SUPPLEMENTARY MATERIALS AND METHODS:

Study subjects and skin samples

Skin biopsies were obtained from 11 volunteers under a protocol approved by The Rockefeller University’s Institutional Review Board. Written, informed consent was obtained from all subjects and the study adhered to the Declaration of Helsinki Principles. All volunteers underwent a rigorous screening process, including medical history, physical examination, complete blood count/blood chemistries, and point-of-care HIV test to ensure they were overall healthy and not on any medication which could interfere with immune reactions. Each volunteer was sensitized to 0.4% DPCP (in a topical gel formulation) on his/her right upper arm and 0.04% DPCP on his/her left lower arm. These concentrations were chosen to ensure effective sensitization while minimizing uncomfortable inflammatory reactions on the arms. Previous work has demonstrated that 0.4% but not 0.04% DPCP is consistently able to induce sensitization in immunocompetent individuals.\(\text{(Levis et al., 2006)}\) Two weeks later, effective sensitization was confirmed by noting induration at the application sites (all subjects were successfully sensitized) and then two challenge applications of 0.04% DPCP were applied to the subject’s left upper thigh. Also at this visit, two placebo applications (identical formulation but without DPCP) were applied to the subject’s right upper thigh. Each application of placebo or DPCP gel was 0.2 mL (80 µg for the 0.04% concentration) placed on a 2.5 x 2.5 cm square area bandage which the subject was instructed to leave on for 24 hours before removal and washing. Three days after these challenge applications, one 6 mm full thickness punch biopsy was taken of a DPCP-treated site and an identical biopsy was taken of a placebo-treated site (day 3 biopsies). Subjects were then observed at 7 and 14 days post-challenge to determine when the DPCP-
induced inflammation was resolving, based on clinical scoring of erythema and induration. At that time (14 days post-challenge), another pair of biopsies was taken, but of the two sites not biopsied at 3 days post-challenge (Figure S1). Six of 11 volunteers were brought back 4-8 months after challenge application for another biopsy of a DPCP-treated site, which clinically no longer exhibited any signs of inflammation. Ultrasound images were acquired using DermaScan C ultrasound scanner (Cortex Technology, Hadsund, Denmark). In these images, dermal inflammation is visualized as a dark zone (brackets) under epidermis and the thickness of this zone correlates with the extent of inflammation/induration. (Kelly et al., 1998) (Hoffmann et al., 1994)

**RNA extraction, quantification, and microarray**

Total RNA was extracted using the miRNeasy Mini Kit (Qiagen, Valencia, CA) according to the manufacturer’s protocol with on-column DNase digestion. The amount of RNA was assessed by NanoDrop 1000 spectrophotometer (Thermo Fisher Scientific Inc., Wilmington, DE). The quality of extracted RNA was examined using Agilent Bioanalyzer 2100 (Agilent Technologies, Palo Alto, CA). RNA was hybridized to HGU133 Plus 2.0 chips (Affymetrix, Santa Clara, CA) to measure relative gene expression.

**Statistical analysis**

Microarray data were analyzed using R/Bioconductor packages (http://www.r-project.org). The Harshlight package (Suárez-Fariñas et al., 2005) was used to scan Affymetrix chips for spatial artifacts. Expression values were obtained using the GCRMA algorithm. Genes with low variation and low expression in most samples were filtered out prior to the analysis. Batch effect
due to hybridization date was adjusted using ComBat. (Johnson et al., 2007) Principal Components Analysis (PCA) was used to represent the high dimensionality of the data along the directions of maximal variance. To identify differentially expressed genes, we fit a mixed effect model with treatment (placebo/DPCP) and day (3/14) as fixed effects and a random intercept for each patient. Hypotheses of interest were tested using contrasts in R’s limma package framework. The p values resultant from the moderated paired Student’s t-tests were adjusted for multiple hypotheses using the Benjamini-Hochberg procedure, which controls for the false discovery rate. The data discussed in this publication have been deposited in the National Center for Biotechnology Information’s Gene Expression Omnibus (GSE accession number GSE52360, http://www.ncbi.nlm.nih.gov/geo/). Ingenuity Pathway Analysis (www.ingenuity.com) was used to determine canonical pathways significantly linked to various gene sets.

**Quantitative RT-PCR**

Pre-amplification quantitative RT-PCR technique was used for measuring various genes in total RNA extracted from skin biopsy samples according to the company’s instructions. Briefly, 5 ng of total RNA was subjected to first-strand cDNA synthesis using High Capacity cDNA Reverse Transcription kits (Applied Biosystems, Carlsbad, CA). The resulting cDNA was subjected to 14 cycles of pre-amplification using TaqMan PreAmp Master Mix Kit (Applied Biosystems) with desired pooled assay mix. The Gene Amp PCR System 9700 (Applied Biosystems) was used for the pre-amplification reaction with the following thermal cycler conditions: 10 min at 95°C and 14 cycles of 15 seconds at 95°C followed by 4 min at 60°C. 12.5 µl of pre-amplified cDNA was then used for quantitative RT-PCR reaction using TaqMan Gene Expression Master Mix (Applied Biosystems). The 7900HT Fast Real-Time PCR System was used for PCR
reactions, and the thermal cycler conditions were as follows: 2 minutes at 50°C, 5 minutes at 95°C, and 40 cycles of 15 seconds at 95°C followed by 60 seconds at 60°C. Data were analyzed by the Applied Biosystems PRISM 7700 software (Sequence Detection Systems, ver. 1.7) and normalized to human acidic ribosomal protein (hARP) housekeeping gene. All assays were from Applied Biosystems and inventoried assays used in this study were as follows: IFNG (Hs00989291_m1), IL2 (Hs00174114_m1), IL2RA (Hs00907779_m1), IL13 (Hs00174379_m1), IL9 (Hs00914237_m1), IL17A (Hs00174383_m1), IL22 (Hs01574154_m1), Foxp3 (Hs01085834_m1), IL10 (Hs00961622_m1), CTLA4 (Hs03044418_m1), PDCD1 (PD1) (Hs01550088_m1), CD274 (PDL1) (Hs01125301_m1), PDCD1LG2 (PDL2) (Hs01057777_m1), IDO1 (Hs00984148_m1), and LAG3 (Hs00158563_m1). For RPLP0/hARP, a custom primer/probe set was used (Forward: CGCTGCTGAACATGCTCAA, Reverse: TGTCGAACACCTGCTGGATG, Probe: 6-FAM-TCCCCCTTCTCCTTTGGCTGG-TAMRA).

**Immunohistochemistry**

Frozen sections of skin biopsies were dried at room temperature and then fixed for 2 minutes in acetone. Next, the samples were blocked with 10% normal serum of the species in which the secondary antibody was made and then the samples were incubated overnight at 4°C with the appropriate primary antibody. Biotin-labeled secondary antibodies (Vector Laboratories, Burlingame, CA) were amplified with avidin-biotin complex (Vector Laboratories) and developed with chromogen 3-amino-9-ethylcarbazole (Sigma Aldrich, St. Louis, MO) to produce a red color indicative of positive staining. The number of positive cells per mm was counted.
manually per field using computer-assisted image analysis (NIH Image 6.1; http://rsb.info.nih.gov/nih-image).

Primary antibodies used in this study are as follows (all are mouse monoclonal unless stated otherwise): CD3 (BD Biosciences, Clone SK7, IgG1, 1:100 dilution), CD8 (BD Biosciences, Clone HIT8a, IgG1, 1:100), CD11c (BD Biosciences, Clone B-ly6, IgG1, 1:100), DC-LAMP (Beckman Coulter, Clone 104.G4, IgG1, 1:50), Langerin (Beckman Coulter, Clone DCGM4, IgG1, 1:100), Foxp3 (Abcam, Clone 236A/E7, IgG1, 1:20), Granulysin (Acris Antibodies, Clone B-R32, IgG2b, 1:100), XCR1 (rabbit polyclonal, LifeSpan Biosciences, Inc., IgG, 1:100).

**Immunofluorescence**

Frozen sections of skin biopsies were dried at room temperature and then fixed with acetone. Next, the samples were blocked with 10% normal goat serum (Vector Laboratories) for 30 minutes. Primary antibody was incubated overnight at 4°C and amplified with the appropriate secondary antibody for 30 minutes. For co-localization, sections were then co-stained overnight with a second antibody, and amplified with the appropriate secondary antibody for 30 minutes. Images were acquired using the appropriate filters of a Zeiss Axioplan 2 wide-field fluorescence microscope (Thornwood, NY) with a Plan Neofluar 20 × 0.7 numerical aperture lens and a Hamamatsu Orca Er-cooled charge-coupled device camera (Bridgewater, NJ), controlled by METAVUE software (MDS Analytical Technologies, Downington, PA). 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 co-express 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.
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**Figure S1.** Schematic of DPCP sensitization and challenge schedule. Subjects were sensitized with DPCP at two sites on their arms at Day 0 followed by challenge and placebo applications at Day 14. At Day 17 (3 days post-challenge), one pair of biopsies was taken and a second pair was taken at Day 28 (14 days post-challenge) when the inflammation induced by DPCP was seen to be clinically resolving. Dark green, light green, and blue squares indicate sensitization, challenge, and placebo applications, respectively. A red X is used to represent a biopsy taken.
Figure S2. DPCP day 14 reactions include many unique genes and XCR1+ DCs not present in day 3 reactions. (a) Venn diagram showing up- and down-regulated probesets (red and green, respectively) in day 3 and day 14 reactions. (b) Immunohistochemistry for XCR1 and (c) immunofluorescence for XCR1 (red)/CD11c (green) on representative placebo-treated (left), DPCP day 3 (middle) and DPCP day 14 (right) samples. Scale bar = 100 µm.
Figure S3. Granulysin co-localizes with CD3+ (both CD8+ and CD8−) and CD11c+ cells.

Immunofluorescence staining of granulysin with (a) CD3 (green), (b) CD8 (red), and (c) CD11c (red). Left panels are placebo-treated samples, middle panels and DPCP day 3 samples, and right panels are DPCP day 14 samples. Shown is a representative subject (subject 013). Scale bar = 100 µm.
Figure S4. Correlations of immunohistochemistry cell counts with immune activation markers by RT-PCR. Shown are scatter plots of (a) CD3+ and (b) CD11c+ cell counts with normalized gene expression measures of IFNγ (top), IL-2 (middle), and IL-2RA (bottom). Only DPCP day 3 and day 14 samples are plotted. *p*-values for all correlations were >0.27 so none reached statistical significance.
Figure S5. RT-PCR and histological analysis of subjects whose CD3+ or CD11c+ infiltrates decrease from 3 days to 14 days post-DPCP challenge (subgroup B, n=6). (a) RT-PCR analysis for IFNγ (left panel), IL-2 (middle panel), and IL-2RA (right panel). Shown are normalized
expression values for each subject individually to highlight that almost all samples have decreased expression of these genes at day 14 compared to day 3. (b-f) H&E (b) and immunohistochemical analysis of samples for (c) CD3, (d) CD11c, (e) DC-LAMP, and (f) Langerin. For all histological images, left panels show placebo reactions, middle panels show DPCP day 3 reactions, and right panels show DPCP day 14 reactions. Shown is a representative subject (subject 015). For immunohistochemical stains, line graphs indicate subgroup-wide average cell counts for placebo, DPCP day 3, DPCP day 14, and DPCP late samples. Asterisks indicate $p<0.05$ when compared to placebo. Scale bar = 100 µm.
Figure S6. Subjects in subgroup B globally have more negative regulatory genes at day 3 than subjects in subgroup A. Heat map of negative regulatory genes for all DPCP samples. Each column represents one sample arranged first by subgroup then by sample type with there being 5 subjects in subgroup A and 6 in subgroup B. DPCP day 3 samples are highlighted as underneath the black bars.
Figure S7. Subjects in subgroup B show resolution of clinical inflammation more quickly than subjects in subgroup A. Plots of ultrasound measurements of extents of inflammatory reactions as reflected by dermal thickness (see Figure 1) versus time for subjects in subgroup A (top) and subjects in subgroup B (bottom). Each subject is shown as an individual line.
**Figure S8.** Comparison of DPCP day 3 vs placebo day 3 reactions to PPD 48 hr vs 6 hr reactions (data from (Tomlinson et al., 2011)). Venn diagram shows 1,187, 780, and 1,017 upregulated genes uniquely in DPCP, in both DPCP and PPD, and uniquely in PPD, respectively (downregulated gene numbers are 1,690, 24, and 112). Tables underneath Venn diagram show selected genes from each section of the Venn diagram.
**Supplemental Table 1.** Demographics and clinical scoring of inflammatory reactions induced by DPCP in all subjects (n=11)

| Subject ID | Gender | Age | Race | Subgroup | day 3 \(^1\) | day 14 \(^1\) | Score | Score |
|------------|--------|-----|------|----------|----------|---------|-------|-------|
| 001        | M      | 55  | White| B        | 4/4 (1.19)| 2/1 (0.20) | 8     | 3     |
| 006        | M      | 52  | Black| A        | 2/2 (0.30)| 0/1 (0.18) | 4     | 1     |
| 008        | F      | 42  | Asian| B        | 3/2 (0.66)| 1/1 (0.19) | 5     | 2     |
| 009        | M      | 58  | White| B        | 2/2 (0.21)| 1/0 (0.18) | 4     | 1     |
| 012        | M      | 44  | White| A        | 3/2 (0.30)| 2/1 (0.10) | 5     | 3     |
| 013        | F      | 46  | Black| A        | 3/3 (0.76)| 2/1 (0.36) | 6     | 3     |
| 014        | M      | 20  | Asian| A        | 3/3 (0.36)| 2/0 (0.15) | 6     | 2     |
| 015        | M      | 55  | Black| B        | 2/2 (0.21)| 1/0 (0.12) | 4     | 1     |
| 016        | F      | 29  | Black| A        | 3/1 (0.24)| 1/0 (0.18) | 4     | 1     |
| 020        | M      | 43  | Black| B        | 3/3 (0.87)| 1/1 (0.24) | 6     | 2     |
| 021        | M      | 40  | Black| B        | 4/4 (1.51)| 2/2 (0.24) | 8     | 4     |

**Average**

5.5 2.1

\( p = 7.8 \times 10^{-8} \) for DPCP day 3 vs day 14 score comparison (paired two-tailed Student's \( t \)-test).

\(^1\)Erythema/induration (0-4 scale for each) - scores are sums of these two measures. In parentheses are the quantifications of the extent of inflammation as measured by ultrasound (in mm, see Figure 1).
**Supplemental Table 2.** Expression of negative regulator genes in DPCP day 3 vs. placebo samples

| Probe     | Symbol | Description                                                                 | FCH  | p        | FDR   |
|-----------|--------|-----------------------------------------------------------------------------|------|----------|-------|
| 207526_s_at | IL1RL1 | interleukin 1 receptor-like 1                                               | 42.8 | 5.3E-11  | 2.1E-09 |
| 227458_at  | CD274  | CD274 molecule                                                             | 34.6 | 1.9E-12  | 1.3E-10 |
| 236341_at  | CTLA4  | associated protein 4                                                        | 21.6 | 3.7E-11  | 1.5E-09 |
| 207238_s_at | PTPRC  | receptor type, C                                                            | 18.0 | 1.6E-12  | 1.2E-10 |
| 206341_at  | IL2RA  | interleukin 2 receptor, alpha                                               | 17.9 | 4.7E-14  | 6.3E-12 |
| 210146_x_at | LILRB2 | member 2                                                                    | 12.5 | 3.6E-08  | 5.4E-07 |
| 222062_at  | IL27RA | interleukin 27 receptor, alpha                                               | 12.3 | 9.9E-13  | 7.6E-11 |
| 217192_s_at | PRDM1  | ZNF domain                                                                  | 11.1 | 8.7E-12  | 4.6E-10 |
| 215719_x_at | FAS    | superfamily, member 6)                                                      | 9.3  | 7.8E-07  | 7.6E-06 |
| 205926_at  | IL27RA | interleukin 27 receptor, alpha                                               | 8.3  | 5.9E-11  | 2.3E-09 |
| Probe ID         | Description                                                                 | Log2 Ratio | Log10(p-value)1 | Log10(p-value)2 |
|-----------------|-------------------------------------------------------------------------------|------------|-----------------|-----------------|
| 204780_s_at     | FAS (TNF receptor superfamily, member 6)                                     | 8.0        | 2.6E-05         | 1.6E-04         |
| 242743_at       | interleukin 4 receptor                                                       | 8.0        | 7.6E-13         | 6.2E-11         |
| 242809_at       | interleukin 1 receptor-like 1 (leukocyte immunoglobulin-like receptor, subfamily B) | 6.6        | 1.5E-06         | 1.3E-05         |
| 207697_x_at     | LILRB2 member 2                                                              | 6.6        | 1.2E-13         | 1.4E-11         |
| 212588_at       | PTPRC receptor type, C                                                        | 6.5        | 2.8E-08         | 4.3E-07         |
| 216252_x_at     | FAS (TNF receptor superfamily, member 6)                                     | 6.3        | 9.4E-08         | 1.2E-06         |
| 230052_s_at     | NFKBID B-cells inhibitor, delta                                              | 6.2        | 1.0E-07         | 1.3E-06         |
| 211336_x_at     | LILRB1 member 1                                                              | 5.2        | 4.8E-16         | 1.5E-13         |
| 212587_s_at     | PTPRC receptor type, C                                                        | 5.1        | 6.5E-13         | 5.5E-11         |
| 207104_x_at     | LILRB1 like receptor, subfamily B                                            | 5.1        | 3.0E-17         | 1.6E-14         |
(with TM and ITIM domains),

| Gene ID       | Symbol | Description                                | Log2FC | Raw P | Adjusted P |
|---------------|--------|--------------------------------------------|--------|-------|------------|
| 211269_s_at   | IL2RA  | interleukin 2 receptor, alpha              | 5.1    | 2.8E-08 | 4.4E-07    |
| 204781_s_at   | FAS    | Fas (TNF receptor superfamily, member 6)   | 4.7    | 3.4E-06 | 2.7E-05    |
| 1552480_s_at  | PTPRC  | receptor type, C                           | 4.5    | 9.0E-08 | 1.2E-06    |
| 203233_at     | IL4R   | interleukin 4 receptor                     | 4.4    | 1.2E-10 | 4.0E-09    |
| 206060_s_at   | PTPN22 | protein tyrosine phosphatase, non-receptor type 22 | 4.3    | 7.6E-06 | 5.5E-05    |
| 223834_at     | CD274  | CD274 molecule                             | 3.8    | 5.7E-09 | 1.1E-07    |
| 235458_at     | HAVCR2 | hepatitis A virus cellular receptor 2      | 3.8    | 6.6E-07 | 6.6E-06    |
| 231794_at     | CTLA4  | cytotoxic T-lymphocyte-associated protein 4 | 3.4    | 1.6E-09 | 3.7E-08    |
| 227900_at     | CBLB   | ubiquitin protein ligase B                 | 3.3    | 1.8E-04 | 8.3E-04    |
| 220418_at     | UBA4H3A| domain containing A                        | 3.3    | 3.0E-05 | 1.8E-04    |
| 202643_s_at   | TNFAIP3| induced protein 3                          | 3.2    | 1.0E-08 | 1.8E-07    |
| 240070_at     | TIGIT  | T cell immunoreceptor with                 | 3.0    | 2.9E-05 | 1.8E-04    |
| Probe    | Gene Symbol | Description                                                | Log2 Fold Change | Adjusted p-value 1 | Adjusted p-value 2 |
|----------|-------------|------------------------------------------------------------|------------------|---------------------|---------------------|
| 201537_s_at | DUSP3       | dual specificity phosphatase 3                             | 3.0              | 4.8E-11             | 1.9E-09             |
|          |             | PR domain containing 1, with                                |                  |                     |                     |
| 228964_at | PRDM1       | ZNF domain                                                 | 2.9              | 3.4E-06             | 2.7E-05             |
| 201538_s_at | DUSP3       | dual specificity phosphatase 3                             | 2.9              | 3.6E-10             | 1.1E-08             |
|          |             | lectin, galactoside-binding,                               |                  |                     |                     |
| 203236_s_at | LGALS9      | soluble, 9                                                 | 2.7              | 3.5E-07             | 3.8E-06             |
|          |             | programmed cell death 1                                    |                  |                     |                     |
| 224399_at | PDCD1LG2    | ligand 2                                                   | 2.7              | 1.3E-07             | 1.7E-06             |
|          |             | nuclear factor of kappa light                              |                  |                     |                     |
|          |             | polypeptide gene enhancer in                               |                  |                     |                     |
| 241889_at | NFKBID      | B-cells inhibitor, delta                                   | 2.6              | 6.5E-06             | 4.8E-05             |
|          |             | zinc finger CCCH-type                                      |                  |                     |                     |
| 223506_at | ZC3H8       | containing 8                                               | 2.6              | 5.6E-04             | 2.2E-03             |
|          |             | itchy E3 ubiquitin protein                                 |                  |                     |                     |
| 209744_x_at | ITCH       | ligase                                                     | 2.6              | 3.8E-07             | 4.1E-06             |
|          |             | phosphoprotein associated with glycosphingolipid           |                  |                     |                     |
| 225622_at | PAG1        | microdomains 1                                             | 2.6              | 3.4E-05             | 2.0E-04             |
|          |             | itchy E3 ubiquitin protein                                 |                  |                     |                     |
| 217094_s_at | ITCH       | ligase                                                     | 2.4              | 1.1E-05             | 7.8E-05             |
| 224211_at | FOXP3       | forkhead box P3                                            | 2.4              | 1.2E-05             | 7.9E-05             |
| 243196_s_at | TRAFD1      | TRAF-type zinc finger                                       | 2.3              | 4.0E-05             | 2.3E-04             |
| Probe Set ID | Description | Fold Change | P-value 1 | P-value 2 |
|-------------|-------------|-------------|----------|----------|
| 228996_at   | RC3H1       | 2.3         | 5.5E-05  | 3.0E-04  |
| 219364_at   | DHX58       | 2.3         | 5.3E-07  | 5.4E-06  |
| 202763_at   | CASP3       | 2.2         | 1.8E-05  | 1.1E-04  |
| 236539_at   | PTPN22      | 2.2         | 6.9E-05  | 3.7E-04  |
| 202644_s_at | TNFAIP3     | 2.2         | 1.4E-06  | 1.3E-05  |
| 205298_s_at | BTN2A2      | 2.2         | 3.7E-04  | 1.6E-03  |
| 217513_at   | MILR1       | 2.1         | 6.0E-06  | 4.4E-05  |
| 205299_s_at | BTN2A2      | 2.0         | 3.9E-05  | 2.2E-04  |
| 242497_at   | TRAFD1      | 1.8         | 4.1E-04  | 1.7E-03  |
| 234066_at   | IL1RL1      | 1.8         | 7.5E-03  | 2.0E-02  |
| 235668_at   | PRDM1       | 1.8         | 3.0E-06  | 2.4E-05  |
| Gene Symbol   | Description                                           | Log2 FC | P value 1 | P value 2 |
|--------------|-------------------------------------------------------|---------|-----------|-----------|
| 1555628_at   | HAVCR2 receptor 2                                      | 1.8     | 6.7E-04   | 2.6E-03   |
| 209682_at    | Cbl proto-oncogene, E3                                 | 1.8     | 6.1E-05   | 3.3E-04   |
| 209354_at    | TNFRSF14 tumor necrosis factor receptor                | 1.8     | 3.2E-06   | 2.6E-05   |
| 227354_at    | PAG1 phosphoprotein associated with glycosphingolipid | 1.7     | 7.0E-02   | 1.3E-01   |
| 209743_s_at  | ITCH itchy E3 ubiquitin protein ligase                 | 1.7     | 4.4E-03   | 1.3E-02   |
| 35254_at     | TRAFD1 TRAF-type zinc finger domain containing 1       | 1.7     | 1.7E-05   | 1.1E-04   |
| 1555629_at   | HAVCR2 receptor 2                                      | 1.7     | 2.4E-04   | 1.1E-03   |
| 202837_at    | TRAFD1 domain containing 1                            | 1.6     | 5.5E-05   | 3.0E-04   |
| 235057_at    | ITCH itchy E3 ubiquitin protein ligase                 | 1.6     | 2.7E-02   | 6.0E-02   |
| 1554285_at   | HAVCR2 receptor 2                                      | 1.6     | 5.4E-04   | 2.2E-03   |
| 225626_at    | PAG1 phosphoprotein associated with glycosphingolipid | 1.5     | 2.3E-02   | 5.2E-02   |
| ProbeID          | Gene Symbol | Description                                                                 | Log2 Fold Change | p-value (FDR) |
|------------------|-------------|------------------------------------------------------------------------------|------------------|---------------|
| 201536_at        | DUSP3       | dual specificity phosphatase 3                                               | 1.5              | 3.2E-04       |
|                  |             | nuclear factor of kappa light polypeptide gene enhancer in                   |                  | 1.4E-03       |
| 1553042_a_at     | NFKBID      | B-cells inhibitor, delta programmed cell death 1                             | 1.5              | 3.0E-03       |
|                  |             |                                                                              |                  | 9.4E-03       |
| 220049_s_at      | PDCD1LG2    | ligand 2                                                                    | 1.4              | 5.4E-03       |
|                  |             | cytotoxic T-lymphocyte-                                                      |                  | 1.5E-02       |
| 221331_x_at      | CTLA4       | associated protein 4                                                         | 1.3              | 4.8E-04       |
|                  |             | cytotoxic T-lymphocyte-                                                      |                  | 2.0E-03       |
| 234362_s_at      | CTLA4       | associated protein 4                                                         | 1.3              | 4.6E-03       |
|                  |             | protein tyrosine phosphatase, non-receptor type 22                           |                  | 1.3E-02       |
| 208010_s_at      | PTPN22      | (lymphoid)                                                                  | 1.3              | 2.4E-03       |
|                  |             | cytotoxic T-lymphocyte-                                                      |                  | 7.8E-03       |
| 234895_at        | CTLA4       | associated protein 4                                                         | 1.1              | 4.9E-02       |
|                  |             | ring finger and CCCH-type                                                    |                  | 9.7E-02       |
| 225893_at        | RC3H1       | domains 1                                                                    | 1.1              | 7.0E-01       |
|                  |             |                                                                              |                  | 7.8E-01       |
| 224859_at        | CD276       | CD276 molecule                                                               | 0.9              | 4.4E-01       |
|                  |             |                                                                              |                  | 5.6E-01       |
| 236235_at        | ITCH        | itchy E3 ubiquitin protein                                                   | 0.8              | 2.6E-01       |
|                  |             |                                                                              |                  | 3.7E-01       |
| 239101_at        | ITCH        | ligase                                                                       | 0.7              | 1.5E-02       |
|                  |             | itchy E3 ubiquitin protein                                                   |                  | 3.6E-02       |
| Probe ID   | Description                               | FCH | FDR       | FDR       |
|-----------|-------------------------------------------|-----|-----------|-----------|
| 1559583_at| CD276 molecule                            | 0.6 | 8.5E-02   | 1.5E-01   |
|           | V-set domain containing T                 |     |           |           |
| 219768_at | VTCN1 cell activation inhibitor 1         | 0.3 | 8.1E-05   | 4.2E-04   |
|           | GTP binding protein                       |     |           |           |
|           | overexpressed in skeletal muscle          |     |           |           |
| 204472_at | GEM muscle                                | 0.3 | 1.1E-05   | 7.6E-05   |

FCH, fold change; FDR, false discovery rate.