Supporting Information

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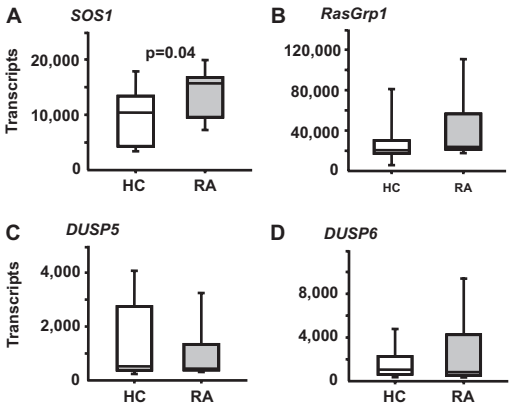

Fig. S1. Expression of ERK pathway genes in RA T cells. Expression of SOS1 (*A*), RasGRP1 (*B*), DUSP5 (*C*), and DUSP6 (*D*) that regulate the ERK pathway in T cells and are not included in the superarray (Table 2) were quantified by SYBR quantitative PCR. Results from 15 controls (open boxes) and 15 patients with RA (shaded boxes) are expressed as the number of transcripts per 10^6 β-actin transcripts and are shown as box plots.

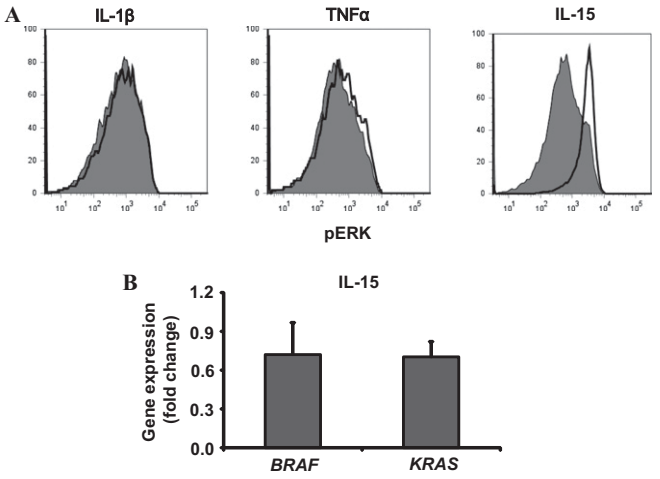

Fig. S2. Modulation of ERK responses by prior cytokine exposure. (*A*) T cells from healthy controls were incubated without cytokine (filled histograms) or with 10 ng/mL IL-1β, TNF-α, or IL-15 (black lines) for 24 h. Following incubation, cytokines were removed by washing, cells were stimulated by anti-CD3 cross-linking, and pERK levels were measured by using PhosFlow. The histograms are representative of three experiments. (*B*) Following preincubation with IL-15, expression of *BRAF* and *KRAS* transcripts was quantified by quantitative PCR. Transcript levels are shown as fold change in IL-15 vs. unstimulated cells. The graphs represent means ± SD of three independent samples.