
10348	ILMN_170979	RAC2	ras-related C3	22	1.097	0.001	0.000	-0.24	-0.03	0.27	-0.04	-0.50	0.37	0.92	0.32	0.87	0.07	0.48	0.99	0.80	0.97	0.11	0	0	0	0	0
10372	ILMN_168213	RAI14	retinoic acid in	5	-1.270	0.000	0.000	-0.10	-0.19	0.31	0.10	-0.16	0.69	0.46	0.23	0.71	0.55	0.77	0.86	0.74	0.91	0.64	0	0	0	0	0
10384	ILMN_172145	RANBP1	RAN binding pr	22	1.136	0.000	0.000	-0.46	0.10	-0.08	-0.14	-0.45	0.01	0.55	0.63	0.40	0.01	0.02	0.90	0.94	0.76	0.02	0	0	0	0	0
10507	ILMN_180823	RBPM52	RNA binding pr	15	-1.051	0.000	0.000	-0.29	-0.05	0.23	0.07	-0.27	0.04	0.71	0.11	0.61	0.06	0.09	0.95	0.61	0.87	0.11	0	0	0	0	0
10540	ILMN_206726	RECK	reversion-indu	9	-1.081	0.000	0.000	0.13	-0.26	-0.10	-0.15	0.29	0.32	0.05	0.45	0.24	0.03	0.44	0.36	0.87	0.65	0.05	0	0	0	0	0
10605	ILMN_165601	RG51	regulator of G-	1	1.207	0.000	0.000	-0.33	-0.50	0.60	0.39	0.09	0.30	0.12	0.06	0.22	0.78	0.41	0.55	0.50	0.63	0.84	0	0	0	0	0
10614	ILMN_173855	RG520	regulator of G-	8	1.711	0.000	0.000	-0.02	-0.18	0.28	0.29	0.01	0.95	0.52	0.33	0.31	0.96	0.96	0.89	0.81	0.70	0.97	0	0	0	0	0
10627	ILMN_180220	RHOB	ras homolog g	2	-1.119	0.000	0.000	-0.15	-0.04	-0.01	-0.21	-0.12	0.23	0.74	0.93	0.08	0.31	0.33	0.96	0.99	0.47	0.40	0	0	0	0	0
10629	ILMN_174494	RHOBTB3	Rho-related BT	5	-1.545	0.000	0.000	0.21	0.21	0.12	0.05	0.04	0.18	0.19	0.43	0.74	0.79	0.28	0.66	0.86	0.92	0.84	0	0	0	0	0
10658	ILMN_240413	RIOK3	RIO kinase 3 (18	1.004	0.000	0.000	0.45	0.03	0.13	0.16	0.60	0.00	0.81	0.26	0.17	0.00	0.00	0.97	0.76	0.58	0.00	0	0	0	0	0
10678	ILMN_177660	RNASE4	ribonuclease 4	14	-1.729	0.000	0.000	0.23	-0.64	-0.64	-0.60	0.26	0.38	0.02	0.02	0.03	0.32	0.50	0.20	0.33	0.32	0.41	0	0	0	0	0
10691	ILMN_181078	RNF11	ring finger pro	1	1.201	0.000	0.000	0.30	-0.01	0.13	0.02	0.49	0.01	0.96	0.24	0.84	0.00	0.03	1.00	0.74	0.95	0.00	0	0	0	0	0
10826	ILMN_177105	RPL29	ribosomal prot	3	1.967	0.000	0.000	-0.72	0.11	-0.17	-0.07	-0.66	0.00	0.54	0.33	0.68	0.00	0.00	0.89	0.81	0.90	0.00	0	0	0	0	0
10827	ILMN_173751	RPL29	ribosomal prot	3	2.135	0.000	0.000	-0.66	0.08	-0.04	-0.02	-0.58	0.00	0.65	0.84	0.89	0.00	0.00	0.94	0.98	0.97	0.01	0	0	0	0	0
10837	ILMN_177482	RPL34	ribosomal prot	4	1.445	0.000	0.000	-0.17	0.22	0.05	0.19	0.05	0.33	0.21	0.77	0.26	0.76	0.44	0.67	0.96	0.66	0.82	0	0	0	0	0
10856	ILMN_171749	RPL6	ribosomal prot	12	1.535	0.000	0.000	-0.26	0.05	-0.08	0.12	-0.17	0.09	0.74	0.61	0.42	0.26	0.16	0.96	0.93	0.77	0.36	0	0	0	0	0
10888	ILMN_221913	RPS15	ribosomal prot	19	1.249	0.000	0.000	-0.45	0.03	-0.14	-0.06	-0.42	0.00	0.79	0.21	0.60	0.00	0.00	0.97	0.72	0.87	0.00	0	0	0	0	0
10902	ILMN_239989	RPS24	ribosomal prot	10	1.505	0.000	0.000	-0.23	0.07	0.17	0.24	-0.21	0.13	0.63	0.25	0.11	0.17	0.21	0.93	0.75	0.51	0.25	0	0	0	0	0
10948	ILMN_207007	RPS7	ribosomal prot	2	1.194	0.000	0.000	-0.49	0.24	0.02	0.06	-0.32	0.00	0.11	0.89	0.69	0.04	0.01	0.53	0.98	0.90	0.07	0	0	0	0	0
10949	ILMN_175072	RPS7	ribosomal prot	2	1.452	0.000	0.000	-0.46	0.34	-0.04	0.11	-0.34	0.01	0.04	0.83	0.51	0.05	0.02	0.33	0.98	0.82	0.08	0	0	0	0	0
10981	ILMN_165787	RSAD2	radical S-adeni	2	1.230	0.000	0.000	4.65	-0.26	-0.03	2.44	5.75	0.00	0.64	0.96	0.00	0.00	0.00	0.93	1.00	0.02	0.00	1	0	0	1	1
11043	ILMN_174891	S100A12	S100 calcium t	1	4.228	0.000	0.000	1.07	-0.20	0.04	0.29	1.19	0.00	0.42	0.88	0.24	0.00	0.00	0.84	0.98							

Table S2.xls

11698	ILMN_168385	SLC7A1	solute carrier f	13	1.171	0.000	0.000	-1.22	0.18	0.22	-0.18	-1.45	0.00	0.44	0.33	0.42	0.00	0.00	0.85	0.81	0.78	0.00	-1	0	0	0	-1
11700	ILMN_172037	SLC7A5	solute carrier f	16	1.649	0.000	0.000	0.20	0.30	0.38	0.36	0.50	0.57	0.38	0.27	0.30	0.16	0.67	0.82	0.77	0.69	0.23	0	0	0	0	0
11727	ILMN_219976	SLITRK4	SLIT and NTRK X	8	-1.036	0.000	0.000	0.46	-0.39	0.29	0.18	0.40	0.01	0.03	0.11	0.32	0.03	0.03	0.28	0.59	0.71	0.06	0	0	0	0	0
11778	ILMN_177538	SMOX	spermine oxid	20	1.747	0.000	0.000	0.04	0.32	0.12	0.15	0.04	0.85	0.14	0.56	0.48	0.85	0.89	0.57	0.92	0.80	0.89	0	0	0	0	0
11779	ILMN_236725	SMOX	spermine oxid	20	1.717	0.000	0.000	0.16	0.42	0.23	0.17	0.19	0.46	0.06	0.30	0.44	0.39	0.58	0.40	0.79	0.78	0.49	0	0	0	0	0
11807	ILMN_170193	SNCA	synuclein, alph	4	-1.109	0.000	0.000	-0.77	-0.56	-0.04	-0.52	-1.10	0.00	0.03	0.89	0.05	0.00	0.01	0.28	0.98	0.39	0.00	0	0	0	0	-1
11855	ILMN_179341	SNTB1	syntrophin, bel	8	-1.016	0.000	0.000	-0.44	-0.77	-0.05	-0.29	-0.70	0.03	0.00	0.80	0.15	0.00	0.07	0.01	0.97	0.56	0.00	0	0	0	0	0
11901	ILMN_240650	SOD2	superoxide dis	6	1.911	0.000	0.000	2.00	-1.20	1.22	1.41	2.47	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.13	0.06	0.00	1	-1	0	1	1
11902	ILMN_233678	SOD2	superoxide dis	6	2.296	0.000	0.000	1.26	-1.04	0.96	1.07	1.46	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.06	0.02	0.00	1	-1	0	1	1
11912	ILMN_174979	SORBS1	sorbin and SH	10	-2.276	0.000	0.000	-0.31	-0.22	0.25	0.08	-0.35	0.09	0.23	0.18	0.65	0.06	0.17	0.70	0.71	0.89	0.10	0	0	0	0	0
11975	ILMN_168925	SPG3A	spastic paraple	14	-1.045	0.000	0.000	-0.22	0.15	0.03	0.11	-0.24	0.18	0.35	0.84	0.50	0.14	0.28	0.80	0.98	0.81	0.21	0	0	0	0	0
11976	ILMN_238147	SPG3A	spastic paraple	14	-1.021	0.000	0.000	-0.29	0.13	-0.02	0.08	-0.30	0.10	0.44	0.89	0.65	0.09	0.18	0.85	0.98	0.89	0.14	0	0	0	0	0
11995	ILMN_165628	SPOCK2	sparc/osteonec	10	1.091	0.001	0.000	0.18	0.14	0.11	0.25	0.56	0.38	0.49	0.58	0.22	0.01	0.50	0.88	0.92	0.63	0.02	0	0	0	0	0
12023	ILMN_177224	SQLE	squalene epoxi	8	1.067	0.000	0.000	0.02	-0.15	0.34	0.05	0.04	0.88	0.27	0.02	0.70	0.80	0.92	0.74	0.33	0.91	0.85	0	0	0	0	0
12024	ILMN_166719	SQRDL	sulfide quinone	15	1.119	0.000	0.000	0.72	-0.24	0.35	0.39	0.76	0.00	0.06	0.01	0.00	0.00	0.00	0.38	0.25	0.15	0.00	0	0	0	0	0
12042	ILMN_176034	SRGN	serglycin (SRG	10	1.040	0.045	0.000	0.90	0.31	0.46	0.52	1.27	0.00	0.08	0.01	0.00	0.00	0.00	0.45	0.27	0.18	0.00	0	0	0	0	1
12067	ILMN_180482	SRXN1	sulfiredoxin 1 l	20	1.026	0.000	0.000	-0.70	0.43	0.44	0.18	-0.69	0.03	0.17	0.16	0.57	0.03	0.07	0.63	0.68	0.86	0.06	0	0	0	0	0
12084	ILMN_177548	SSPN	sarcospan (Krs	12	-1.337	0.000	0.000	0.50	-0.29	0.32	0.28	0.49	0.00	0.09	0.06	0.09	0.01	0.01	0.48	0.49	0.48	0.01	0	0	0	0	0
12149	ILMN_169010	STAT1	signal transduc	2	1.906	0.000	0.000	3.09	0.13	0.41	1.46	3.22	0.00	0.56	0.06	0.00	0.00	0.00	0.90	0.49	0.00	0.00	1	0	0	1	1
12150	ILMN_169136	STAT1	signal transduc	2	1.611	0.000	0.000	2.81	0.08	0.41	1.38	2.81	0.00	0.69	0.06	0.00	0.00	0.00	0.95	0.49	0.00	0.00	1	0	0	1	1
12151	ILMN_177732	STAT1	signal transduc	2	1.048	0.000	0.000	2.04	0.08	0.16	0.93	1.95	0.00	0.62	0.33	0.00	0.00	0.00	0.92	0.81	0.00	0.00	1	0	0	0	1
12153	ILMN_241098	STAT3	signal transduc	17	1.105	0.000	0.000	0.54	-0.07	0.14	0.28	0.86	0.00	0.58	0.30	0.04	0.00	0.00	0.91	0.79	0.37	0.00	0	0	0	0	0
12154	ILMN_166361	STAT3	signal transduc	17	1.128	0.000	0.000	0.52	-0.06	0.04	0.19	0.82	0.00	0.66	0.80	0.18	0.00	0.00	0.94	0.97	0.59	0.00	0	0	0	0	0
12295	ILMN_172774	SYNCRIP	synaptotagmin	6	1.164	0.000	0.000	-0.09	0.09	0.14	0.13	-0.09	0.36	0.37	0.16	0.19	0.36	0.47	0.82	0.68	0.59	0.46	0	0	0	0	0
12352	ILMN_177866	TAGLN	transgelin (TAC	11	-1.346	0.000	0.000	0.59	0.37	-0.34	-0.08	0.68	0.00	0.06	0.08	0.68	0.00	0.01	0.39	0.54	0.90	0.00	0	0	0	0	0
12353	ILMN_240093	TAGLN	transgelin (TAC	11	-1.869	0.000	0.000	0.01	-0.01	-0.05	-0.02	0.19	0.95	0.94	0.72	0.88	0.21	0.97	0.99	0.96	0.97	0.29	0	0	0	0	0
12536	ILMN_180517	TGFA	transforming q	2	1.205	0.000	0.000	0.43	1.52	-0.09	0.04	0.78	0.09	0.00	0.70	0.86	0.00	0.16	0.00	0.95	0.96	0.01	0	1	0	0	0
12537	ILMN_208394	TGFA	transforming q	2	1.312	0.000	0.000	0.49	1.64	-0.28	0.01	0.80	0.06	0.00	0.28	0.95	0.00	0.12	0.00	0.78	0.99	0.01	0	1	0	0	0
12542	ILMN_178428	TGFBR3	transforming g	1	-1.382	0.000	0.000	0.19	0.21	0.08	0.01	0.18	0.11	0.07	0.49	0.95	0.13	0.19	0.41	0.89	0.99	0.20	0	0	0	0	0
12625	ILMN_170146	TIMP3	TIMP metallopr	22	-1.702	0.000	0.000	-0.99	-0.03	-0.23	-0.32	-1.31	0.02	0.94	0.57	0.43	0.00	0.05	0.99	0.92	0.78	0.01	0	0	0	0	-1
12639	ILMN_180603	TK1	thymidine kinase 1, s	15	1.193	0.000	0.000	-0.31	-0.58	0.00	-0.37	-0.52	0.16	0.01	0.99	0.10	0.02	0.25	1.00	1.00	0.49	0.04	0	0	0	0	0
12643	ILMN_223441	TLE3	transducin-like	15	1.225	0.000	0.000	-0.82	-0.53	-0.43	-0.33	-0.93	0.00	0.00	0.01	0.05	0.00	0.00	0.04	0.27	0.39	0.00	0	0	0	0	0
12716	ILMN_205287	TMEM116	transmembran	12	-1.141	0.000	0.000	0.07	0.17	0.23	0.17	0.00	0.40	0.05	0.01	0.05	0.97	0.52	0.36	0.25	0.40	0.98	0	0	0	0	0
12756	ILMN_177393	TMEM165	transmembran	4	1.193	0.000	0.000	0.33	0.04	0.28	0.16	0.46	0.02	0.76	0.05	0.27	0.00	0.05	0.96	0.47	0.67	0.01	0	0	0	0	0
12817	ILMN_177112	TMEM45B	transmembran	11	1.814	0.000	0.000	-0.55	0.57	-0.14	-0.10	-0.45	0.00	0.00	0.37	0.52	0.00	0.00	0.02	0.83	0.82	0.01	0	0	0	0	0
12828	ILMN_171883	TMEM57	transmembran	1	1.018	0.000	0.000	0.27	0.05	0.01	0.03	0.27	0.01	0.61	0.93	0.78	0.01	0.03	0.92	0.99	0.94	0.03	0	0	0	0	0
12852	ILMN_221106	TMEM91	transmembrane prote	1	-1.102	0.000	0.000	-1.08	0.51	-0.35	-0.34	-1.39	0.00	0.07	0.21	0.22	0.00	0.00	0.41	0.72	0.63	0.00	-1	0	0	0	-1
12858	ILMN_175817	TMEM99	transmembran	17	-1.573	0.000	0.000	-0.87	-0.11	-0.25	-0.25	-1.10	0.00	0.48	0.13	0.12	0.00	0.00	0.87	0.65	0.53	0.00	0	0	0	0	-1
12900	ILMN_169969	TNFRSF21	tumor necrosis	6	1.241	0.000	0.000	-1.29	0.04	-0.10	-0.25	-1.64	0.00	0.90	0.78	0.47	0.00	0.00	0.99	0.97	0.80	0.00	-1	0	0	0	-1
12904	ILMN_233123	TNFRSF6B	tumor necrosis	20	1.164	0.000	0.000	0.66	0.48	0.17	0.33	0.83	0.01	0.05	0.48	0.18	0.00	0.02	0.36	0.89	0.59	0.00	0	0	0	0	0
12923	ILMN_170759	TNIP3	TNFAIP3 intera	4	1.604	0.000	0.000	1.62	0.06	0.65	1.08	2.14	0.00	0.90	0.17	0.03	0.00	0.01	0.99	0.70	0.32	0.00	1	0	0	0	1
12957	ILMN_168609	TOP2A	topoisomerase	17	1.057	0.000	0.000	-0.18	-0.49	0.18	-0.40	-0.50	0.51	0.08	0.52	0.15	0.07	0.62	0.45	0.90	0.56	0.12	0	0	0	0	0
12995	ILMN_171668	TPM1	tropomyosin 1	15	-1.256	0.000	0.000	-0.20	-0.13	-0.13	-0.15	-0.08	0.04	0.18	0.15	0.12	0.40	0.08	0.64	0.67	0.53	0.50	0	0	0	0	0
12996	ILMN_236071	TPM1	tropomyosin 1	15	-1.255	0.000	0.000	-0.28	-0.25	-0.29	-0.29	-0.27	0.03	0.06	0.02	0.03	0.04	0.07	0.38	0.37	0.32	0.07	0	0	0	0	0
12997	ILMN_178919	TPM2	tropomyosin 2	9	-1.770	0.000	0.000	-0.73	0.10	-0.46	-0.61	-1.10	0.00	0.66	0.05	0.01	0.00	0.01	0.94	0.47	0.26	0.00	0	0	0	0	-1
12998	ILMN_175760	TPM2	tropomyosin 2	9	-1.925	0.000	0.000	-0.65	0.14	-0.43	-0.50	-0.95	0.00	0.53	0.05	0.03	0.00	0.01	0.89	0.47	0.32	0.00	0	0	0	0	0
13037	ILMN_178169	TRAK2	trafficking prot	2	-1.023	0.000	0.000	-0.58	-0.23	0.04	-0.23	-0.80	0.00	0.08	0.74	0.08	0.00	0.00	0.45	0.96	0.47	0.00	0	0	0	0	0
13068	ILMN_174507	TRIM2	tripartite motif	4	-1.067	0.000	0.000	-0.18	-0.48	0.32	-0.13	-0.26	0.20	0.00	0.03	0.35	0.08	0.31	0.04	0.38	0.73	0.13	0	0	0	0	0
13070	ILMN_177925	TRIM22	tripartite motif	11	1.604	0.000	0.000	1.72	0.10	0.01	0.77	2.32	0.00	0.67	0.98	0.00	0.00	0.00	0.94	1.00	1.03	0.00	1	0	0	0	1
13151	ILMN_178756	TSC22D1	TSC22 domain	13	-1.016	0.001	0.000	0.33	-0.89	0.93	0.64	0.58	0.28	0.00	0.00	0.04	0.06										

Table S2.xls

14314	ILMN_236649	ZNF706	zinc finger pro	8	-1.069	0.000	0.000	-0.45	-0.09	0.13	-0.12	-0.66	0.00	0.43	0.26	0.31	0.00	0.00	0.85	0.76	0.70	0.00	0	0	0	0	0
14315	ILMN_170238	ZNF706	zinc finger pro	8	-1.049	0.000	0.000	-0.50	-0.15	-0.01	-0.23	-0.71	0.00	0.24	0.95	0.09	0.00	0.00	0.71	0.99	0.47	0.00	0	0	0	0	0
14351	ILMN_180205	ZNF91	zinc finger pro	19	-1.178	0.000	0.000	-0.04	0.04	0.01	-0.02	-0.08	0.79	0.82	0.93	0.87	0.63	0.85	0.97	0.99	0.97	0.71	0	0	0	0	0
14369	ILMN_165494	ZSCAN18	zinc finger and	19	-1.622	0.000	0.000	-0.28	0.04	-0.01	-0.19	-0.25	0.04	0.75	0.95	0.17	0.08	0.09	0.96	0.99	0.58	0.13	0	0	0	0	0

Table S4. Gene Set Enrichment Analysis (GSEA) of cytokine-treated macrophage pathways in psoriasis compared to control

PATHWAY	No of Genes	ES^a	NES^b	FDR
LPS- UP	70	0.84	2.77	0.000
IFN γ - UP	478	0.63	2.49	0.000
LPS & IFN γ - UP	630	0.57	2.31	0.000
TNF α - UP	29	0.59	1.64	0.003
IL4- DOWN	23	0.58	1.49	0.013
IL4- UP	105	0.28	0.97	0.549
LPS & IFN γ DOWN	519	-0.35	-1.68	0.009
IFN γ DOWN	297	-0.32	-1.43	0.037

^aES, enrichment score

^bNES, normalized enrichment score

Connectivity Score

We quantified the relationship between the UP and DOWN genes by calculating the connectivity score (CS) (Lamb *et al.*, 2006). The CS was determined for the IFN γ , LPS+IFN γ and IL-4 pathways, by subtracting the enrichment score (ES) for UP and DOWN genes for each pathway. A CS near 1 would indicate perfect agreement between a pathway and our psoriasis gene set, whereas 0 would indicate no agreement, and -1 a negative correlation. The highest CS was for IFN γ (0.63- [-0.32] =0.95), next was LPS+IFN γ (0.57- [-0.35] =0.92), and the IL-4 CS was lowest (0.58-0.28=0.3). TNF-DOWN and LPS-DOWN pathways did not have sufficient genes to generate a CS. Overall, this analysis showed that there was a significant over-expression of IFN γ - and LPS-induced “M1” macrophage genes in psoriasis, with little “M2” signature.

Table S5. Upregulated and downregulated genes in IL-4 and TNF-treated macrophages in common with Psoriasis

Upregulated genes in IL-4 treated macrophages common with Psoriasis		
Gene Symbol	Description	FCH
DCUN1DS	DCN1,defective in cullin neddylation 1, domain containing 3	3.32
TGFA	Transforming growth factor, alpha	3.12
DNASEIL3	Deoxyribonuclease I-like 3	2.70
QSOX1	Quiescin Q6 sulfhydryl oxidase 1	2.60
CTSC	Cathepsin C	2.08
Downregulated genes in IL-4 treated macrophages common with Psoriasis		
FAM134B	Family with sequence similarity 134, member B	0.48
AKR1C3	Aldo-keto reductase family 1, member C3	0.34

Upregulated genes in TNF-α treated macrophages common with Psoriasis		
Gene Symbol	Description	FCH
CCL5	Chemokine (C-C motif) ligand 5	5.91
CCL4L2	Chemokine (C-C motif) ligand 4-Like 2	3.48
CCL4L1	Chemokine (C-C motif) ligand 4-Like 1	3.29
GBP1	Guanylate binding protein 1	2.35

Table S6. Antibodies for Immunohistochemistry and Immunofluorescence

Antigen	Manufacturer	Clone ^a	Iso	Dil	Amplification/ detection ^b
CD163	Acris	5C6-FAT	IgG1	1:100	Goat anti-mouse IgG1-A568
RFD7	Abcam	RFD7	IgG1	1:100	Goat anti-mouse IgG1-A488
LAMP-2/ CD107b (FITC)	eBioscience	EBioH4B4	IgG1	1:50	Goat anti-FITC-A488
CD68	BD Pharmingen	Y1/82A	IgG2b	1:100	Goat anti-mouse IgG2b-A488
STABILIN/ MS1	Gift *	Rabbit polyclonal	IgG	1:100	Goat anti-mouse IgG1-A488
MARCO	Hycult biotechnology	PLK-1	IgG3	1:10	Goat anti-mouse IgG3-A488
CD163-FITC	Acris	5C6-FAT	IgG1	1:100	Goat anti-FITC-A488
Factor XIIIa	Enzyme Research	AP Polyclonal Sheep	Nil	1:100	Donkey anti-sheep-A568
CD11c	BD Pharmingen	B-ly6	IgG1	1:100	Goat anti-mouse IgG1-A568
MMR/CD206	GeneTex	15-2	IgG1	1:100	Goat anti-mouse IgG1-A488
DC-SIGN/ CD209-FITC	BD Pharmingen	DCN46	IgG2b	1:50	Goat anti-FITC-A488
CD86(FITC)	RDI	BU63	IgG1	1:100	Goat anti-FITC-A488
CD40(FITC)	BD Pharmingen	5C3	IgG1	1:100	Goat anti-FITC-A488
DC-LAMP/ CD208-PE	Immunotech	104.G4	IgG1	1:50	Goat anti-mouse IgG1-A568
DEC-205/CD205	R.M. Steinman	MG38	IgG2b	1:100	Goat anti-mouse IgG2b-A568
CD83	Immunotech	HB15a	IgG2b	1:50	Goat anti-FITC-A488
STAT 1	BD Biosciences	1/Stat1	IgG1	1:25	Goat anti-mouse IgG1-A568
CXCL9	R&D	49106.11	IgG1	1:50	Goat anti-mouse IgG1-A568
MxA/Mx1	Santa Cruz	Goat polyclonal D-14	IgG	1:20	Chicken anti-goat-A-594
HLA-DR	BD	L243	IgG2a	1:100	Goat anti-mouse IgG2a-A488
IL23p19	Biolegend	HLT2736	IgG1	1:50	Goat anti-mouse IgG1-A568
IL23p40(FITC)	Biolegend	C11.5	IgG1	1:50	Goat anti-FITC-A488
INOS	Santa Cruz Biotechnology	Rabbit polyclonal N-20	IgG	1:20	Chicken anti-rabbit IgG-A488
TNF- α (FITC)	BD Biosciences	6401.1111	IgG1	1:10	Goat anti-FITC-A488
CD14 (FITC)	BD Biosciences	M phi P9	IgG2b	1:50	Goat anti-FITC-A488
CD16 (FITC)	BD Biosciences	3G8	IgG1	1:50	Goat anti-FITC-A488
CD11a (FITC)	Immunotech	25.3	IgG1	1:50	Goat anti-FITC-A488

^aAll are murine monoclonals unless stated

^bAll amplification/ detection antibodies are from Invitrogen /Molecular Probes unless stated

.