Supplementary Methods

a) Study design

This study was designed as an investigator-initiated clinical study to investigate the molecular signatures of AD and psoriasis. Procedures were conducted according to the Declaration of Helsinki principles. Informed written consent was obtained from human subjects under a protocol approved by the local ethics board at the University Hospital Schleswig-Holstein, Campus Kiel, Germany (reference: A100/12). Adult patients with a history of AD or psoriasis for at least 3 years attending the dermatology department as well as adult volunteers without personal or familial history of atopic and chronic-inflammatory diseases of German ethnicity were invited to participate. Inclusion criteria for patients were a dermatologist-confirmed diagnosis of active chronic plaque-type psoriasis or AD. Exclusion criteria were presence of any other chronic skin disease, systemic treatment with immune-efficient medication ever, and topical treatment within one week prior to material sampling. AD or psoriasis was diagnosed on the basis of a skin examination by experienced dermatologists according to standard criteria (for AD, the American Academy of Dermatology Consensus Criteria were used) (Boehncke and Schon, 2015, Weidinger and Novak, 2015). From all participants, 9 ml of blood (collected into EDTA) as well as 5mm skin punch biopsies from the upper extremities (under local anesthesia) were obtained. From control individuals, a single biopsy was taken, while pairs of biopsies were taken and from adjacent (at least 50 mm from active lesions) clinically normal (i.e. no signs of erythema, edema, crusting, thickening, scaling or scratch marks) skin in psoriatic or AD patients. Skin tissue specimen were stored in PaxGene tissue containers (PreAnalytiX, Hombrechtikon, Switzerland) at -80°C according to the manufacturer's manual until further processing. A detailed cohort description can be found in **Supplementary Table 1**.

b) Filaggrin gene genotyping

Genomic DNA was isolated from peripheral EDTA blood with the automated chemagic Star workstation protocol (Hamilton Company, Reno, NV) and used to determine the *filaggrin* gene (FLG) status of AD patients and healthy controls. The four most common European mutations R501X, 2282del4, R2447X and S3247X were analyzed with the TaqMan allelic discrimination

method (Applied Biosystems, Carlsbad, CA) following the standard procedures based on the manufacturer's reagents. Probe detection was performed with the Applied Biosystems 7900HT Fast Real-Time PCR System. Results are presented in **Supplementary Table 1**.

c) Sample processing

Total RNA was isolated from PAXgene® fixed tissue samples using the AllPrep DNA/RNA Mini Kit (Qiagen, Hilden, Germany) following the manufacturers specifications. Samples of cases and controls were randomly distributed across the plates and pools before sequencing to minimize batch effects; in total we used 3 runs to obtain RNA-seq data. Preceding RNA isolation all samples were disrupted using innuSPEED Lysis Tubes W (1,4 - 1,6 mm steel beads & 3,5 mm ceramic beads) (Analytik Jena, Jena, Germany) in a SpeedMill Plus (3x 1min intervals) (Analytik Jena) together with 600µl of RLT-Plus-Buffer (Qiagen) including ß-Mercaptoethanol and additionally homogenized with QIAshredder spin-columns (Qiagen). In order to assure sufficient concentration, integrity and purity of isolated RNA all samples were measured with the Qubit 2.0 Fluorometer (Qubit RNA HS Assay) (LifeTechnologies, Carlsbad, CA) and the 2200 Tape Station (R6K ScreenTape Assay) (Agilent, Santa Clara, CA) following the manufacturer's instructions. Only samples with a concentration of >50ng/µl, an OD260/280 ≥1.8 and a RNA integrity number (RIN) >7 were included in subsequent library preparation and sequencing.

d) RNA library preparation and sequencing

RNA samples were prepared for sequencing using the Illumina Truseq® Stranded total RNA Protocol in combination with the RiboZero rRNA removal Kit, and sequenced on the HiSeq2500 in pools of 10 samples with 2x125bp, producing paired-end reads according to the manufacturer's protocol (Illumina, San Diego, CA). The case and control samples were randomly distributed across the plates and pools before sequencing to minimize batch effects. We sequenced libraries prepared from total RNA extracted from 147 skin biopsies (38 control;

27 psoriasis non-lesional (NL); 28 psoriasis lesional (LL); 27 AD NL; 27 AD LL) donated by 93 individuals.

e) RNA-seq data processing

Low quality reads were filtered from the data using the Illumina CASAVA FASTQ filter. Illumina standard primers were trimmed, and the quality of the data was assessed using FastQC (vs 0.11.3) (Andrews, 2010). Paired reads were mapped to the human reference genome (b37) using STAR (Dobin et al., 2013), only uniquely mapped read pairs were retained Number of reads for each gene was counted using HTSeq (Anders et al., 2015), only genes with on average ≥1 read/sample were used in our analysis. TMM was used to normalize the RNA-seq data (Robinson and Oshlack, 2010), and we applied voom transformation to model the mean-variance relationship of the expression data (Law C. W. et al., 2014).

f) Statistical and bioinformatics analysis

We conducted differential expression analysis between different conditions using empirical Bayes linear model as implemented in the limma package (Ritchie et al., 2015), controlling for individual specific effect (for nonlesional vs. lesional skin comparison) and gender effect (for normal vs. nonlesional/lesional skin comparison); False discovery rate (FDR) ≤5% and |log2 Fold Change (FC)| ≥1 were used to declare significance. Functional enrichment analysis was performed using the hypergeometric test for pathways/functions compiled from Gene Ontology (Ashburner et al., 2000), KEGG (Kanehisa et al., 2012), and Biocarta (Nishimura, 2001), and only those with ≥10 and ≤300 annotated genes were examined; FDR≤10% and Observed/Expected ratio ≥2 were declared significant. By using the current criteria (i.e. FDR<=5% and with more than 2 fold change between two groups) and assuming >10% of genes truly differentially expressed (with on average>500 read counts/sample, estimated from our cohort)

from the 31,364 genes we examined, retrospective power calculation estimates >75% of statistical power (Guo et al., 2014).

For illustration purposes, we grouped similar functions and presented the groupings in a piechart using ClueGO (Bindea et al., 2009). To identify genes that are close to T-cell specific chromatin marks, we first retrieved T-cell H3K27ac peak signals from a previous study (Farh et al., 2015), and, for each cell type, we computed the cell-type specific ratio of each peak's by comparing the signal in the cell type with the average of the remaining cell types. The 10,000 peaks with the highest ratios for each cell type were screened for cell-specific genes within a 5k bp interval. We performed the classification task (e.g. psoriatic vs AD lesional skin) using the Random Forest classifier in the MLR package (Bischl et al., 2016), and the top features were selected according to backward selection with permutation importance; the final Area under Receiver Operating Characteristic (AUROC) was estimated (using the selected features) from three-fold cross validation with 100-repetitions.

We compiled the expert-curated chemical/drug -- gene interactions from the Comparative Toxicogenomics Database (CTD) (Davis et al., 2016), DrugBank (Law V. et al., 2014) and PharmGKB (Hewett et al., 2002), and the chemical/drug -- disease associations from CTD and National Drug File-Reference Terminology (NDF-RT) (Carter et al., 2002). Although these resources also include chemicals, we apply a lexicon to only include associations/interactions involving three types of drugs (antibiotics, clinical drugs and pharmacologic active substances). All the resources use customized identifiers for drugs and diseases, thus recognizing duplicates across the resources is challenging. We therefore replaced the drug identifiers with customized identifiers from our previous work (Raja et al., 2017), plus the diseases' concept identifier (CUI) from UMLS Metathesaurus.

g) Cytokine stimulation in keratinocytes

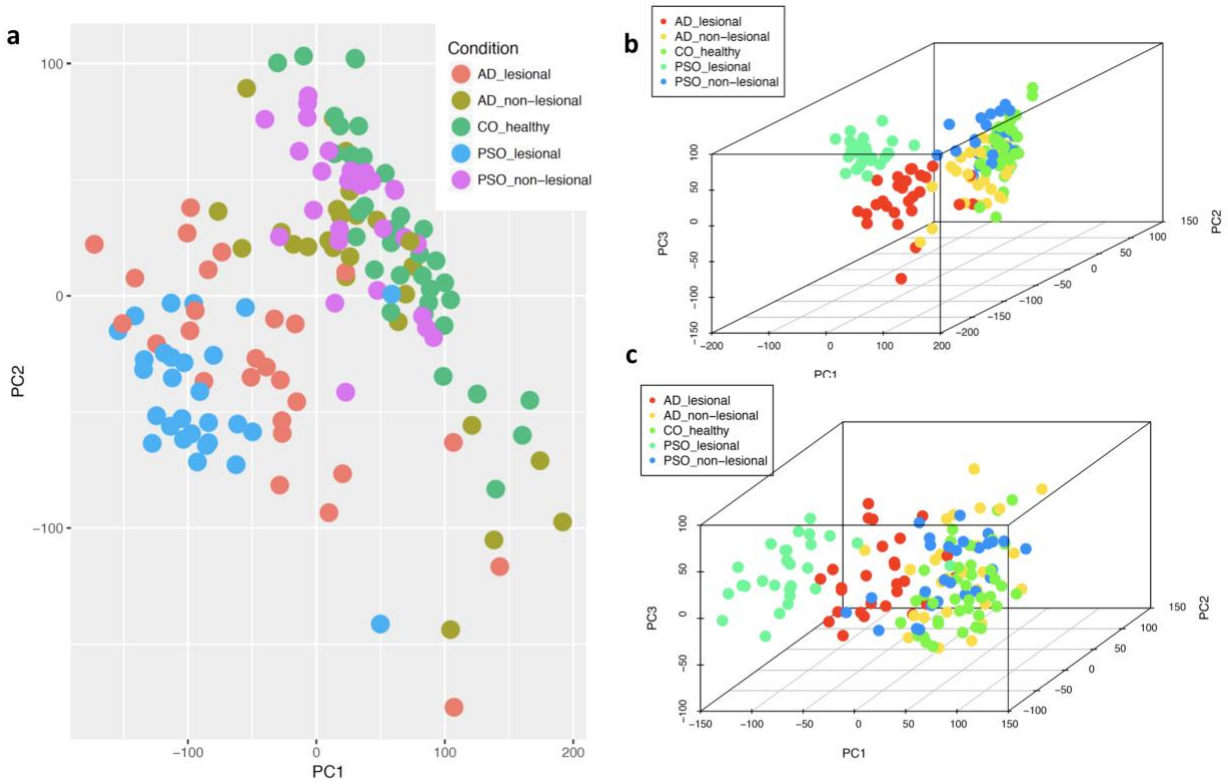
We determined whether the DEGs identified in our experiments were regulated by stimulations with various cytokines in keratinocytes. We obtained 50 normal human keratinocytes from 50 different healthy adults. Keratinocytes were grown in 12 well plate in 154 CF medium (Thermo Fisher #M154CF500) with human keratinocyte growth supplement (Thermo Fisher #S0015). Keratinocytes were grown to confluency at which time the complete medium (with supplements) was replaced by basal 154 CF medium (without supplements). Cells were then stimulated with cytokines (IL-4, IL-13, IFN-α, IFN-γ, TNF-α, IL-17A, IL-36α, IL-36β, IL-36γ, R&D Systems) individually at 10 ng/ml concentration. After 8 hrs cells were harvested and RNA was isolated using RNeasy Plus Mini kit (Qiagen # 74136). RNA was analyzed by RNA Nano Chips (Agilent Technologies) and sequenced (Sarkar et al., 2018).

h) Immunohistology

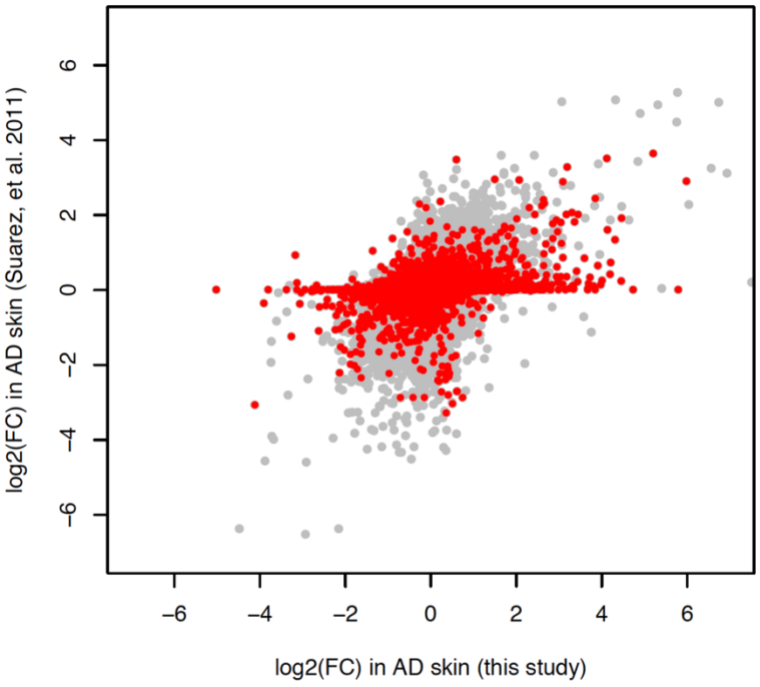
Sections were taken from formalin-fixed, paraffin-embedded biopsies. Tissue slides underwent thorough manual quality control check for the following parameters: dermis and epidermis present on the slide, tissue is well aligned on the glass without loss of large parts of the biopsy material, staining intensity is visible and present in the expected cell component. If any of the criteria were not met, reevaluation on freshly cut material from the identical biopsy was performed. If the second evaluation did not show concordance with the criteria, the slide was excluded from further processing for the digital image analysis. Tissue slides, stained with CD8, were digitally scanned at x20 magnification using a Hamamatsu Nanozoomer in brightfield mode. Quantitative image analysis was performed by on whole slide scanned images using Definiens Tissue Studio® software. A customized algorithm was developed per marker in Tissue Studio® using a subset of the study images. The customized algorithm was developed to accurately detect the whole tissue or if required, segment the specified regions of interest (ROI)

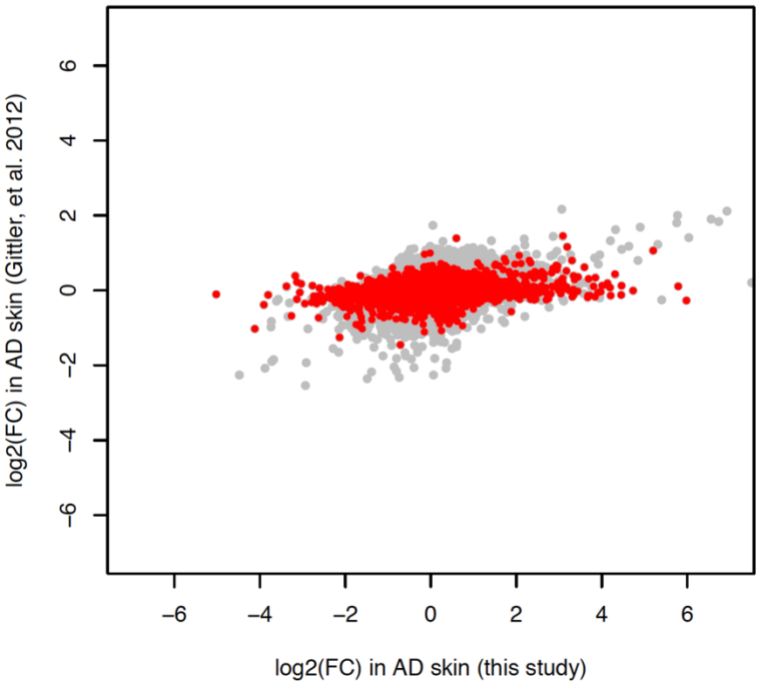
within the whole tissue section. Cellular analysis thresholds were then optimized per algorithm to specifically detect positive cells for the immunohistochemistry markers within the tissue ROI. The algorithms were then applied objectively to each section to quantify the required parameters. Evaluation was performed for total cell count (sum of epidermal and dermal cell counts) on the CD8 stains. The analyzed area was measured in mm2 and based on the absolute cell counts calculation of cells per mm2 was performed.

Supplementary Figures

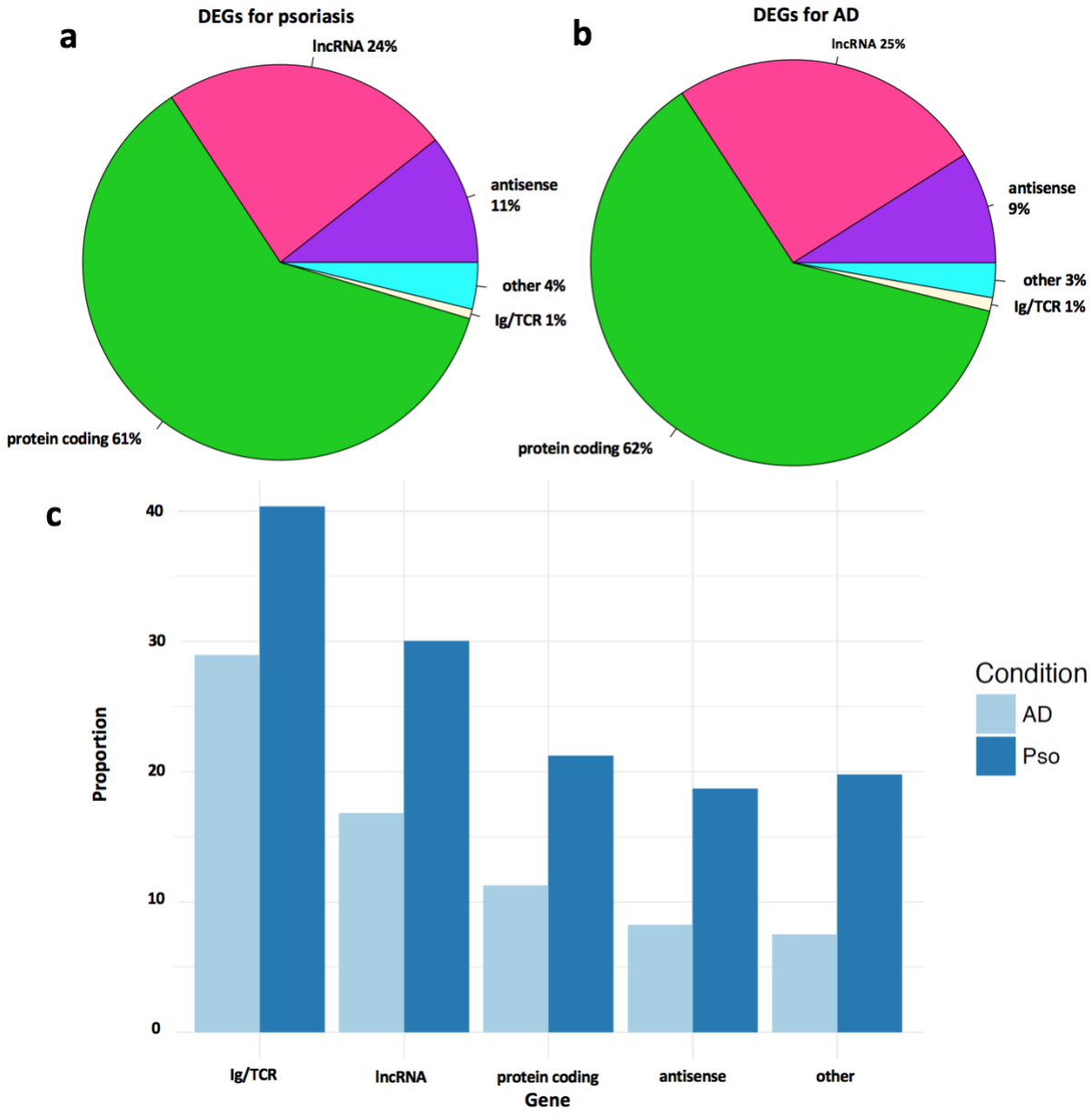


Supplementary Figure 1. a) top two principal components computed using the transcriptomes of the samples; b) the top three principal components using the transcriptome of the samples; c) the top three principal components after adjusting the batch variable estimated by the SVA algorithm.

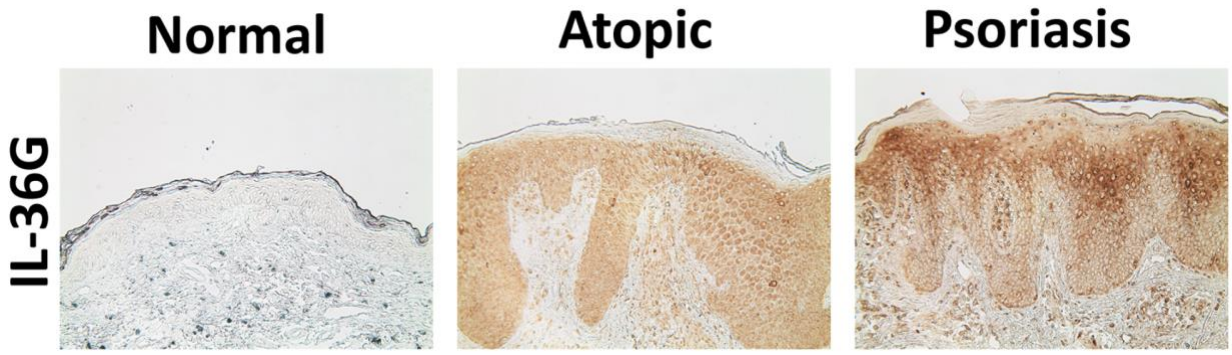




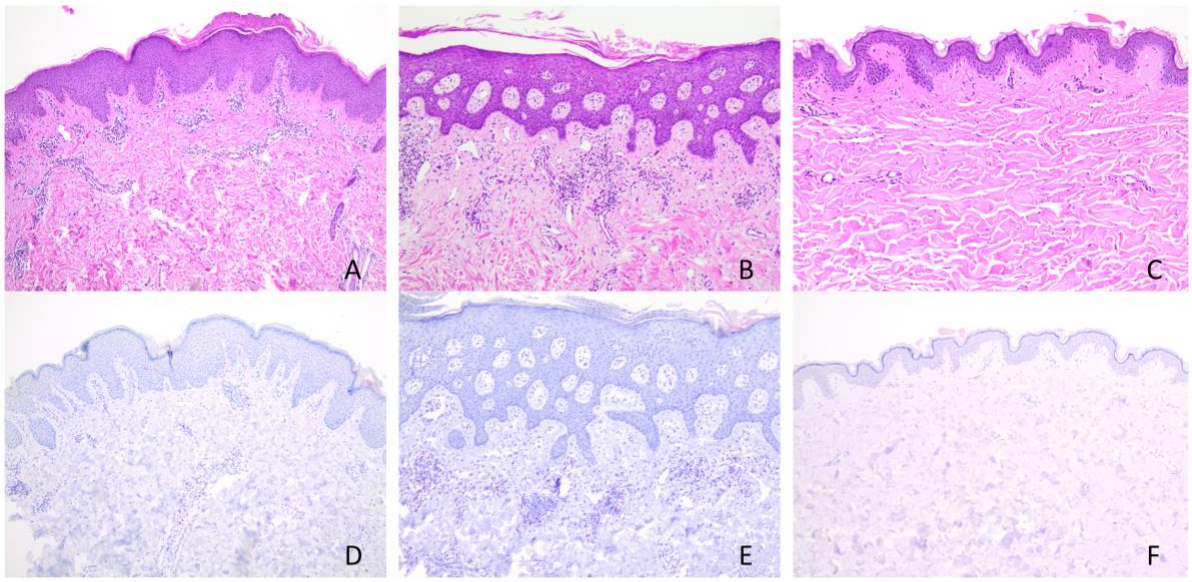
Supplementary Figure 2. Comparing the magnitude of dysregulation (Fold Change in logarithmic scale) in AD skin measured in this study (x-axis) versus previous microarray studies. Each point represents a gene that is common in both platforms; red color represents genes expressing in the lower 25% of the transcriptome.



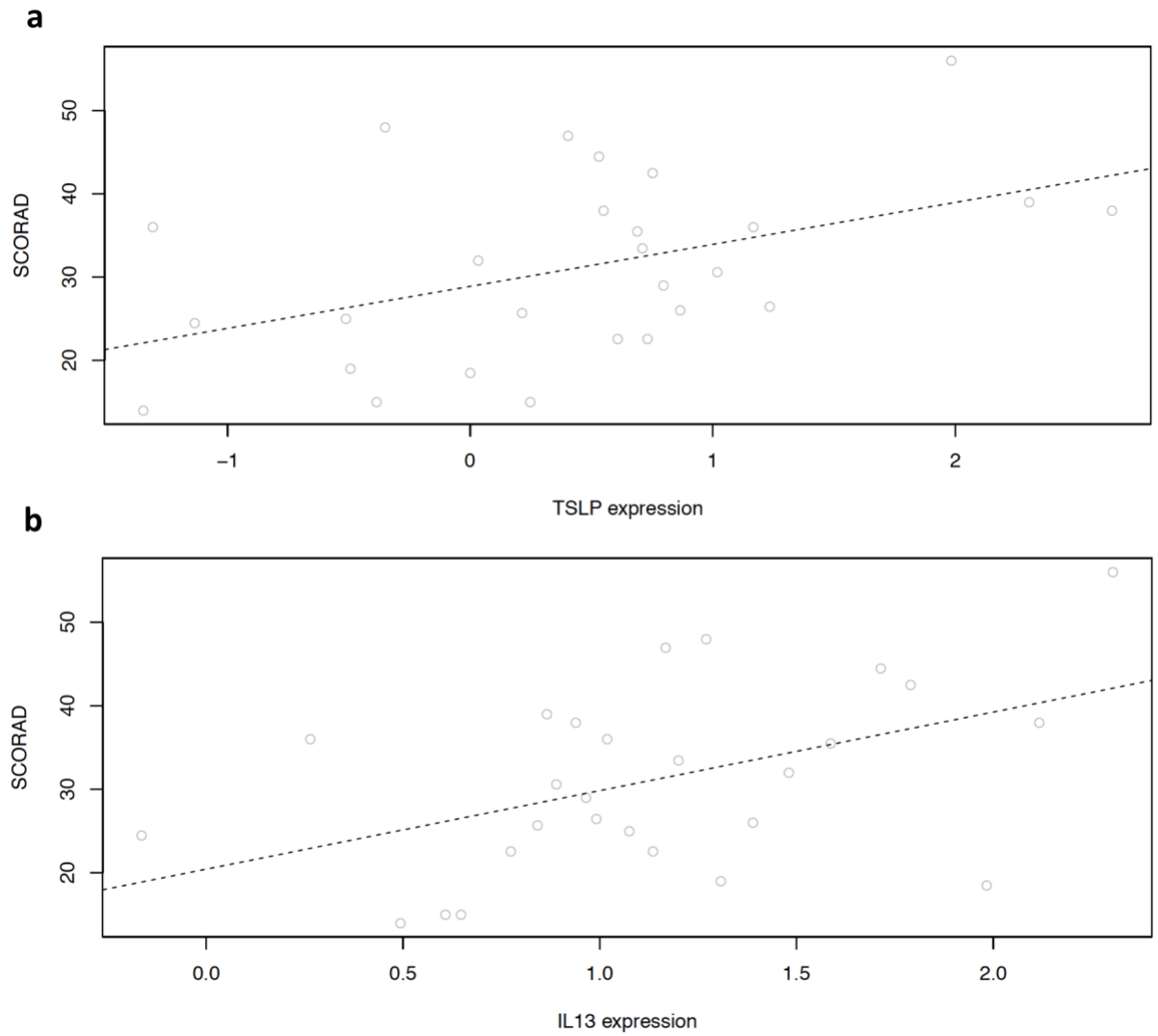
Supplementary Figure 3. The proportion of different gene categories in the DEGs for psoriasis (a) and atopic dermatitis (b). (c). For each category, the proportion of DEGs.



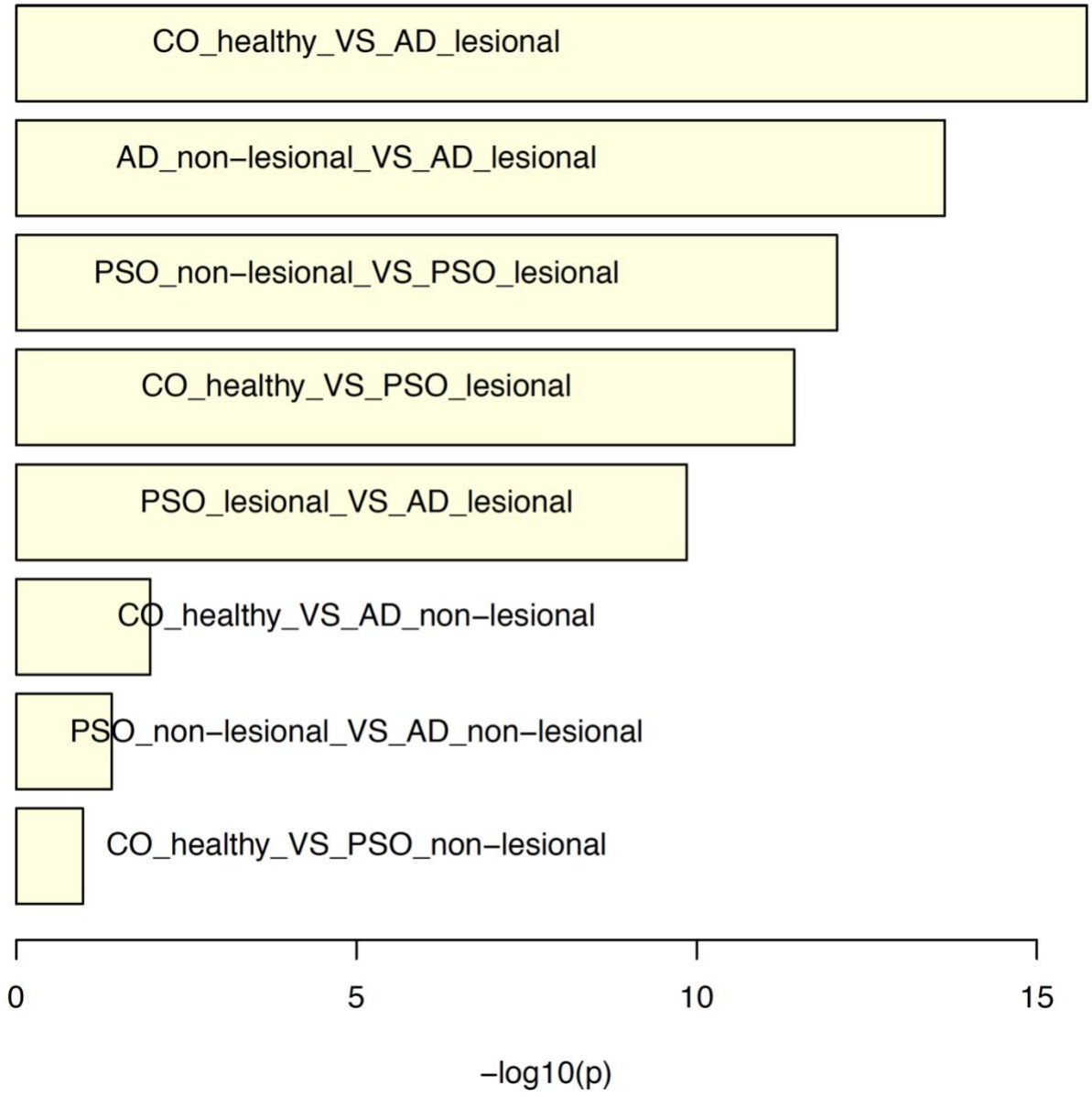
Supplementary Figure 4. Immunohistochemistry illustrates the detection of IL-36G in the skin of atopic dermatitis and psoriasis, concordant with the expression data.



Supplementary Figure 5. Lesional AD skin (A) with acanthotic thickening of the epidermis and parakeratosis. Perivascular infiltration of lymphomononuclear cells mainly in the dermis and focal epidermotropic lymphocytes. The lesional psoriatic skin (B) shows an acanthotic epidermis with parakeratosis and hypogranulosis and perivascular lymphomononuclear infiltrates in the upper dermis. The healthy control skin (C) displays a thin epidermis with regular structure and scarce perivascular lymphomononuclear infiltrates. CD8 is expressed in lymphocytic cells in the dermal compartment in lesional AD (D), lesional psoriasis (E) and control skin (F), accounting approximately for a quarter of all lymphocytes in each sample. In relation to the amount of lymphocytic infiltrates, the absolute count of CD8 positive cells is higher in D and E. Original magnification x100 in A-F.



Supplementary Figure 6. Correlation between SCORAD with normalized expression of TSLP (a) and IL13 (b) of AD lesional skin samples



Supplementary Figure 7. The enrichment analysis for AD drug targets among the genes dysregulated in different differential expression analysis.

Supplementary Tables

Supplementary Table 1. Cohort description: Continuous traits as mean and standard deviation for atopic dermatitis patients (AD), psoriasis patients (Pso) and healthy control individuals (Healthy). Filaggrin (FLG) status (R501X, 2282del4, R2447X, S3247X) determined in AD and healthy control individuals only.

	AD	Pso	Healthy
Number of individuals (male/female)	27 (17/10)	28 (14/14)	38 (16/22)
Age	34.07+/-10.96	41.89+/-15.74	32.63+/-11.64
Objective Scorad / PASI	31.11+/-10.96	9.54+/-3.49	-
BMI	25.07+/-5.1	28.65+/-5.69	24.16+/-4.22
Age onset <6	80.77	7.14	-
FLG mutation carriers N (%)	7 (25.93)	NA	1 (2.63)
Asthma/Rhinitis (%)	48.15/62.96	-/-	0/0
Dennie-Morgan lines: weak/moderate/strong (%)	37.04/11.11/0	-/-/-	0/0/0
Herthoge's sign: weak/moderate/strong (%)	14.81/0/0	5.26/0/0	-/-/-
Palmar hyperlinearity: weak/moderate/strong (%)	37.04 /22.22/3.7	-/-/-	5.26/0/0
Sebostasis weak/moderate/strong (%)	29.63/44.44/22. 22	-/-/-	2.63/0/0
Keratosis pilaris weak/moderate/strong	37.04/11.11/0	-/-/-	7.89/5.26/0
PsA: questionable/yes (%)	-/-	28.57/14.29	-/-

Supplementary Table 2. Sample description. Clinical and molecular features collected for each samples used in the RNA-seq analysis.

ID.pheno	Trait	Sex	Age	FLG Mutation	Severity (ScorAD/PASI)	Rhinitis	Asthma	PsA	biopsy site non-lesional	biopsy site lesional	Dennie	Hertoghe	Palmar hyperlinearity	Xerosis	Keratosis pilaris
AD_004	AD	female	48	no	35.5	yes	yes		upper arm flexural right	upper arm flexural left	moderate	no	weak	moderate	no
AD_005	AD	male	43	no	44.5	yes	yes		upper arm flexural left	upper arm flexural right	no	no	moderate	moderate	weak
AD_006	AD	male	25	2282del4	25	no	no		upper arm flexural left	upper arm flexural right	weak	weak	moderate	moderate	weak
AD_007	AD	male	33	R244X	15	yes	no		upper arm flexural left	antecubital fossa left	no	no	moderate	weak	weak
AD_009	AD	male	45	2282del4	32	yes	yes		upper arm flexural left	antecubital fossa left	no	no	moderate	moderate	weak
AD_011	AD	male	45	no	36	yes	yes		upper arm flexural left	upper arm flexural left	no	no	weak	weak	moderate
AD_014	AD	male	37	no	48	yes	no		upper arm flexural left	upper arm flexural left	no	no	weak	moderate	no
AD_016	AD	female	25	no	18.5	no	no		upper arm flexural left	upper arm flexural left	no	no	weak	moderate	moderate
AD_017	AD	female	42	no	38	yes	yes		upper arm flexural left	upper arm flexural left	weak	no	moderate	strong	weak
AD_019	AD	female	22	no	24.5	no	no		upper arm flexural left	antecubital fossa left	no	no	no	moderate	weak
AD_020	AD	female	43	no	42.5	yes	yes		upper arm flexural right	antecubital fossa	weak	no	weak	strong	weak
AD_021	AD	female	29	no	15	no	no		upper arm flexural left	antecubital fossa left	weak	no	no	weak	no
AD_023	AD	male	47	R244X/2282del4	47	yes	yes		upper arm flexural left	upper arm flexural left	weak	weak	strong	strong	weak
AD_024	AD	female	45	no	22.6	no	yes		upper arm flexural right	upper arm flexural right	no	no	weak	strong	weak
AD_025	AD	female	22	no	22.6	no	no		upper arm flexural left	antecubital fossa left	weak	no	no	moderate	no
AD_026	AD	male	19	no	33.5	yes	yes		upper arm flexural left	antecubital fossa left	no	no	weak	weak	no
AD_027	AD	female	22	no	14	yes	yes		upper arm flexural left	upper upper arm flexural left	no	weak	no	moderate	no
AD_028	AD	male	31	no	19	yes	yes		upper arm flexural right	upper arm flexural right	weak	no	weak	moderate	no
AD_029	AD	male	21	no	25.7	yes	no		upper arm flexural left	upper arm flexural left	moderate	no	weak	no	no
AD_030	AD	female	23	no	26.5	no	no		upper arm flexural right	antecubital fossa right	no	no	no	weak	no
AD_031	AD	male	24	no	30.6	no	no		upper arm flexural left	upper arm flexural left	weak	no	no	moderate	moderate
AD_032	AD	male	53	2282del4	29	no	no		upper arm flexural left	antecubital fossa right	no	no	moderate	moderate	weak
AD_033	AD	male	48	no	39	yes	yes		upper leg flexural right	upper leg flexural right	moderate	no	no	strong	no
AD_034	AD	male	30	R501X	38	yes	yes		upper arm flexural right	upper arm flexural right	no	no	moderate	moderate	no
AD_035	AD	male	19	no	26	yes	no		upper arm flexural left	lower arm left	weak	no	no	weak	no
AD_036	AD	male	45	R501X/2282del4	56	yes	no		upper arm flexural left	upper arm flexural left	no	no	moderate	strong	no
AD_037	AD	male	34	no	36	no	no		upper arm flexural left	upper arm flexural left	weak	weak	no	weak	no
PSO_001	PSO	female	28		3.3			yes	upper arm extensor left	ellbow left					
PSO_002	PSO	male	50		5			no	upper arm flexural left	upper arm flexural left					
PSO_003	PSO	female	50		6.2			yes	upper leg flexural left	upper leg flexural left					
PSO_005	PSO	female	33		4.3			no	lower leg flexural right	lower leg flexural right					

ID.pheno	Trait	Sex	Age	FLG Mutation	Severity (ScorAD/PASI)	Rhinitis	Asthma	PsA	biopsy site non-lesional	biopsy site lesional	Dennie	Hertoghe	Palmar hyperlinearity	Xerosis	Keratosis pilaris
PSO_006	PSO	female	50		7			no	lower leg flexural left	lower leg flexural left					
PSO_007	PSO	female	68		3.8			unknown	upper arm extensor right	upper arm extensor right					
PSO_008	PSO	female	35		5			no	upper arm flexural left	ellbow left					
PSO_009	PSO	male	71		6.2			yes	lower leg flexural left	lower arm flexural left					
PSO_011	PSO	male	53		8.3			yes	lower leg extensor left	lower leg extensor left					
PSO_012	PSO	female	46		5.8			unknown	lower leg extensor left	lower leg extensor left					
PSO_014	PSO	male	22		6.8			no	upper arm extensor left	upper arm extensor left					
PSO_015	PSO	male	49		22.4			unknown	upper arm extensor left	upper arm extensor left					
PSO_016	PSO	male	23		5.4			no	upper arm extensor left	upper arm extensor left					
PSO_017	PSO	male	30		6.6			no	lower arm extensor left	lower arm extensor left					
PSO_018	PSO	female	38		1.8			no	upper arm extensor left	upper arm extensor left					
PSO_020	PSO	female	21		2.7			unknown	upper leg flexural left	upper leg flexural left					
PSO_023	PSO	female	36		1.2			unknown	upper arm extensor left	ellbow left					
PSO_024	PSO	male	69		2.9			no	upper arm extensor right	ellbow right					
PSO_027	PSO	male	46		3.6			no	upper arm flexural left	ellbow left					
PSO_028	PSO	male	41		9.7			no	upper arm extensor left	upper arm extensor left					
PSO_029	PSO	female	70		2			unknown	upper arm extensor right	ellbow right					
PSO_030	PSO	male	52		6.8			no	upper arm extensor right	ellbow right					
PSO_031	PSO	male	40		11.4			no	upper arm extensor right	ellbow right					
PSO_033	PSO	female	28		4.5			no	upper arm extensor right	upper arm extensor right					
PSO_034	PSO	male	28		4			unknown	upper arm flexural left	upper arm flexural left					
PSO_035	PSO	male	24		1.3			no	upper arm flexural left	upper arm flexural left					
PSO_036	PSO	female	18		3.5			no	upper arm extensor left	upper arm extensor left					
PSO_037	PSO	female	54		10.5			unknown	upper arm extensor right	upper arm extensor right					
CTRL_002	CTRL	female	42	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_003	CTRL	female	25	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_004	CTRL	female	28	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_006	CTRL	female	24	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_008	CTRL	male	28	no		no	no		upper arm flexural right		no	no	no	no	weak
CTRL_009	CTRL	female	33	no		no	no		upper arm flexural left		no	no	no	no	weak
CTRL_010	CTRL	female	27	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_011	CTRL	male	26	no		no	no		upper arm flexural left		no	no	no	no	moderate
CTRL_013	CTRL	male	42	no		no	no		upper arm extensor right		no	no	no	no	no

ID.pheno	Trait	Sex	Age	FLG Mutation	Severity (ScorAD/PASI)	Rhinitis	Asthma	PsA	biopsy site non-lesional	biopsy site lesional	Dennie	Hertoghe	Palmar hyperlinearity	Xerosis	Keratosis pilaris
CTRL_014	CTRL	male	24	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_015	CTRL	female	28	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_016	CTRL	female	32	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_017	CTRL	male	30	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_018	CTRL	male	23	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_019	CTRL	female	40	no		no	no		upper arm extensor left		no	no	weak	no	moderate
CTRL_020	CTRL	male	26	no		no	no		upper arm flexural left		no	no	no	weak	no
CTRL_022	CTRL	male	47	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_024	CTRL	female	47	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_025	CTRL	female	25	no		no	no		upper arm flexural left		no	weak	no	no	no
CTRL_026	CTRL	female	31	no		no	no		upper arm flexural left		no	weak	no	no	no
CTRL_029	CTRL	male	40	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_030	CTRL	male	40	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_031	CTRL	male	54	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_032	CTRL	male	37	no		no	no		upper arm flexural right		no	no	no	no	no
CTRL_033	CTRL	female	52	no		no	no		upper arm extensor left		no	no	no	no	no
CTRL_034	CTRL	male	61	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_035	CTRL	female	29	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_036	CTRL	female	25	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_037	CTRL	male	22	no		no	no		upper arm flexural left		no	no	no	no	weak
CTRL_038	CTRL	female	20	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_039	CTRL	female	19	no		no	no		upper arm extensor left		no	no	weak	no	no
CTRL_040	CTRL	female	20	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_041	CTRL	female	57	no		no	no		upper arm extensor right		no	no	no	no	no
CTRL_042	CTRL	female	20	2282del4		no	no		upper arm flexural left		no	no	no	no	no
CTRL_043	CTRL	female	24	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_044	CTRL	male	18	no		no	no		upper arm flexural right		no	no	no	no	no
CTRL_045	CTRL	female	25	no		no	no		upper arm flexural right		no	no	no	no	no
CTRL_046	CTRL	male	49	no		no	no		upper arm flexural left		no	no	no	no	no

Supplementary Table 3. Transcriptomic studies conducted for AD/Eczema. Only show the number of samples that have been profiled for transcriptome, remained after quality control, and presented in the paper (if the number cannot be determined in the paper, the number of samples deposited in the corresponding GEO was used). ^same control individuals; *same patients; [#]the study used skin tape strip for profiling the transcriptome.

Study	Platform	Study treatment response	Control	Pso uninvolved	Pso lesional	AD/Eczema uninvolved	AD/Eczema lesional
Nomura I, et al. 2003. *JACI*	Microarray	NA	NA	NA	**6**	NA	**7**
Guttman-Yassky E et al. 2009. *JACI*	Microarray	NA	**9^**	NA	**15**	NA	**9**
Suarez-Farinas Mayte, et al. 2011. *JACI*	Microarray	NA	**8**	NA	NA	**12**	**13**
Tintle S, et al. 2011. *JACI*	Microarray	UVB phototherapy	NA	NA	NA	**12**	**12**
Choy DF et al. 2012. *JACI*	Microarray	NA	**5**	NA	14	NA	**12**
Gittler JK et al. 2012. *JACI*	Microarray	NA	**15^**	NA	NA	**8**	**8 chronic/8 acute**
Cole C et al. 2014. *JACI*	**RNA-Seq**	NA	**10**	NA	NA	**26**	NA
Quaranta M et al. 2014. *Sci Trans Med*	Microarray	NA	NA	NA	**24** psoriatic patients also with eczema	NA	**24 eczema patients also with psoriasis**
Rodriguez E, et al. 2014. *JID*	Microarray	NA	**14 epidermal**	NA	NA	**7 epidermal**	**12 epidermal**
Khattri S, et al. 2014. *JACI*	Microarray	Cyclosporine	NA	NA	NA	**19***	**19***
Beck LA, et al. 2014. *NEJM*	microarray	dupilumab	NA	NA	NA	**7**	**16**
Suarez-Farinas M, et al. 2015. *JACI*	**Microarray & RNA-seq**	NA	NA	NA	NA	**18***	**18***
Brunner, PM, et al. 2016. *JACI*	Microarray	Topical glucocorticosteroids	NA	NA	NA	**9**	**14**
Malik K. et al. 2017. *Clin Exp Allergy*	Microarray	House dust mite atopy patch test	**14**	NA	NA	**8**	**8**
Dyjack N, et al. 2018. *JACI*[#]	RNA-seq	NA	**13**	NA	NA	**18**	**12**
This study	**RNA-seq**	NA	**38**	**27**	**28**	**27**	**27**

Supplementary Table 4. Number of differentially expressed genes in each of the comparisons.

	Number of Genes		
DE analysis	**DEGs**	**Up-regulated**	**Down-regulated**
Healthy vs Pso non-lesional	246	82	164
Healthy vs Pso lesional	6763	2502	4261
Pso non-lesional vs Pso lesional	5156	2232	2924
Healthy vs AD non-lesional	180	98	82
Healthy vs AD lesional	3450	1529	1921
AD non-lesional vs AD lesional	1785	919	866
Pso non-lesional vs AD non-lesional	185	117	68
Pso lesional vs AD lesional	2030	1259	771

Supplementary Table 5. Functional enrichment results for lesional DEGs In Excel Table

Supplementary Table 6. Functional enrichment results for uninvolved DEGs In Excel Table

Supplementary Table 7. Read counts obtained for IL4 and IL13 for all samples

Supplementary Table 8. Cell type enrichment analysis for different differential expression analysis

Supplementary Table 9. Proportion of CD8 cells obtained from the quantitative immunochemistry results.

Supplementary Table 10. Table for top features in classification.

	Ranking of selected features	Selected features
Normal vs uninvolved AD	1	*IL13*
	2	*EBI3*
	3	*IL26*
	4	*IL20*
	5	*IL5*
	6	*IL36A*
	7	*IL36G*
Normal vs uninvolved Pso	1	*IL36G*
	2	*IL19*
	3	*IL18*
	4	*IL36A*
	5	*EBI3*
	6	*IL13*

Supplementary Table 11. Spearman correlation and significance level between gene expression and severity score in psoriatic lesional (PASI) and AD lesional (SCORAD) skin.

Supplementary Table 12. Current AD drugs (from the drug databases used in this study) whose targets are differentially expressed in AD lesioanl skin.

References

Anders S, Pyl PT, Huber W. HTSeq--a Python framework to work with high-throughput sequencing data. Bioinformatics 2015;31(2):166-9.

Andrews S. FastQC: a quality control tool for high throughput sequence data., http://www.bioinformatics.babraham.ac.uk/projects/fastqc; 2010 [accessed.

Ashburner M, Ball CA, Blake JA, Botstein D, Butler H, Cherry JM, et al. Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. Nature genetics 2000;25(1):25-9.

Bindea G, Mlecnik B, Hackl H, Charoentong P, Tosolini M, Kirilovsky A, et al. ClueGO: a Cytoscape plug-in to decipher functionally grouped gene ontology and pathway annotation networks. Bioinformatics 2009;25(8):1091-3.

Bischl B, Lang M, Kotthoff L, Schiffner J, Richter J, Studerus E, et al. mlr: Machine Learning in R. Journal of Machine Learning Research 2016;17(170):1-5.

Boehncke WH, Schon MP. Psoriasis. Lancet 2015;386(9997):983-94.

Carter JS, Brown SH, Erlbaum MS, Gregg W, Elkin PL, Speroff T, et al. Initializing the VA medication reference terminology using UMLS metathesaurus co-occurrences. Proc AMIA Symp 2002:116-20.

Davis AP, Grondin CJ, Johnson RJ, Sciaky D, King BL, McMorran R, et al. The Comparative Toxicogenomics Database: update 2017. Nucleic Acids Res 2016.

Dobin A, Davis CA, Schlesinger F, Drenkow J, Zaleski C, Jha S, et al. STAR: ultrafast universal RNA-seq aligner. Bioinformatics 2013;29(1):15-21.

Farh KK, Marson A, Zhu J, Kleinewietfeld M, Housley WJ, Beik S, et al. Genetic and epigenetic fine mapping of causal autoimmune disease variants. Nature 2015;518(7539):337-43.

Guo Y, Zhao S, Li CI, Sheng Q, Shyr Y. RNAseqPS: A Web Tool for Estimating Sample Size and Power for RNAseq Experiment. Cancer Inform 2014;13(Suppl 6):1-5.

Hewett M, Oliver DE, Rubin DL, Easton KL, Stuart JM, Altman RB, et al. PharmGKB: the Pharmacogenetics Knowledge Base. Nucleic Acids Res 2002;30(1):163-5.

Kanehisa M, Goto S, Sato Y, Furumichi M, Tanabe M. KEGG for integration and interpretation of large-scale molecular data sets. Nucleic Acids Res 2012;40(Database issue):D109-14.

Law CW, Chen Y, Shi W, Smyth GK. voom: Precision weights unlock linear model analysis tools for RNA-seq read counts. Genome Biol 2014;15(2):R29.

Law V, Knox C, Djoumbou Y, Jewison T, Guo AC, Liu Y, et al. DrugBank 4.0: shedding new light on drug metabolism. Nucleic Acids Res 2014;42(Database issue):D1091-7.

Nishimura D. Biocarta. Biotech Software & Internet Report 2001;2(3):117-20.

Raja K, Patrick M, Elder JT, Tsoi LC. Machine learning workflow to enhance predictions of Adverse Drug Reactions (ADRs) through drug-gene interactions: application to drugs for cutaneous diseases. Sci Rep 2017;7(1):3690.

Ritchie ME, Phipson B, Wu D, Hu Y, Law CW, Shi W, et al. limma powers differential expression analyses for RNA-sequencing and microarray studies. Nucleic Acids Res 2015;43(7):e47.

Robinson MD, Oshlack A. A scaling normalization method for differential expression analysis of RNA-seq data. Genome Biol 2010;11(3):R25.

Sarkar MK, Hile GA, Tsoi LC, Xing X, Liu J, Liang Y, et al. Photosensitivity and type I IFN responses in cutaneous lupus are driven by epidermal-derived interferon kappa. Ann Rheum Dis 2018.

Weidinger S, Novak N. Atopic dermatitis. Lancet 2015.

	Significant in	NumFunGenes	DEGs_both_Pso_AD_x	DEGs_both_Pso_AD_p	DEGs_both_Pso_AD_FDR	DEGs_both_Pso_AD_FC	DEGs_both_Pso_AD_g	DEGs_only_Pso_x
CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	DEGs_Pso_&_AD	229	73	5.53E-22	3.29E-18	3.40	CXCL13; IL24; CCR1; C	17
CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	DEGs_AD_only	229	73	5.53E-22	3.29E-18	3.40	CXCL13; IL24; CCR1; C	17
CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	DEGs_Pso_vs_AD	229	73	5.53E-22	3.29E-18	3.40	CXCL13; IL24; CCR1; C	17
CYTOKINE_ACTIVITY	DEGs_Pso_&_AD	168	57	6.35E-19	1.89E-15	3.62	AREG; BMP3; BMP5; C	11
CYTOKINE_ACTIVITY	DEGs_AD_only	168	57	6.35E-19	1.89E-15	3.62	AREG; BMP3; BMP5; C	11
CYTOKINE_ACTIVITY	DEGs_Pso_vs_AD	168	57	6.35E-19	1.89E-15	3.62	AREG; BMP3; BMP5; C	11
CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	DEGs_Pso_&_AD	44	26	1.59E-16	3.15E-13	6.30	CXCL13; CCR1; CCR4; C	3
RESPONSE_TO_BACTERIUM	DEGs_Pso_&_AD	278	70	4.65E-15	6.92E-12	2.68	ACP5; ADH7; ADM; ALI	17
EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	DEGs_Pso_&_AD	182	53	1.59E-14	1.89E-11	3.10	AMOT; APOE; CCR1; C	19
RESPONSE_TO_VIRUS	DEGs_Pso_&_AD	200	56	1.91E-14	1.89E-11	2.98	APOBEC3A; APOBEC3B	16
CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS	DEGs_Pso_&_AD	212	57	7.65E-14	6.06E-11	2.87	CXCL13; CYSLTR1; HRH	21
CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS	DEGs_Pso_vs_AD	212	57	7.65E-14	6.06E-11	2.87	CXCL13; CYSLTR1; HRH	21
GPCR_LIGAND_BINDING	DEGs_Pso_&_AD	274	67	8.15E-14	6.06E-11	2.61	CXCL13; CYSLTR1; HRH	28
GPCR_LIGAND_BINDING	DEGs_Pso_vs_AD	274	67	8.15E-14	6.06E-11	2.61	CXCL13; CYSLTR1; HRH	28
CHEMOKINE_RECEPTOR_BINDING	DEGs_Pso_&_AD	46	23	1.05E-12	6.94E-10	5.33	CCL17; CCL18; CCL19;	4
CHEMOKINE_RECEPTOR_BINDING	DEGs_Pso_vs_AD	46	23	1.05E-12	6.94E-10	5.33	CCL17; CCL18; CCL19;	4
CHEMOKINE_ACTIVITY	DEGs_Pso_&_AD	39	21	1.46E-12	7.98E-10	5.74	CCL17; CCL18; CCL19;	2
EXPRESSION_OF_IFN_INDUCED_GENES	DEGs_Pso_&_AD	32	19	1.49E-12	7.98E-10	6.33	IRF9; IFITM3; IFI6; IRF8	1
RESPONSE_TO_LIPOPOLYSACCHARIDE	DEGs_Pso_&_AD	190	51	1.61E-12	7.98E-10	2.86	ACP5; ADM; ALPL; CCL	12
RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN	DEGs_Pso_&_AD	199	52	3.05E-12	1.35E-09	2.79	ACP5; ADM; ALPL; CCL	12
KERATINIZATION	DEGs_Pso_&_AD	44	22	3.19E-12	1.35E-09	5.33	CNFN; HRNR; IVL; KRT1	1
REGULATION_OF_INFLAMMATORY_RESPONSE	DEGs_Pso_&_AD	180	48	9.17E-12	3.63E-09	2.84	ACP5; ADAM8; ADCYA	12
REGULATION_OF_INFLAMMATORY_RESPONSE	DEGs_Pso_vs_AD	180	48	9.17E-12	3.63E-09	2.84	ACP5; ADAM8; ADCYA	12
CELLULAR_RESPONSE_TO_TYPE_I_INTERFERON	DEGs_Pso_&_AD	47	22	1.73E-11	6.03E-09	4.99	IFI27; IFI35; IFI6; IFIT3;	2
TYPE_I_INTERFERON_MEDIATED_SIGNALING_PATHWAY	DEGs_Pso_&_AD	47	22	1.73E-11	6.03E-09	4.99	IFI27; IFI35; IFI6; IFIT3;	2
REGULATION_OF_LYMPHOCYTE_ACTIVATION	DEGs_Pso_&_AD	274	62	2.44E-11	8.04E-09	2.41	ADAM8; BLM; CARD11	16
RESPONSE_TO_TYPE_I_INTERFERON	DEGs_Pso_&_AD	48	22	2.92E-11	9.13E-09	4.89	IFI27; IFI35; IFI6; IFIT3;	2
LYMPHOCYTE_ACTIVATION	DEGs_Pso_&_AD	263	60	3.54E-11	1.05E-08	2.43	BATF; BCL3; BLM; CARI	14
POSITIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	DEGs_Pso_&_AD	96	32	4.29E-11	1.21E-08	3.55	C6; CCL19; CCL2; CCR2	7
POSITIVE_REGULATION_OF_CELL_ACTIVATION	DEGs_Pso_&_AD	218	52	1.22E-10	3.31E-08	2.54	ADAM8; BLM; CARD11	13
INTERFERON_ALPHA_BETA_SIGNALING	DEGs_Pso_&_AD	43	20	1.58E-10	4.09E-08	4.96	IRF9; IFITM3; USP18; I	1
CYTOKINE_RECEPTOR_BINDING	DEGs_Pso_&_AD	182	46	1.75E-10	4.31E-08	2.69	CCL17; CCL18; CCL19;	10
CYTOKINE_RECEPTOR_BINDING	DEGs_AD_only	182	46	1.75E-10	4.31E-08	2.69	CCL17; CCL18; CCL19;	10
CYTOKINE_RECEPTOR_BINDING	DEGs_Pso_vs_AD	182	46	1.75E-10	4.31E-08	2.69	CCL17; CCL18; CCL19;	10
REGULATION_OF_LYMPHOCYTE_PROLIFERATION	DEGs_Pso_&_AD	140	39	1.81E-10	4.31E-08	2.97	BLM; CARD11; CCL19;	9
NEGATIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	DEGs_Pso_&_AD	52	22	2.02E-10	4.49E-08	4.51	APOBEC3A; CAMP; CCI	4
POSITIVE_REGULATION_OF_LEUKOCYTE_ACTIVATION	DEGs_Pso_&_AD	208	50	2.04E-10	4.49E-08	2.56	ADAM8; BLM; CARD11	13
REGULATION_OF_MONONUCLEAR_CELL_PROLIFERATION	DEGs_Pso_&_AD	141	39	2.29E-10	4.85E-08	2.95	BLM; CARD11; CCL19;	9
DEFENSE_RESPONSE_TO_BACTERIUM	DEGs_Pso_&_AD	97	31	2.84E-10	5.82E-08	3.41	ACP5; BCL3; CAMP; CC	5
CORNIFIED_ENVELOPE	DEGs_Pso_&_AD	22	14	3.15E-10	6.24E-08	6.78	CNFN; FLG; IVL; LOR; S	1
KERATINOCYTE_DIFFERENTIATION	DEGs_Pso_&_AD	87	29	3.32E-10	6.36E-08	3.55	CNFN; EPHA2; FLG; HR	1
PEPTIDE_LIGAND_BINDING_RECEPTORS	DEGs_Pso_&_AD	120	35	3.73E-10	6.94E-08	3.11	CXCL13; CCR1; CCR4; C	13
PEPTIDE_LIGAND_BINDING_RECEPTORS	DEGs_Pso_vs_AD	120	35	3.73E-10	6.94E-08	3.11	CXCL13; CCR1; CCR4; C	13
CYTOKINE_MEDIATED_SIGNALING_PATHWAY	DEGs_Pso_&_AD	258	57	4.00E-10	7.21E-08	2.36	AIM2; CCL2; CCL5; CCR	18
REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	DEGs_Pso_&_AD	206	49	4.53E-10	7.93E-08	2.54	AIM2; AP1S3; BIRC3; C	14
REGULATION_OF_LEUKOCYTE_PROLIFERATION	DEGs_Pso_&_AD	145	39	5.64E-10	9.58E-08	2.87	BLM; CARD11; CCL19;	10
REGULATION_OF_T_CELL_ACTIVATION	DEGs_Pso_&_AD	203	48	8.38E-10	1.38E-07	2.52	ADAM8; BLM; CARD11	8
POSITIVE_REGULATION_OF_T_CELL_ACTIVATION	DEGs_Pso_&_AD	147	39	8.73E-10	1.40E-07	2.83	ADAM8; BLM; CARD11	5
EPIDERMAL_CELL_DIFFERENTIATION	DEGs_Pso_&_AD	102	31	1.16E-09	1.78E-07	3.24	CNFN; EPHA2; FA2H; F	2
POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	DEGs_Pso_&_AD	192	46	1.17E-09	1.78E-07	2.55	ADAM8; ADCYAP1; AF	10
POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	DEGs_Pso_vs_AD	192	46	1.17E-09	1.78E-07	2.55	ADAM8; ADCYAP1; AF	10
DEFENSE_RESPONSE_TO_VIRUS	DEGs_Pso_&_AD	123	34	3.10E-09	4.60E-07	2.95	APOBEC3A; APOBEC3B	12
RESPONSE_TO_INTERFERON_GAMMA	DEGs_Pso_&_AD	84	27	3.23E-09	4.69E-07	3.43	CCL2; CCL3; CCL5; CYP	8
POSITIVE_REGULATION_OF_LYMPHOCYTE_ACTIVATION	DEGs_Pso_&_AD	193	45	4.39E-09	6.21E-07	2.49	ADAM8; BLM; CARD11	12
CELLULAR_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORI	DEGs_Pso_&_AD	91	28	5.12E-09	7.08E-07	3.28	CCL2; CCL3; CCL5; CCR	6
POSITIVE_REGULATION_OF_T_CELL_PROLIFERATION	DEGs_Pso_&_AD	65	23	5.37E-09	7.26E-07	3.77	BLM; CARD11; CCL19;	2
CELLULAR_RESPONSE_TO_LIPOPOLYSACCHARIDE	DEGs_Pso_&_AD	86	27	5.77E-09	7.47E-07	3.35	CCL2; CCL3; CCL5; CCR	6
REGULATION_OF_LYMPHOCYTE_CHEMOTAXIS	DEGs_Pso_&_AD	13	10	5.78E-09	7.47E-07	8.20	CCL2; CCL3; CCL4; CCL	0
LEUKOCYTE_MIGRATION	DEGs_Pso_&_AD	195	45	6.18E-09	7.82E-07	2.46	ADAM8; AMICA1; CCL	15
LEUKOCYTE_MIGRATION	DEGs_AD_only	195	45	6.18E-09	7.82E-07	2.46	ADAM8; AMICA1; CCL	15
POSITIVE_REGULATION_OF_INFLAMMATORY_RESPONSE	DEGs_Pso_&_AD	66	23	7.54E-09	9.00E-07	3.71	ADAM8; AGTR1; ALOX	3
POSITIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	DEGs_Pso_&_AD	98	29	7.57E-09	9.00E-07	3.15	BLM; CARD11; CCL19;	7
REGULATION_OF_T_CELL_PROLIFERATION	DEGs_Pso_&_AD	98	29	7.57E-09	9.00E-07	3.15	BLM; CARD11; CCL19;	2
T_CELL_ACTIVATION	DEGs_Pso_&_AD	172	41	1.04E-08	1.21E-06	2.54	BATF; BCL3; BLM; CARI	9
REGULATION_OF_SYMBIOSIS__ENCOMPASSING_MUTUALI	DEGs_Pso_&_AD	20	12	1.45E-08	1.63E-06	6.40	CAMP; CD36; HS3ST5;	1
REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	DEGs_Pso_&_AD	58	21	1.47E-08	1.63E-06	3.86	BLM; CCL19; CCR2; CD	2
POSITIVE_REGULATION_OF_LYMPHOCYTE_PROLIFERATION	DEGs_Pso_&_AD	95	28	1.48E-08	1.63E-06	3.14	BLM; CARD11; CCL19;	7
CYTOKINE_PRODUCTION	DEGs_Pso_&_AD	90	27	1.73E-08	1.87E-06	3.20	AIM2; BATF; CCL19; CC	8
POSITIVE_REGULATION_OF_MONONUCLEAR_CELL_PROLIF	DEGs_Pso_&_AD	96	28	1.92E-08	2.03E-06	3.11	BLM; CARD11; CCL19;	7
REGULATION_OF_LEUKOCYTE_MIGRATION	DEGs_Pso_&_AD	85	26	1.99E-08	2.07E-06	3.26	ADAM8; APOD; BMP5;	8
CELLULAR_RESPONSE_TO_BIOTIC_STIMULUS	DEGs_Pso_&_AD	102	29	2.06E-08	2.11E-06	3.03	CCL2; CCL3; CCL5; CCR	7
SERINE_TYPE_ENDOPEPTIDASE_ACTIVITY	DEGs_Pso_&_AD	120	32	2.26E-08	2.27E-06	2.84	CFB; CFD; CTSC; ELANE	14
REGULATION_OF_INTERLEUKIN_10_PRODUCTION	DEGs_Pso_&_AD	25	13	3.97E-08	3.93E-06	5.54	BCL3; CD274; CD83; FC	3
CELL_KILLING	DEGs_Pso_&_AD	33	15	4.04E-08	3.93E-06	4.85	ALB; APOL1; CAMP; CL	2
CELL_ADHESION_MOLECULES_CAMS	DEGs_Pso_&_AD	105	29	4.20E-08	4.02E-06	2.94	CDH2; CDH3; CDH4; CD	10
REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	DEGs_Pso_&_AD	88	26	4.41E-08	4.16E-06	3.15	CCL19; CCR2; CD226; C	3
CYTOKINE_RECEPTOR_ACTIVITY	DEGs_Pso_&_AD	72	23	4.95E-08	4.60E-06	3.41	CCR1; CCR2; CCR4; CCF	5
CYTOKINE_RECEPTOR_ACTIVITY	DEGs_Pso_vs_AD	72	23	4.95E-08	4.60E-06	3.41	CCR1; CCR2; CCR4; CCF	5
CELLULAR_RESPONSE_TO_INTERFERON_GAMMA	DEGs_Pso_&_AD	67	22	5.39E-08	4.93E-06	3.50	CCL2; CCL3; CCL5; GAP	6
REGULATION_OF_LYMPHOCYTE_MIGRATION	DEGs_Pso_&_AD	22	12	6.33E-08	5.71E-06	5.81	ADAM8; APOD; CCL2;	2
JAK_STAT_SIGNALING_PATHWAY	DEGs_Pso_&_AD	125	32	6.47E-08	5.74E-06	2.73	IRF9; IL24; CNTFR; CSF	5
POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVAT	DEGs_Pso_&_AD	43	17	6.93E-08	5.97E-06	4.21	BLM; CCL19; CCR2; CD	1
REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	DEGs_Pso_&_AD	43	17	6.93E-08	5.97E-06	4.21	ADAM8; AURKB; CCL1	2
POSITIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	DEGs_Pso_&_AD	63	21	7.84E-08	6.66E-06	3.55	ADAM8; CCL19; CCL2;	6
POSITIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STI	DEGs_Pso_&_AD	145	35	8.21E-08	6.88E-06	2.57	ADAM8; AGTR1; ALOX	12
POSITIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STI	DEGs_Pso_vs_AD	145	35	8.21E-08	6.88E-06	2.57	ADAM8; AGTR1; ALOX	12
REGULATION_OF_CYTOKINE_SECRETION	DEGs_Pso_&_AD	74	23	8.78E-08	7.25E-06	3.31	AIM2; CCL19; CCL3; CC	7
POSITIVE_REGULATION_OF_LYMPHOCYTE_MIGRATION	DEGs_Pso_&_AD	16	10	1.28E-07	1.04E-05	6.66	ADAM8; CCL3; CCL4; C	1
PEPTIDE_CROSS_LINKING	DEGs_Pso_&_AD	27	13	1.30E-07	1.04E-05	5.13	BGN; DCN; IVL; LOR; N	2
PEPTIDE_CROSS_LINKING	DEGs_Pso_vs_AD	27	13	1.30E-07	1.04E-05	5.13	BGN; DCN; IVL; LOR; N	2
G_PROTEIN_COUPLED_RECEPTOR_BINDING	DEGs_Pso_&_AD	161	37	1.41E-07	1.07E-05	2.45	ADCYAP1; ADM; ADRB	10
CCR_CHEMOKINE_RECEPTOR_BINDING	DEGs_Pso_&_AD	13	9	1.44E-07	1.07E-05	7.38	CCL19; CCL2; CCL3; CC	0
MODULATION_OF_GROWTH_OF_SYMBIONT_INVOLVED_IN	DEGs_Pso_&_AD	13	9	1.44E-07	1.07E-05	7.38	CAMP; CD36; IL10; IL1	0
NEGATIVE_REGULATION_OF_GROWTH_OF_SYMBIONT_IN_	DEGs_Pso_&_AD	13	9	1.44E-07	1.07E-05	7.38	CAMP; CD36; IL10; IL1	0
NEGATIVE_REGULATION_OF_GROWTH_OF_SYMBIONT_IN\	DEGs_Pso_&_AD	13	9	1.44E-07	1.07E-05	7.38	CAMP; CD36; IL10; IL1	0
REGULATION_OF_GROWTH_OF_SYMBIONT_IN_HOST	DEGs_Pso_&_AD	13	9	1.44E-07	1.07E-05	7.38	CAMP; CD36; IL10; IL1	0
CELLULAR_DIVALENT_INORGANIC_CATION_HOMEOSTASIS	DEGs_Pso_&_AD	213	44	2.80E-07	2.02E-05	2.20	ADCYAP1; ADM; AGTR	24
G_ALPHA_I_SIGNALLING_EVENTS	DEGs_Pso_&_AD	139	33	2.83E-07	2.02E-05	2.53	CXCL13; HRH3; CHRM2	12
SERINE_TYPE_PEPTIDASE_ACTIVITY	DEGs_Pso_&_AD	139	33	2.83E-07	2.02E-05	2.53	CFB; CFD; CTSC; ELANE	17
G_ALPHA_I_SIGNALLING_EVENTS	DEGs_Pso_vs_AD	139	33	2.83E-07	2.02E-05	2.53	CXCL13; HRH3; CHRM2	12
REGULATION_OF_T_CELL_DIFFERENTIATION	DEGs_Pso_&_AD	73	22	3.00E-07	2.12E-05	3.21	ADAM8; CARD11; CCL1	1
DIVALENT_INORGANIC_CATION_HOMEOSTASIS	DEGs_Pso_&_AD	228	46	3.17E-07	2.22E-05	2.15	ADCYAP1; ADM; AGTR	27
CHEMOKINE_SIGNALING_PATHWAY	DEGs_Pso_&_AD	173	38	3.36E-07	2.33E-05	2.34	RASGRP2; CXCL13; CCF	8
CALCIUM_ION_HOMEOSTASIS	DEGs_Pso_&_AD	216	44	4.23E-07	2.89E-05	2.17	ADCYAP1; ADM; AGTR	26
REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE_BASED_	DEGs_Pso_&_AD	80	23	4.27E-07	2.89E-05	3.06	CCL19; CCR2; CD226; C	2
IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMF	DEGs_Pso_&_AD	53	18	4.46E-07	2.98E-05	3.62	CD96; LILRB2; CD226;	3
NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	DEGs_Pso_&_AD	231	46	4.70E-07	3.10E-05	2.12	CYSLTR1; HRH3; CHRM	23
NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	DEGs_Pso_vs_AD	231	46	4.70E-07	3.10E-05	2.12	CYSLTR1; HRH3; CHRM	23
SERINE_HYDROLASE_ACTIVITY	DEGs_Pso_&_AD	142	33	4.80E-07	3.13E-05	2.48	CFB; CFD; CTSC; ELANE	17
CELLULAR_CALCIUM_ION_HOMEOSTASIS	DEGs_Pso_&_AD	203	42	4.88E-07	3.16E-05	2.21	ADCYAP1; ADM; AGTR	23
LEUKOCYTE_CHEMOTAXIS	DEGs_Pso_&_AD	82	23	6.95E-07	4.44E-05	2.99	ADAM8; AMICA1; CCL	8
REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	DEGs_Pso_&_AD	88	24	7.20E-07	4.55E-05	2.91	CCR2; CD226; CD28; C	6
POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_PROLIFE	DEGs_Pso_&_AD	15	9	8.64E-07	5.35E-05	6.40	BLM; CCR2; CD28; CD3	0
REGULATION_OF_INTERLEUKIN_12_PRODUCTION	DEGs_Pso_&_AD	40	15	8.64E-07	5.35E-05	4.00	ACP5; CCL19; CCR7; CD	2
REGULATION_OF_INTERLEUKIN_12_PRODUCTION	DEGs_Pso_vs_AD	40	15	8.64E-07	5.35E-05	4.00	ACP5; CCL19; CCR7; CD	2
CELL_CHEMOTAXIS	DEGs_Pso_&_AD	103	26	1.34E-06	8.19E-05	2.69	ADAM8; AGTR1; AMIC	12
POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	DEGs_Pso_&_AD	219	43	1.59E-06	9.67E-05	2.09	ADAM8; AGTR1; AIM2	15
EPITHELIAL_CELL_DIFFERENTIATION	DEGs_Pso_&_AD	242	46	1.84E-06	1.11E-04	2.03	AR; CNFN; DHRS9; EHF	12
REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	DEGs_Pso_&_AD	58	18	2.01E-06	1.20E-04	3.31	CCL19; CCL2; CCL3; CC	5
REGULATION_OF_ALPHA_BETA_T_CELL_PROLIFERATION	DEGs_Pso_&_AD	20	10	2.14E-06	1.26E-04	5.33	BLM; CCR2; CD28; CD3	0
CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	DEGs_Pso_&_AD	215	42	2.39E-06	1.39E-04	2.08	IRF9; IFITM3; USP18; G	17
REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIAT	DEGs_Pso_&_AD	59	18	2.66E-06	1.53E-04	3.25	CD28; CD36; DEFB103	5
REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIAT	DEGs_Pso_vs_AD	59	18	2.66E-06	1.53E-04	3.25	CD28; CD36; DEFB103	5
REGULATION_OF_CD4_POSITIVE__ALPHA_BETA_T_CELL_A	DEGs_Pso_&_AD	29	12	2.86E-06	1.63E-04	4.41	CCL19; CD80; CD83; FC	0
LEUKOCYTE_MEDIATED_IMMUNITY	DEGs_Pso_&_AD	120	28	2.99E-06	1.69E-04	2.49	BATF; BCL3; C6; C7; CC	11
POSITIVE_REGULATION_OF_T_CELL_DIFFERENTIATION	DEGs_Pso_&_AD	49	16	3.31E-06	1.84E-04	3.48	ADAM8; CCL19; CD80;	1
NEGATIVE_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PRO	DEGs_Pso_&_AD	25	11	3.43E-06	1.88E-04	4.69	AURKB; CCL19; CCL5;	2
CYTOSOLIC_CALCIUM_ION_HOMEOSTASIS	DEGs_Pso_&_AD	134	30	3.44E-06	1.88E-04	2.39	ADCYAP1; ADM; AGTR	13
CYTOSOLIC_CALCIUM_ION_HOMEOSTASIS	DEGs_Pso_vs_AD	134	30	3.44E-06	1.88E-04	2.39	ADCYAP1; ADM; AGTR	13
ELEVATION_OF_CYTOSOLIC_CALCIUM_ION_CONCENTRATI	DEGs_Pso_&_AD	121	28	3.55E-06	1.92E-04	2.47	ADCYAP1; ADM; AGTR	10
ELEVATION_OF_CYTOSOLIC_CALCIUM_ION_CONCENTRATI	DEGs_Pso_vs_AD	121	28	3.55E-06	1.92E-04	2.47	ADCYAP1; ADM; AGTR	10
POSITIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	DEGs_Pso_&_AD	50	16	4.47E-06	2.39E-04	3.41	CCL19; CCL2; CCL3; CC	5
REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	DEGs_Pso_&_AD	61	18	4.53E-06	2.40E-04	3.15	BCL3; CCR2; CCR7; CD3	4
REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	DEGs_Pso_vs_AD	61	18	4.53E-06	2.40E-04	3.15	BCL3; CCR2; CCR7; CD3	4
REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	DEGs_Pso_&_AD	97	24	4.76E-06	2.46E-04	2.64	ADAM8; CARD11; CCL1	3
POSITIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONS	DEGs_Pso_&_AD	45	15	4.85E-06	2.46E-04	3.55	CCR2; CD226; FCER1G;	2
POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMU	DEGs_Pso_&_AD	45	15	4.85E-06	2.46E-04	3.55	CD226; CRTAM; FCER1	4
POSITIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMM	DEGs_Pso_&_AD	45	15	4.85E-06	2.46E-04	3.55	CD226; CRTAM; FCER1	4
REGULATION_OF_CELL_KILLING	DEGs_Pso_&_AD	35	13	4.91E-06	2.47E-04	3.96	CD226; CRTAM; FCER2	3
REGULATION_OF_T_CELL_MIGRATION	DEGs_Pso_&_AD	14	8	5.62E-06	2.81E-04	6.09	ADAM8; APOD; CCL5;	1
REGULATION_OF_INTERLEUKIN_1_BETA_SECRETION	DEGs_Pso_&_AD	18	9	6.64E-06	3.29E-04	5.33	AIM2; CCL19; CCL3; CC	3
REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	DEGs_Pso_&_AD	159	33	6.85E-06	3.36E-04	2.21	ADAM8; CARD11; CCL1	8
CELLULAR_RESPONSE_TO_LIPID	DEGs_Pso_&_AD	196	38	8.27E-06	4.03E-04	2.07	ADCYAP1; APOE; CCL2	14
CELLULAR_RESPONSE_TO_LIPID	DEGs_Pso_vs_AD	196	38	8.27E-06	4.03E-04	2.07	ADCYAP1; APOE; CCL2	14
NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	DEGs_Pso_&_AD	113	26	8.49E-06	4.10E-04	2.45	CLEC2A; KLRF2; RAET1	8
ANCHORED_TO_MEMBRANE	DEGs_Pso_&_AD	120	27	9.08E-06	4.35E-04	2.40	ALPL; CD177; CD2; CD	13
ANCHORED_TO_MEMBRANE	DEGs_Pso_vs_AD	120	27	9.08E-06	4.35E-04	2.40	ALPL; CD177; CD2; CD	13
CYTOKINE_BINDING	DEGs_Pso_&_AD	64	18	9.59E-06	4.55E-04	3.00	CCR1; CCR2; CCR4; CCF	6
EXPRESSION_OF_IFNG_STIMULATED_GENES	DEGs_Pso_&_AD	32	12	9.72E-06	4.55E-04	4.00	IRF9; GBP5; ICAM1; IRI	4
REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	DEGs_Pso_&_AD	32	12	9.72E-06	4.55E-04	4.00	CD226; CRTAM; ICAM1	3
REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	DEGs_Pso_&_AD	70	19	9.92E-06	4.61E-04	2.89	CD226; CD28; CRTAM;	4
GLYCOSAMINOGLYCAN_BINDING	DEGs_Pso_&_AD	155	32	1.04E-05	4.77E-04	2.20	APOE; BGN; CCL2; CCL	23
GLYCOSAMINOGLYCAN_BINDING	DEGs_Pso_vs_AD	155	32	1.04E-05	4.77E-04	2.20	APOE; BGN; CCL2; CCL	23
POSITIVE_REGULATION_OF_CYTOKINE_SECRETION	DEGs_Pso_&_AD	53	16	1.04E-05	4.77E-04	3.22	AIM2; CCL19; CCL3; CD	6
DENDRITIC_CELL_CHEMOTAXIS	DEGs_Pso_&_AD	15	8	1.12E-05	5.07E-04	5.69	CCL19; CCL5; CCR1; CC	0
POSITIVE_REGULATION_OF_CD4_POSITIVE__ALPHA_BETA_	DEGs_Pso_&_AD	19	9	1.17E-05	5.26E-04	5.05	CCL19; CD80; CD83; FC	0
POSITIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONS	DEGs_Pso_&_AD	48	15	1.19E-05	5.32E-04	3.33	CCR2; CD226; FCER1G;	3
REGULATION_OF_MULTI_ORGANISM_PROCESS	DEGs_Pso_&_AD	207	39	1.29E-05	5.71E-04	2.01	AIM2; AP1S3; APOBEC	14
LYMPHOCYTE_MEDIATED_IMMUNITY	DEGs_Pso_&_AD	96	23	1.30E-05	5.73E-04	2.55	BATF; BCL3; C6; C7; CD	9
NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATIO	DEGs_Pso_&_AD	33	12	1.41E-05	6.10E-04	3.88	APOBEC3A; CCL5; HM	3
NEGATIVE_REGULATION_OF_VIRAL_REPRODUCTION	DEGs_Pso_&_AD	33	12	1.41E-05	6.10E-04	3.88	APOBEC3A; CCL5; HM	3
CARBOHYDRATE_DERIVATIVE_BINDING	DEGs_Pso_&_AD	172	34	1.52E-05	6.57E-04	2.11	APOE; BGN; CCL2; CCL	24
CARBOHYDRATE_DERIVATIVE_BINDING	DEGs_Pso_vs_AD	172	34	1.52E-05	6.57E-04	2.11	APOE; BGN; CCL2; CCL	24
LEUKOCYTE_MEDIATED_CYTOTOXICITY	DEGs_Pso_&_AD	24	10	1.65E-05	7.07E-04	4.44	CLEC2A; CRTAM; CTSC	2
PD_1_SIGNALING	DEGs_Pso_&_AD	12	7	1.74E-05	7.22E-04	6.22	CD274; LCK; PDCD1; CI	0
POSITIVE_REGULATION_OF_HUMORAL_IMMUNE_RESPON	DEGs_Pso_&_AD	12	7	1.74E-05	7.22E-04	6.22	C6; CCR7; FCER2; LTA;	1
POSITIVE_REGULATION_OF_T_CELL_MIGRATION	DEGs_Pso_&_AD	12	7	1.74E-05	7.22E-04	6.22	ADAM8; CCL5; CCR2; C	1
RESPONSE_TO_INTERFERON_BETA	DEGs_Pso_&_AD	12	7	1.74E-05	7.22E-04	6.22	AIM2; IFITM1; IFITM3;	1
REGULATION_OF_PROTEIN_SECRETION	DEGs_Pso_&_AD	118	26	1.93E-05	7.98E-04	2.35	ADAM8; AIM2; CCL19;	10
REGULATION_OF_INTERLEUKIN_1_SECRETION	DEGs_Pso_&_AD	20	9	1.96E-05	8.05E-04	4.80	AIM2; CCL19; CCL3; CC	4
HUMORAL_IMMUNE_RESPONSE	DEGs_Pso_&_AD	86	21	2.16E-05	8.80E-04	2.60	AIRE; BCL3; C6; C7; CCI	12
PPAR_SIGNALING_PATHWAY	DEGs_Pso_&_AD	62	17	2.37E-05	9.58E-04	2.92	SORBS1; CYP8B1; FABF	6
CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WAL	DEGs_Pso_&_AD	87	21	2.61E-05	1.04E-03	2.57	MERTK; SLC7A9; AMIC	3
TYPE_I_DIABETES_MELLITUS	DEGs_Pso_&_AD	35	12	2.81E-05	1.11E-03	3.65	CPE; GZMB; FASLG; IL1	3
METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	DEGs_Pso_&_AD	57	16	2.89E-05	1.14E-03	2.99	UGT2A1; ADH1B; ADH	4
POSITIVE_REGULATION_OF_ACUTE_INFLAMMATORY_RESP	DEGs_Pso_&_AD	21	9	3.18E-05	1.24E-03	4.57	ADAM8; ALOX5AP; CCI	0
POSITIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTIO	DEGs_Pso_&_AD	13	7	3.50E-05	1.35E-03	5.74	CD83; FCER1G; IL12B;	1
INTERFERON_SIGNALING	DEGs_Pso_&_AD	122	26	3.58E-05	1.35E-03	2.27	IRF9; IFITM3; USP18; G	9
AUTOIMMUNE_THYROID_DISEASE	DEGs_Pso_&_AD	17	8	3.63E-05	1.35E-03	5.02	CTLA4; GZMB; FASLG;	2
CHEMOKINE_BINDING	DEGs_Pso_&_AD	17	8	3.63E-05	1.35E-03	5.02	CCR1; CCR2; CCR4; CCF	0
DENDRITIC_CELL_MIGRATION	DEGs_Pso_&_AD	17	8	3.63E-05	1.35E-03	5.02	CCL19; CCL5; CCR1; CC	0
NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	DEGs_Pso_&_AD	17	8	3.63E-05	1.35E-03	5.02	CLEC2A; KLRF2; RAET1	2
POSITIVE_REGULATION_OF_INTERLEUKIN_1_BETA_SECRET	DEGs_Pso_&_AD	17	8	3.63E-05	1.35E-03	5.02	AIM2; CCL19; CCL3; NL	3
CYTOKINE_SECRETION	DEGs_Pso_&_AD	26	10	3.82E-05	1.40E-03	4.10	AIM2; CCL19; CCR7; KL	1
NATURAL_KILLER_CELL_ACTIVATION	DEGs_Pso_&_AD	26	10	3.82E-05	1.40E-03	4.10	CD2; IL12B; IL21R; KLR	2
REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_	DEGs_Pso_&_AD	36	12	3.88E-05	1.41E-03	3.55	CD36; FCER1G; FOXP3;	3
LYMPHOCYTE_DIFFERENTIATION	DEGs_Pso_&_AD	151	30	4.10E-05	1.47E-03	2.12	BATF; BCL3; BLM; CARI	9
MALARIA	DEGs_Pso_&_AD	47	14	4.11E-05	1.47E-03	3.18	COMP; HBA1; HBA2; H	2
POSITIVE_REGULATION_OF_JAK_STAT_CASCADE	DEGs_Pso_&_AD	47	14	4.11E-05	1.47E-03	3.18	AGAP2; CCL5; CSF2; ER	4
POSITIVE_REGULATION_OF_JAK_STAT_CASCADE	DEGs_Pso_vs_AD	47	14	4.11E-05	1.47E-03	3.18	AGAP2; CCL5; CSF2; ER	4
NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	DEGs_Pso_&_AD	166	32	4.42E-05	1.57E-03	2.05	ADCYAP1; APOD; BMP	10
POSITIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PRO	DEGs_Pso_&_AD	53	15	4.45E-05	1.58E-03	3.02	BCL3; CARD11; CCR2;	4
POSITIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATIC	DEGs_Pso_&_AD	59	16	4.62E-05	1.62E-03	2.89	ADAM8; CCL19; CD80;	3
HEPARAN_SULFATE_SULFOTRANSFERASE_ACTIVITY	DEGs_Pso_&_AD	10	6	5.37E-05	1.88E-03	6.40	HS3ST1; HS3ST2; HS3S	0
BICARBONATE_TRANSPORT	DEGs_Pso_&_AD	27	10	5.60E-05	1.92E-03	3.95	CA1; CA13; CA3; CA9;	4
REGULATION_OF_CD4_POSITIVE__ALPHA_BETA_T_CELL_D	DEGs_Pso_&_AD	27	10	5.60E-05	1.92E-03	3.95	CCL19; CD80; CD83; FC	0
PRIMARY_IMMUNODEFICIENCY	DEGs_Pso_&_AD	32	11	5.64E-05	1.92E-03	3.66	ICOS; AIRE; IL2RG; IL7R	2
REGULATION_OF_BLOOD_COAGULATION	DEGs_Pso_&_AD	54	15	5.67E-05	1.92E-03	2.96	APOE; CD36; F12; F3; F	5
REGULATION_OF_HEMOSTASIS	DEGs_Pso_&_AD	54	15	5.67E-05	1.92E-03	2.96	APOE; CD36; F12; F3; F	5
NEGATIVE_REGULATION_OF_LEUKOCYTE_ACTIVATION	DEGs_Pso_&_AD	98	22	5.74E-05	1.94E-03	2.39	CCR2; CD274; CDKN2A	6
REGULATION_OF_COAGULATION	DEGs_Pso_&_AD	60	16	5.78E-05	1.94E-03	2.84	APOE; CD36; F12; F3; F	5
POSITIVE_REGULATION_OF_INTERLEUKIN_1_SECRETION	DEGs_Pso_&_AD	18	8	6.06E-05	2.02E-03	4.74	AIM2; CCL19; CCL3; NL	4
POSITIVE_REGULATION_OF_PROTEIN_SECRETION	DEGs_Pso_&_AD	79	19	6.31E-05	2.10E-03	2.56	ADAM8; AIM2; CCL19;	9
POSITIVE_REGULATION_OF_PROTEIN_SECRETION	DEGs_Pso_vs_AD	79	19	6.31E-05	2.10E-03	2.56	ADAM8; AIM2; CCL19;	9
LYMPHOCYTE_CHEMOTAXIS	DEGs_Pso_&_AD	14	7	6.50E-05	2.15E-03	5.33	ADAM8; CCL2; CCL3; C	1
REGULATION_OF_CHEMOTAXIS	DEGs_Pso_&_AD	99	22	6.75E-05	2.21E-03	2.37	CCL19; CCL2; CCL3; CC	13
T_CELL_DIFFERENTIATION	DEGs_Pso_&_AD	99	22	6.75E-05	2.21E-03	2.37	BATF; BCL3; BLM; CARI	6
NEGATIVE_REGULATION_OF_CELL_ACTIVATION	DEGs_Pso_&_AD	106	23	7.04E-05	2.29E-03	2.31	APOE; CCR2; CD274; C	8
IMMUNOLOGICAL_SYNAPSE	DEGs_Pso_&_AD	23	9	7.57E-05	2.43E-03	4.17	CD3E; CD53; GZMA; G	0
POSITIVE_REGULATION_OF_INTERLEUKIN_1_BETA_PRODU	DEGs_Pso_&_AD	23	9	7.57E-05	2.43E-03	4.17	AIM2; CCL19; CCL3; IFI	3
REGULATION_OF_INTERLEUKIN_1_BETA_PRODUCTION	DEGs_Pso_&_AD	33	11	7.80E-05	2.48E-03	3.55	ACP5; AIM2; CCL19; C	6
REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	DEGs_Pso_&_AD	33	11	7.80E-05	2.48E-03	3.55	FOXP3; IL12B; IL12RB1	1
G_PROTEIN_COUPLED_AMINE_RECEPTOR_ACTIVITY	DEGs_Pso_&_AD	28	10	8.05E-05	2.53E-03	3.81	ADRB1; CHRM1; CHRM	2
REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE	DEGs_Pso_&_AD	50	14	8.76E-05	2.74E-03	2.98	ADAM8; ADCYAP1; AL	3
ANTIGEN_BINDING	DEGs_Pso_&_AD	39	12	9.47E-05	2.95E-03	3.28	CD48; IGHA1; IGHA2; I	5
CHEMOKINE_MEDIATED_SIGNALING_PATHWAY	DEGs_Pso_&_AD	19	8	9.70E-05	2.99E-03	4.49	CCL2; CCL5; CCR1; CCR	1
REGULATION_OF_INFLAMMATORY_RESPONSE_TO_ANTIGE	DEGs_Pso_&_AD	19	8	9.70E-05	2.99E-03	4.49	ADCYAP1; CCR7; CD28	1
CHEMOKINE_MEDIATED_SIGNALING_PATHWAY	DEGs_Pso_vs_AD	19	8	9.70E-05	2.99E-03	4.49	CCL2; CCL5; CCR1; CCR	1
REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	DEGs_Pso_&_AD	34	11	1.06E-04	3.26E-03	3.45	CCL3; CCL4; CD3E; CD8	1
REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCI	DEGs_Pso_&_AD	102	22	1.08E-04	3.30E-03	2.30	ADCYAP1; ADM; ADRB	9
DENDRITIC_CELL_DIFFERENTIATION	DEGs_Pso_&_AD	11	6	1.10E-04	3.34E-03	5.81	BATF3; CCL19; CCR7; C	1
NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	DEGs_Pso_&_AD	51	14	1.11E-04	3.35E-03	2.93	ADCYAP1; CCR2; FOXP	1
POSITIVE_REGULATION_OF_CELL_KILLING	DEGs_Pso_&_AD	29	10	1.13E-04	3.39E-03	3.68	CD226; CRTAM; FCER2	3
POSITIVE_REGULATION_OF_INTERFERON_GAMMA_PRODU	DEGs_Pso_&_AD	29	10	1.13E-04	3.39E-03	3.68	BCL3; CCR2; CD3E; IL1	1
POSITIVE_REGULATION_OF_INTERFERON_GAMMA_PRODU	DEGs_Pso_vs_AD	29	10	1.13E-04	3.39E-03	3.68	BCL3; CCR2; CD3E; IL1	1
NEGATIVE_REGULATION_OF_REPRODUCTIVE_PROCESS	DEGs_Pso_&_AD	76	18	1.18E-04	3.51E-03	2.52	APOBEC3A; CCL3; CCL	6
PEPTIDASE_INHIBITOR_ACTIVITY	DEGs_Pso_&_AD	138	27	1.23E-04	3.65E-03	2.09	BIRC5; CST7; CSTB; OV	16
PEPTIDASE_INHIBITOR_ACTIVITY	DEGs_Pso_vs_AD	138	27	1.23E-04	3.65E-03	2.09	BIRC5; CST7; CSTB; OV	16
REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	DEGs_Pso_&_AD	83	19	1.29E-04	3.79E-03	2.44	BCL3; CARD11; CCR2;	7
REGULATION_OF_NEUROLOGICAL_SYSTEM_PROCESS	DEGs_Pso_vs_AD	199	35	1.45E-04	4.24E-03	1.87	ADCYAP1; APOE; ARC;	18
CHEMOKINE_RECEPTOR_ACTIVITY	DEGs_Pso_&_AD	20	8	1.50E-04	4.28E-03	4.26	CCR1; CCR2; CCR4; CCF	2
G_PROTEIN_COUPLED_CHEMOATTRACTANT_RECEPTOR_A	DEGs_Pso_&_AD	20	8	1.50E-04	4.28E-03	4.26	CCR1; CCR2; CCR4; CCF	2
LYMPHOCYTE_MIGRATION	DEGs_Pso_&_AD	20	8	1.50E-04	4.28E-03	4.26	ADAM8; CCL2; CCL3; C	2
POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INV	DEGs_Pso_&_AD	20	8	1.50E-04	4.28E-03	4.26	CD36; FCER1G; NOD2;	1
REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	DEGs_Pso_&_AD	20	8	1.50E-04	4.28E-03	4.26	CCL19; CCR2; CD80; IL	0
CHEMOKINE_RECEPTOR_ACTIVITY	DEGs_Pso_vs_AD	20	8	1.50E-04	4.28E-03	4.26	CCR1; CCR2; CCR4; CCF	2
G_PROTEIN_COUPLED_CHEMOATTRACTANT_RECEPTOR_A	DEGs_Pso_vs_AD	20	8	1.50E-04	4.28E-03	4.26	CCR1; CCR2; CCR4; CCF	2
REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	DEGs_Pso_vs_AD	20	8	1.50E-04	4.28E-03	4.26	CCL19; CCR2; CD80; IL	0
FATTY_ACID_BINDING	DEGs_Pso_&_AD	25	9	1.62E-04	4.56E-03	3.84	ALB; ALOX5AP; APOC1	1
POSITIVE_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	DEGs_Pso_&_AD	25	9	1.62E-04	4.56E-03	3.84	AIM2; CCL19; CCL3; IFI	4
CELL_RECOGNITION	DEGs_Pso_&_AD	65	16	1.63E-04	4.56E-03	2.62	CCL19; CCR7; CD226;	9
REGULATION_OF_JAK_STAT_CASCADE	DEGs_Pso_&_AD	65	16	1.63E-04	4.56E-03	2.62	AGAP2; CCL5; CDK5R1;	4
REGULATION_OF_TUMOR_NECROSIS_FACTOR_PRODUCTIC	DEGs_Pso_&_AD	65	16	1.63E-04	4.56E-03	2.62	ACP5; BCL3; CCL19; CC	6
CARGO_RECEPTOR_ACTIVITY	DEGs_Pso_&_AD	59	15	1.71E-04	4.73E-03	2.71	CD36; CD5L; CD6; HPN	4
DRUG_METABOLISM___CYTOCHROME_P450	DEGs_Pso_&_AD	59	15	1.71E-04	4.73E-03	2.71	UGT2A1; ADH1B; ADH	7
IRON_ION_BINDING	DEGs_Pso_&_AD	141	27	1.79E-04	4.92E-03	2.04	ACP5; CH25H; CYP1A1	20
IRON_ION_BINDING	DEGs_Pso_vs_AD	141	27	1.79E-04	4.92E-03	2.04	ACP5; CH25H; CYP1A1	20
DEFENSE_RESPONSE_TO_GRAM_NEGATIVE_BACTERIUM	DEGs_Pso_&_AD	16	7	1.87E-04	5.02E-03	4.66	CAMP; IL12B; IL6; NOS	1
MAST_CELL_ACTIVATION	DEGs_Pso_&_AD	16	7	1.87E-04	5.02E-03	4.66	CD48; FCER1G; LAT2; L	2
NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPON	DEGs_Pso_&_AD	16	7	1.87E-04	5.02E-03	4.66	FOXP3; IL7R; LILRB1; N	0
POSITIVE_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PRO	DEGs_Pso_&_AD	16	7	1.87E-04	5.02E-03	4.66	ADAM8; CCL5; CDKN2A	0
REGULATION_OF_INTERLEUKIN_1_PRODUCTION	DEGs_Pso_&_AD	36	11	1.90E-04	5.06E-03	3.26	ACP5; AIM2; CCL19; C	7
C_C_CHEMOKINE_BINDING	DEGs_Pso_&_AD	12	6	2.06E-04	5.34E-03	5.33	CCR1; CCR2; CCR4; CCF	0
DEFENSE_RESPONSE_TO_PROTOZOAN	DEGs_Pso_&_AD	12	6	2.06E-04	5.34E-03	5.33	BATF; BCL3; CLEC7A; IL	0
NEGATIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTIC	DEGs_Pso_&_AD	12	6	2.06E-04	5.34E-03	5.33	ACP5; IL10; JAK3; NOD	1
NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMM	DEGs_Pso_&_AD	12	6	2.06E-04	5.34E-03	5.33	FOXP3; IL7R; LILRB1; N	0
NEGATIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IM	DEGs_Pso_&_AD	12	6	2.06E-04	5.34E-03	5.33	FOXP3; IL7R; LILRB1; N	0
POSITIVE_REGULATION_OF_PROTEIN_PROCESSING	DEGs_Pso_&_AD	12	6	2.06E-04	5.34E-03	5.33	ADAM8; C6; CLEC3B; C	2
NEGATIVE_REGULATION_OF_LYMPHOCYTE_ACTIVATION	DEGs_Pso_&_AD	86	19	2.12E-04	5.45E-03	2.36	CD274; CDKN2A; CTLA	5
REGULATION_OF_IMMUNOGLOBULIN_MEDIATED_IMMUN	DEGs_Pso_&_AD	31	10	2.14E-04	5.45E-03	3.44	CD226; CD28; FCER1G;	1
LYMPHOCYTE_COSTIMULATION	DEGs_Pso_&_AD	54	14	2.17E-04	5.45E-03	2.76	CARD11; CCL19; CD24	2
PROTEIN_SECRETION	DEGs_Pso_&_AD	54	14	2.17E-04	5.45E-03	2.76	AIM2; CBLN4; CCL19;	2
T_CELL_COSTIMULATION	DEGs_Pso_&_AD	54	14	2.17E-04	5.45E-03	2.76	CARD11; CCL19; CD24	2
INTERFERON_GAMMA_MEDIATED_SIGNALING_PATHWAY	DEGs_Pso_&_AD	48	13	2.17E-04	5.45E-03	2.89	ICAM1; IRF1; IRF7; IRF	4
MONOCARBOXYLIC_ACID_BINDING	DEGs_Pso_&_AD	48	13	2.17E-04	5.45E-03	2.89	ALB; ALOX5AP; APOC1	3
REGULATION_OF_VIRAL_GENOME_REPLICATION	DEGs_Pso_&_AD	48	13	2.17E-04	5.45E-03	2.89	APOBEC3A; CCL5; CD2	5
REGULATION_OF_WOUND_HEALING	DEGs_Pso_&_AD	73	17	2.20E-04	5.50E-03	2.48	APOE; CD36; F12; F3; F	6
POSITIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPH	DEGs_Pso_&_AD	114	23	2.25E-04	5.60E-03	2.15	AFAP1L2; CCK; CCL5; C	6
POSITIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPH	DEGs_Pso_vs_AD	114	23	2.25E-04	5.60E-03	2.15	AFAP1L2; CCK; CCL5; C	6
POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTO	DEGs_Pso_&_AD	26	9	2.29E-04	5.67E-03	3.69	CD226; CRTAM; IL12B;	3
REGULATION_OF_B_CELL_ACTIVATION	DEGs_Pso_&_AD	80	18	2.37E-04	5.84E-03	2.40	CARD11; CD28; CD38;	7
POSITIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	DEGs_Pso_&_AD	87	19	2.49E-04	6.11E-03	2.33	ADAM8; CCL19; CCR1;	6
POSITIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	DEGs_Pso_vs_AD	87	19	2.49E-04	6.11E-03	2.33	ADAM8; CCL19; CCR1;	6
ANION_TRANSPORT	DEGs_Pso_vs_AD	268	43	2.51E-04	6.14E-03	1.71	ABCB11; ALB; APBA1;	26
POSITIVE_REGULATION_OF_CHEMOTAXIS	DEGs_Pso_&_AD	74	17	2.62E-04	6.39E-03	2.45	CCL19; CCL2; CCL3; CC	9
POSITIVE_REGULATION_OF_CHEMOTAXIS	DEGs_Pso_vs_AD	74	17	2.62E-04	6.39E-03	2.45	CCL19; CCL2; CCL3; CC	9
REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	DEGs_Pso_&_AD	32	10	2.88E-04	6.98E-03	3.33	CD226; CD28; FCER1G;	1
HEPARIN_BINDING	DEGs_Pso_&_AD	116	23	2.94E-04	7.04E-03	2.11	APOE; CCL2; CCL7; CCL	18
HEPARIN_BINDING	DEGs_Pso_vs_AD	116	23	2.94E-04	7.04E-03	2.11	APOE; CCL2; CCL7; CCL	18
ACETYLCHOLINE_RECEPTOR_ACTIVITY	DEGs_Pso_&_AD	17	7	2.96E-04	7.04E-03	4.39	CHRM1; CHRM2; CHRN	0
POSITIVE_REGULATION_OF_CD4_POSITIVE__ALPHA_BETA_	DEGs_Pso_&_AD	17	7	2.96E-04	7.04E-03	4.39	CCL19; CD80; CD83; FC	0
REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICITY	DEGs_Pso_&_AD	17	7	2.96E-04	7.04E-03	4.39	IL12B; IL12RB1; IL7R; L	1
SULFUR_COMPOUND_BINDING	DEGs_Pso_vs_AD	153	28	3.08E-04	7.29E-03	1.95	APOE; CCL2; CCL7; CCL	24
AMINE_LIGAND_BINDING_RECEPTORS	DEGs_Pso_&_AD	27	9	3.18E-04	7.50E-03	3.55	HRH3; CHRM1; CHRM2	2
ALLOGRAFT_REJECTION	DEGs_Pso_&_AD	22	8	3.27E-04	7.59E-03	3.88	GZMB; FASLG; IL10; IL1	2
GLUTATHIONE_TRANSFERASE_ACTIVITY	DEGs_Pso_&_AD	22	8	3.27E-04	7.59E-03	3.88	ALOX5AP; GSTM2; GST	2
POSITIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALI	DEGs_Pso_&_AD	22	8	3.27E-04	7.59E-03	3.88	CCL3; CCL4; CD3E; CD8	0
POSITIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTIO	DEGs_Pso_&_AD	22	8	3.27E-04	7.59E-03	3.88	CCL19; CCR7; CD36; ID	0
JAK_STAT_CASCADE	DEGs_Pso_&_AD	44	12	3.39E-04	7.84E-03	2.91	CCL2; CCR2; EGF; JAK3	3
POSITIVE_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	DEGs_Pso_&_AD	13	6	3.56E-04	8.18E-03	4.92	CD226; FCER1G; FCER2	1
POSITIVE_REGULATION_OF_IMMUNOGLOBULIN_MEDIATE	DEGs_Pso_&_AD	13	6	3.56E-04	8.18E-03	4.92	CD226; FCER1G; FCER2	1
ALPHA_BETA_T_CELL_DIFFERENTIATION	DEGs_Pso_&_AD	33	10	3.81E-04	8.68E-03	3.23	BATF; BCL3; BLM; FOXI	2

; 23A; PDGFC; CCL1; CCL3L1; CCL13; CXCL1; CXCL12; BMP4; BMPR1B; TNFSF11; TNFSF12; TNFSF9; CD70
; 23A; PDGFC; CCL1; CCL3L1; CCL13; CXCL1; CXCL12; BMP4; BMPR1B; TNFSF11; TNFSF12; TNFSF9; CD70
; 23A; PDGFC; CCL1; CCL3L1; CCL13; CXCL1; CXCL12; BMP4; BMPR1B; TNFSF11; TNFSF12; TNFSF9; CD70
L13; IL17A; IL17F; IL1B; IL23A; IL33; IL34RN; IL9; NDP; TNFSF11; TNFSF12; TNFSF9
L13; IL17A; IL17F; IL1B; IL23A; IL33; IL34RN; IL9; NDP; TNFSF11; TNFSF12; TNFSF9
L13; IL17A; IL17F; IL1B; IL23A; IL33; IL34RN; IL9; NDP; TNFSF11; TNFSF12; TNFSF9

I; MMP7; NR1D1; PGLYRP4; PLA2G2A; PTGER2; PTGER3; RARA; REN; SFTPC; SOD2; STAT1
RTN4RL2; SCNN1G; SLC2A4; THBS1; THY1; VTCN1

MCSR; MTMR14; NT5; OXTR; PTGDR; PTGER2; PTGER3; RLN2; CCL3L1; CXCL5; CXCL12; TACR3; GAL R2; CCKBR; P2RY14
MCSR; MTMR14; NT5; OXTR; PTGDR; PTGER2; PTGER3; RLN2; CCL3L1; CXCL5; CXCL12; TACR3; GAL R2; CCKBR; P2RY14
FFAR4; CXCR2; MCSR; MTMR14; NT5; OXTR; PTGDR; PTGER2; PTGER3; RLN2; CCL3L1; CXCL5; CXCL12; TACR3; WNT7B; WNT9A; FZD5; GAL R2; CCKBR; GABBR2; P2RY14
FFAR4; CXCR2; MCSR; MTMR14; NT5; OXTR; PTGDR; PTGER2; PTGER3; RLN2; CCL3L1; CXCL5; CXCL12; TACR3; WNT7B; WNT9A; FZD5; GAL R2; CCKBR; GABBR2; P2RY14

REN; SFTPC; SOD2; STAT1
IARA; REN; SFTPC; SOD2; STAT1

MGFV; PLA2G2A; PTGER3; PTGIS; TLR7; TNFSF11
MGFV; PLA2G2A; PTGER3; PTGIS; TLR7; TNFSF11

VFSK14; PGLYRP4; RARA; SFRP1; SOX11; TBX21; THY1; TNFSF11; VNN1; VTCN1

I1; MAP3K14; RARA; TBX21; THBS1; THY1; TNFSF11; VNN1

'; IL1B; IL23A; IL23R; IL36RN; IL9; ITGB3; LIFR; NTF3; STAT1; TNFSF11; TNFSF12; TNFSF9
'; IL1B; IL23A; IL23R; IL36RN; IL9; ITGB3; LIFR; NTF3; STAT1; TNFSF11; TNFSF12; TNFSF9
'; IL1B; IL23A; IL23R; IL36RN; IL9; ITGB3; LIFR; NTF3; STAT1; TNFSF11; TNFSF12; TNFSF9

I1; MAP3K14; RARA; TBX21; THBS1; THY1; TNFSF11; VNN1

GAL R2; CCKBR
GAL R2; CCKBR
IFI1; GPR17; IFIT1; IFNG; IL13RA2; IL1B; IL23R; IL31RA; IRAK3; KRT18; LIFR; STAT1; TNFSF11
IP4; RARA; RBP4; TBX21; TRIL

I1; VNN1; VTCN1
I1

.33; IGJ; KLHL1; LURAP1; RARA; SULF1; SULF2; THBS1; TLR7; TWIST1
.33; IGJ; KLHL1; LURAP1; RARA; SULF1; SULF2; THBS1; TLR7; TWIST1

TBX21; THY1; TNFSF11; VNN1

$3; LILDAM; RET; SLC7A11; TBX21; TNFSF11
$3; LILDAM; RET; SLC7A11; TBX21; TNFSF11

SUIT2; THBS1; TH8S4; TLR7; TNFSF11
SUIT2; THBS1; TH8S4; TLR7; TNFSF11

NT7B; WNT9A

IAJ; JPH2; OXTR; PTGER3; SLC8A3; TRPV4
CLS; CXCL12; GAL R2; GABBR2; P2RY14

CLS; CXCL12; GAL R2; GABBR2; P2RY14

;; EDN2; GAL R2; JPH2; OXTR; PTGER3; SLC8A3; TRPV4
; LS2; STAT1
;; EDN2; GAL R2; JPH2; OXTR; PTGER3; SLC8A3; TRPV4

8A2; GRIK3; GRIN2A; MCSR; MTMR14; NT5; OXTR; PTGDR; PTGER2; PTGER3; TACR3; VIPR1; GAL R2; CCKBR; GABBR2; P2RY14
8A2; GRIK3; GRIN2A; MCSR; MTMR14; NT5; OXTR; PTGDR; PTGER2; PTGER3; TACR3; VIPR1; GAL R2; CCKBR; GABBR2; P2RY14

IAJ; JPH2; OXTR; PTGER3; SLC8A3; TRPV4

TLR7; TNFSF11; TBIL
I; MES1P1; MS1; SPOX7; SFRP4; TNMD; WNT7B

DBA3; TRPV4
DBA3; TRPV4
PX4
PX4

P1; TES1; TNFSF11; VNN1
1DR; PTGER2; RARA; RET; SFRP1; STAT1; STRA8; TES1; WNT7B; WNT9A
1DR; PTGER2; RARA; RET; SFRP1; STAT1; STRA8; TES1; WNT7B; WNT9A

G2; PSCA; RGMA; RTN4RL2; THY1; VNN1; VNN2
G2; PSCA; RGMA; RTN4RL2; THY1; VNN1; VNN2

; LAMC2; LYVE1; PCOLCE2; PGLYRP4; POSTN; PRELP; RSPO4; SFRP1; SUIT2; TH8S1; TH8S4; TNFAIP6; TNN
; LAMC2; LYVE1; PCOLCE2; PGLYRP4; POSTN; PRELP; RSPO4; SFRP1; SUIT2; TH8S1; TH8S4; TNFAIP6; TNN

1; ITGAM; LILDAM; LAMC2; LYVE1; PCOLCE2; PGLYRP4; POSTN; PRELP; RSPO4; SFRP1; SUIT2; ST8SIA2; TH8S1; TH8S4; TNFAIP6; TNN
1; ITGAM; LILDAM; LAMC2; LYVE1; PCOLCE2; PGLYRP4; POSTN; PRELP; RSPO4; SFRP1; SUIT2; ST8SIA2; TH8S1; TH8S4; TNFAIP6; TNN

H8S1; THY1; VTCN1

7; SLPI; TFPI2; TIMP1; WFDC2; WFDC3
7; SLPI; TFPI2; TIMP1; WFDC2; WFDC3

RHX2; GRIN2A; IFNG; NR3IN1; NTF3; NTRK2; OXTR; RNS1; RXRG; SLC6A1

I; CYP4B1; CYP4F2; CYP4Z1; CYP4Z2P; FADS2F1; MB; MFI2; PTGIS
I; CYP4B1; CYP4F2; CYP4Z1; CYP4Z2P; FADS2F1; MB; MFI2; PTGIS

3; NTF3; SRCIN1; TGFA; TH8S4
3; NTF3; SRCIN1; TGFA; TH8S4

SLC1A2; SLC1A6; SLC22A16; SLC23A2; SLC26A2; SLC26A4; SLC26A7; SLC34A2; SLC40A1; SLC4A4; SLC5A5; SLC6A1; SLC6A20; SLC7A11; SLCO2A1; SLCO3A1; SLCO4C1

2; POSTN; PRELP; RSPO4; SFRP1; SUIT2; TH8S1; TH8S4; TNN
2; POSTN; PRELP; RSPO4; SFRP1; SUIT2; TH8S1; TH8S4; TNN

GPC6; ITGAM; LAMC2; PCOLCE2; POSTN; PRELP; RSPO4; SFRP1; SUIT2; TH8S1; TH8S4; TNN