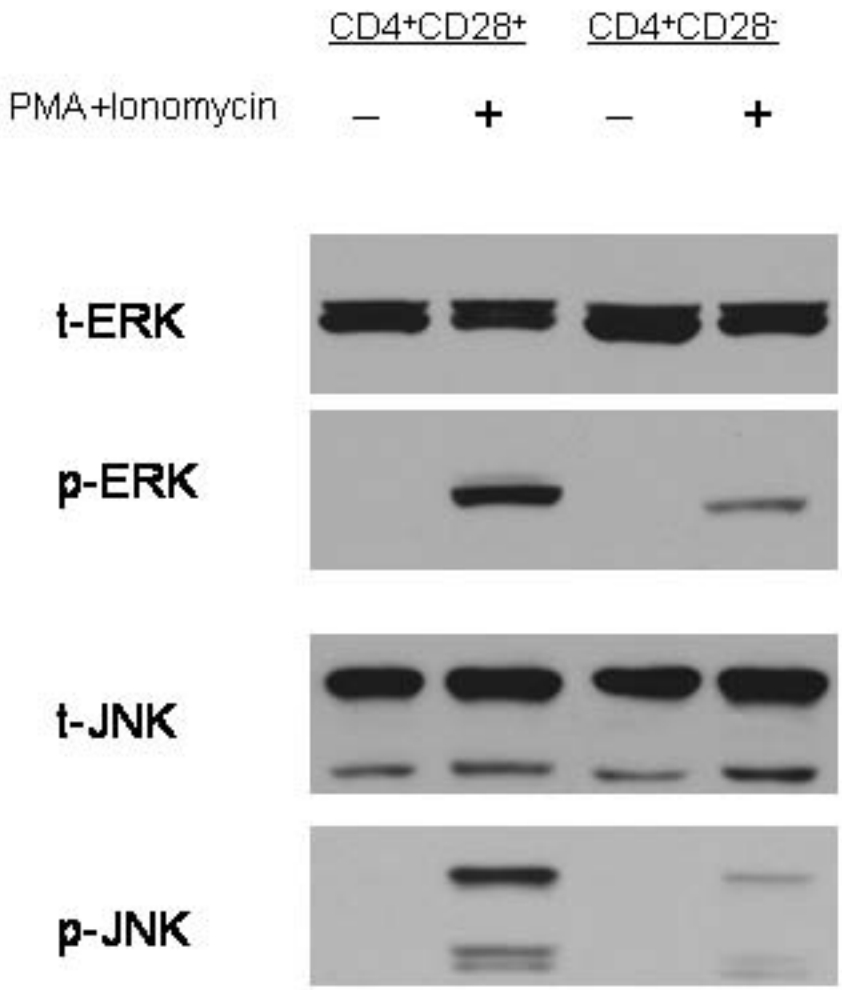


Fig. S1. Chronically activated CD4+ T cells were generated as described in Materials and Methods, then CD28+ and CD28- subsets were purified and stimulated (+) or not (-) with PMA + ionomycin for 15 min. Total ERK (t-ERK), phospho-ERK (p-ERK), total JNK (t-JNK) and phospho-JNK (p-JNK) were measured by immunoblotting.

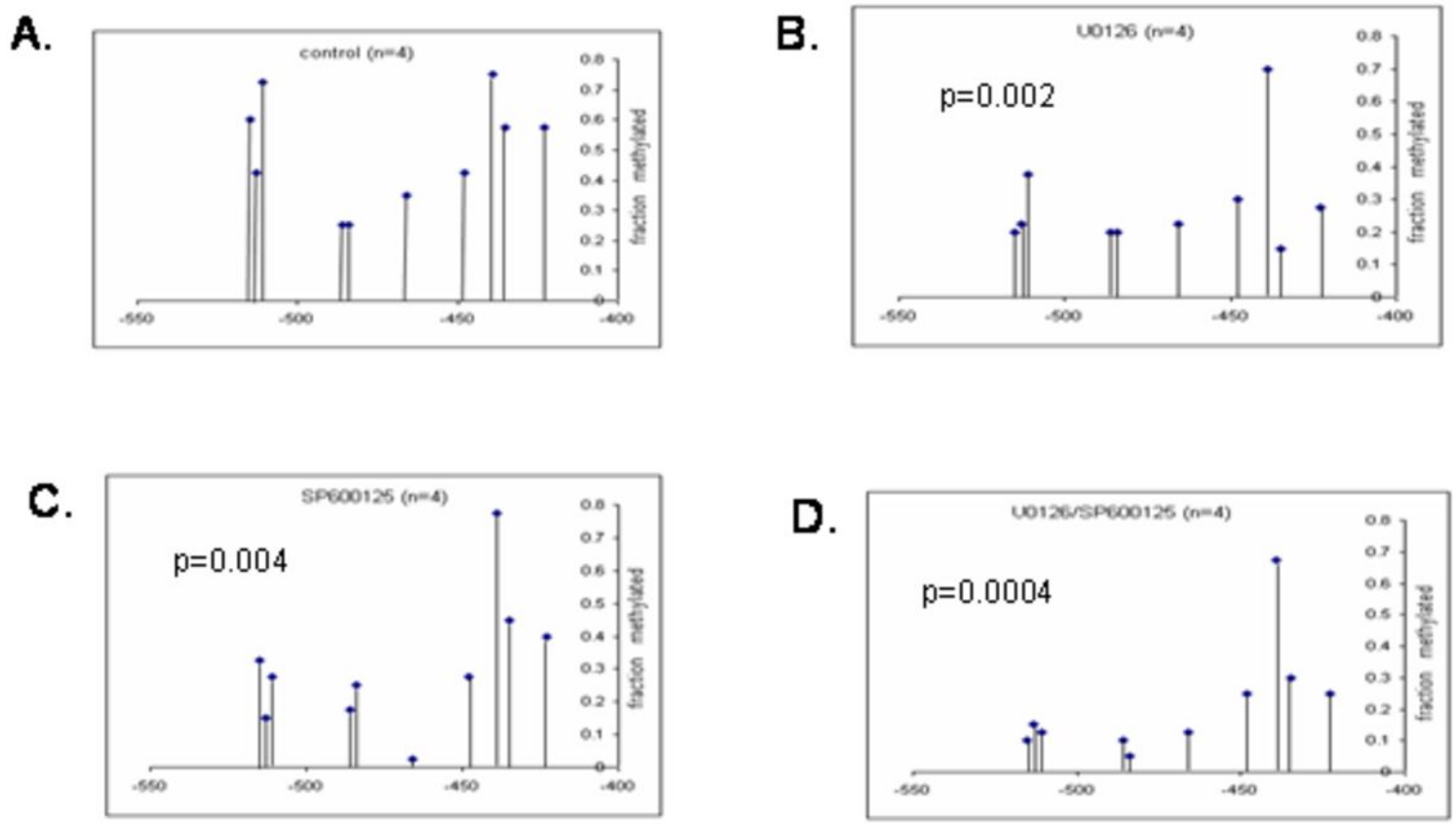


Fig. S2. *Effect of ERK and JNK pathway inhibitors on CD4+ T cell TNFSF7 (CD70) methylation*. **A**. PBMC from 4 healthy controls were stimulated with PHA and 72 hours later CD4+ T cells were isolated, DNA purified and treated with sodium bisulfite, then the indicated region of the *TNFSF7* promoter was amplified and 10 fragments cloned and sequenced from each subject. The location of each CG pair in the region is shown on the X axis numbered relative to the transcription start site, and the average methylation of the 40 determinations for each CG pair is shown on the Y axis. **B**. PHA stimulated PBMC from the same donors were treated with U0126 as in panel A and promoter methylation measured by cloning and sequencing of 10 bisulfite treated DNA fragments 72 hours later as in panel B. **C**. CD4+ T cells were treated with SP600125 as in panel A then methylation compared to untreated cells by bisulfite sequencing of 10 cloned fragments as in panel C. **D**. CD4+ T cells were treated U0126 and SP600125 as in panel A and overall methylation for each CG pair measured as in panel B.

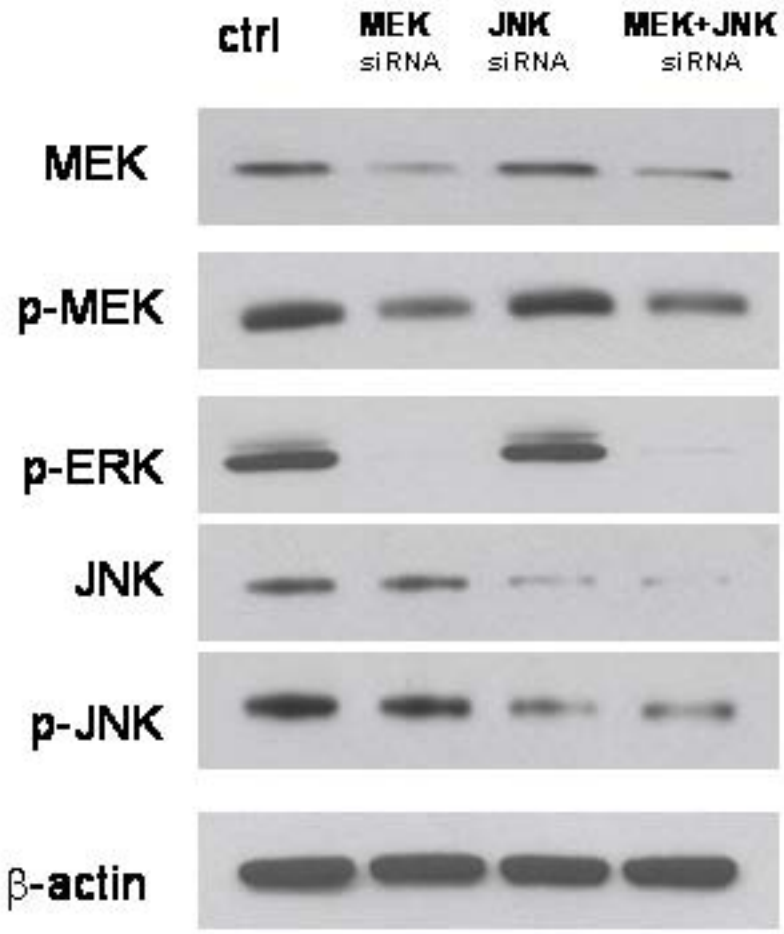
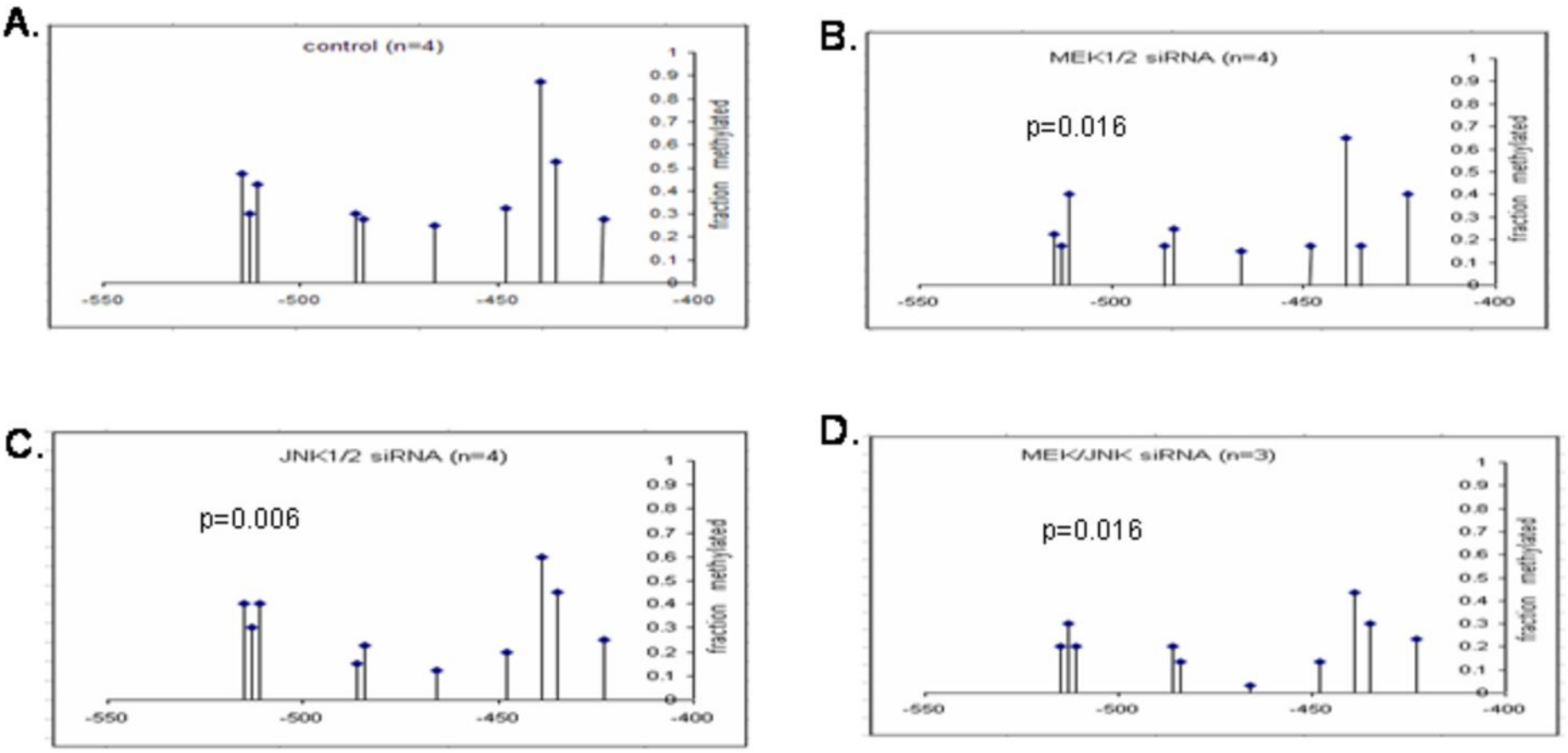


Fig. S3. *T cell MEK and/or JNK RNi knockdowns.* Representative immunoblots of total and phosphorylated MEK and JNK in CD4+ T cells transfected with control siRNA, MEK siRNA, JNK siRNA, or MEK + JNK siRNA as described in Materials and Methods. 72 hours later the cells were stimulated with PMA, and 15 minutes later the cells were lysed and MEK, p-MEK, p-ERK, JNK and p-JNK measured by immunoblotting. β-actin loading controls are also shown.



S4. *Effects of MEK and/or JNK siRNA on CD4+ T cell TNFSF7 (CD70) methylation.* **A**. T cells from 4 healthy controls were transfected with control siRNA, stimulated with PHA 48 hours later, and 24 hours later DNA was isolated and *TNFSF7* promoter methylation measured as in Fig. S2, cloning and sequencing 10 fragments of bisulfite treated DNA from each of the 4 subjects. **B**. *TNFSF7* promoter methylation was measured in T cells transfected with MEK siRNA as described in panels A. **C**. *TNFSF7* promoter methylation was similarly measured in T cells transfected with JNK siRNA as described in panels A and B. **D**. *TNFSF7* promoter methylation was similarly measured in T cells from 3 healthy controls transfected with MEK + JNK siRNA as described in panels A and B.