Table S2. Gene expression in psoriasis lesions (PP) and uninvolved skin samples (PN) at baseline prior to etanercept treatment. We used RT-PCR to evaluate gene expression at baseline for six genes and compared estimated fold-change values (PP/PN) to those obtained using Affymetrix microarray analysis. RT-PCR results were based on n = 4-18 patients per gene (see table). Patients for which expression was not detected using RT-PCR were excluded from analyses. All microarray results are based upon n = 7 patients, with expression estimates calculated using robust multichip average (RMA). In some cases, a given gene was represented by multiple probe set features included on the array platform. In these instances, the probe set for which the most significant result was obtained (i.e., lowest p-value) is listed in the table below.

below.		RT-PCR Resu	ulte	Microarray Results		
Symbol	n	Fold-Change	P-value	Probe Set	Fold-Change	P-value
IL17A	4	67.1	0.0047*	216876_s_at	2.82	0.001*
IL17RA	12	1.15	0.26	229295_at	1.20	0.047*
IL17RC	18	0.85	0.28	224514_x_at	0.78	0.0018*
IL22	5	3.01	0.12	221165_s_at	1.08	0.23
CXCL11	18	0.85	0.28	211122_s_at	2.15	0.0081*
CCL20	12	8.00	0.0035*	205476_at	7.70	0.000013*