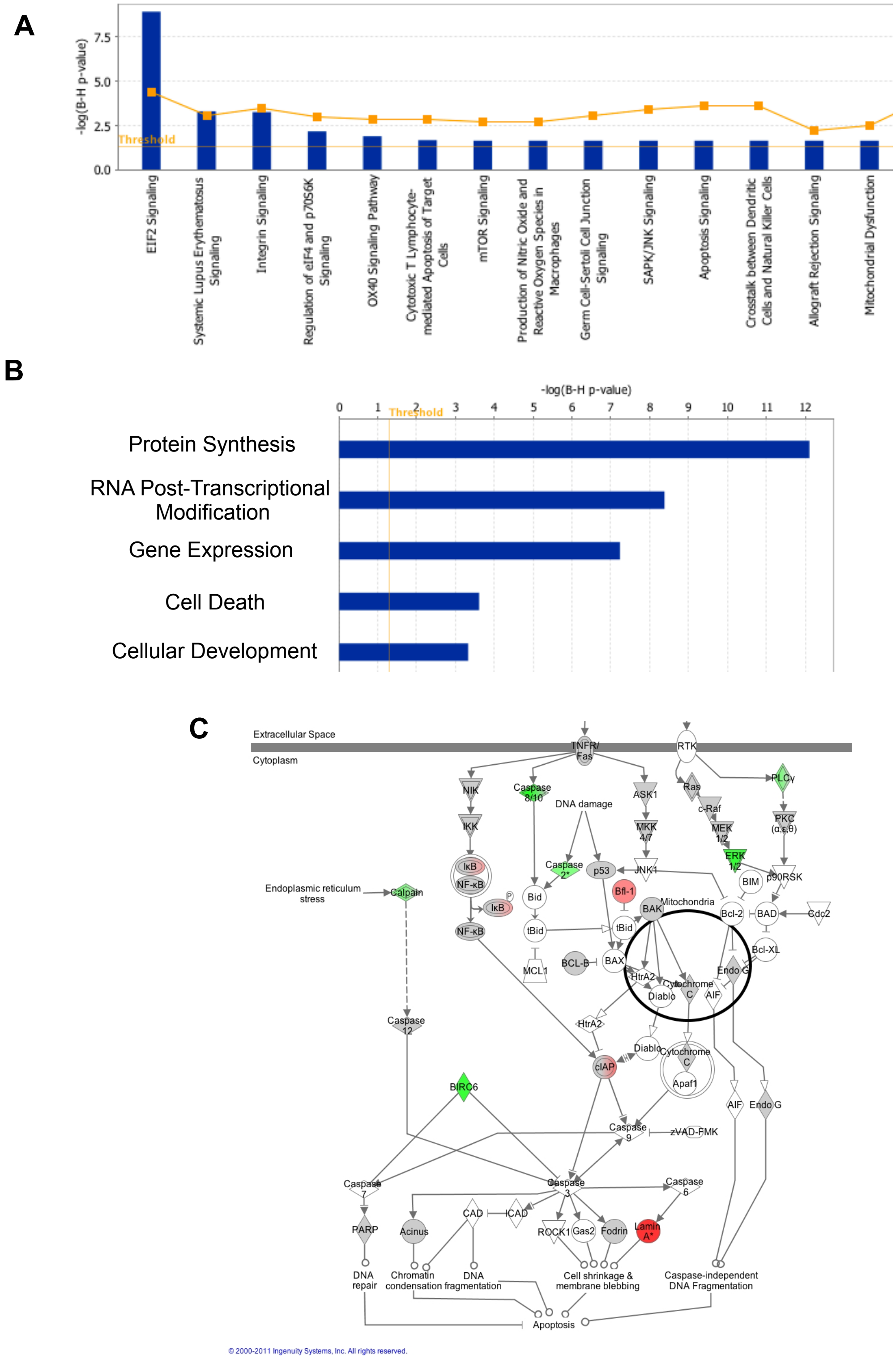

Figure S3. Pathway and functional analysis of the transcriptome in CD8$^+$ T cells with strong VIA and weak VIA in the presence or absence of TCR stimulation.
(A) Canonical pathways from IPA analysis that were substantially changed in the comparison between CD8$^+$ T cells with strong VIA and weak VIA are shown. The yellow line indicates the 5% FDR estimate from Fisher's exact test for over-representation of canonical pathways in the list of differentially expressed genes. (B) IPA biological functions that were substantially changed in the comparison between CD8$^+$ T cells with strong VIA and weak VIA. The yellow line has the same meaning as in (A). (C) IPA's Apoptosis Signaling canonical pathway (strong VIA versus weak VIA) is shown. The red color indicates up-regulation (fold change >= 1.5, *P*<0.01); the green color indicates down-regulation (fold change <= -1.5, *P*<0.01); the grey color indicates genes that do not meet statistical significance, while the white color indicates molecules not probed by the microarray. Diamonds represents enzymes; circles represent mitochondria.