

Table S1. Description of additional microarray datasets. We identified early gene expression shifts in psoriasis lesions following etanercept treatment and compared these patterns to those observed in an independent set of microarray datasets (see Figure 5). The table below describes the additional microarray datasets used in these comparisons. For each dataset, condition A lists the experimental treatment group and condition B lists the control group. In all cases, expression patterns were compared between the two treatments (A versus B) using empirical Bayes methods and moderated t-statistics (R package: limma). The table lists the total number of unique genes assayed in each experiment, along with the number of genes significantly increased in condition A (versus condition B), and the number of unique genes significantly decreased in condition A (versus condition B). Significantly increased genes included only those for which the estimated fold-change (condition A/condition B) was greater than 1.50, while significantly decreased genes included only those for which the estimated fold-change (condition A/condition B) was less than 0.67. The table lists the number of genes significantly altered based upon a raw p-value threshold ($P < 0.05$) as well as the number of genes significantly altered based upon a false discovery rate criterion ($FDR < 0.10$; Benjamini-Hochberg correction).

GEO Series	Condition A	Condition B	No. Genes	Increased ($P < 0.05$)	Decreased ($P < 0.05$)	Increased ($FDR < 0.10$)	Decreased ($FDR < 0.10$)
GSE12109 ^a	IL17-treated KCs ($n = 3$)	untreated KCs ($n = 3$)	12701	60	15	42	5
GSE31652 ^b	Lesion LY2439821 ($n = 6$)	Lesion placebo ($n = 8$)	12701	1346	1094	1228	1050
GSE36287 ^c	TNF-treated KCs ($n = 3$)	untreated KCs ($n = 3$)	20184	934	1184	119	39
GSE36287 ^d	IFN γ -treated KCs ($n = 3$)	untreated KCs ($n = 3$)	20184	1756	1676	1547	1487
GSE7216 ^e	IL22-treated KCs ($n = 3$)	untreated KCs ($n = 3$)	20184	550	855	550	855

^aFigure 5A. Cultured KCs were treated with 200 ng IL17A for 24 hours. Expression was profiled using the Affymetrix Human Genome U133A 2.0 array platform. Nograles et al. 2008, Br J Dermatol 159:1092-1102.

^bFigure 5B. Patients were given 2 subcutaneous injections of ixekizumab (150 mg) over two weeks. Placebo injections were given to a separate group of patients. Expression was profiled using the Affymetrix Human Genome U133A 2.0 array platform. Krueger et al. 2012, J Allergy Clin Immunol 130:145-154.

^cFigure 5C. Cultured KCs were treated with 10 ng TNF for 24 hours. Expression was profiled using the Affymetrix Human Genome U133 Plus 2.0 array platform. Swindell et al. 2012, PLoS ONE 7:e34594.

^dFigure 5D. Cultured KCs were treated with 20 ng IFN- γ for 24 hours. Expression was profiled using the Affymetrix Human Genome U133 Plus 2.0 array platform. Swindell et al. 2012, PLoS ONE 7:e34594.

^eData not shown. Cultured KCs were treated with 20 ng IL-22 for 4 days. Expression was profiled using the Affymetrix Human Genome U133 Plus 2.0 array platform. Sa et al. 2007, J Immunol 178:2229-2240.