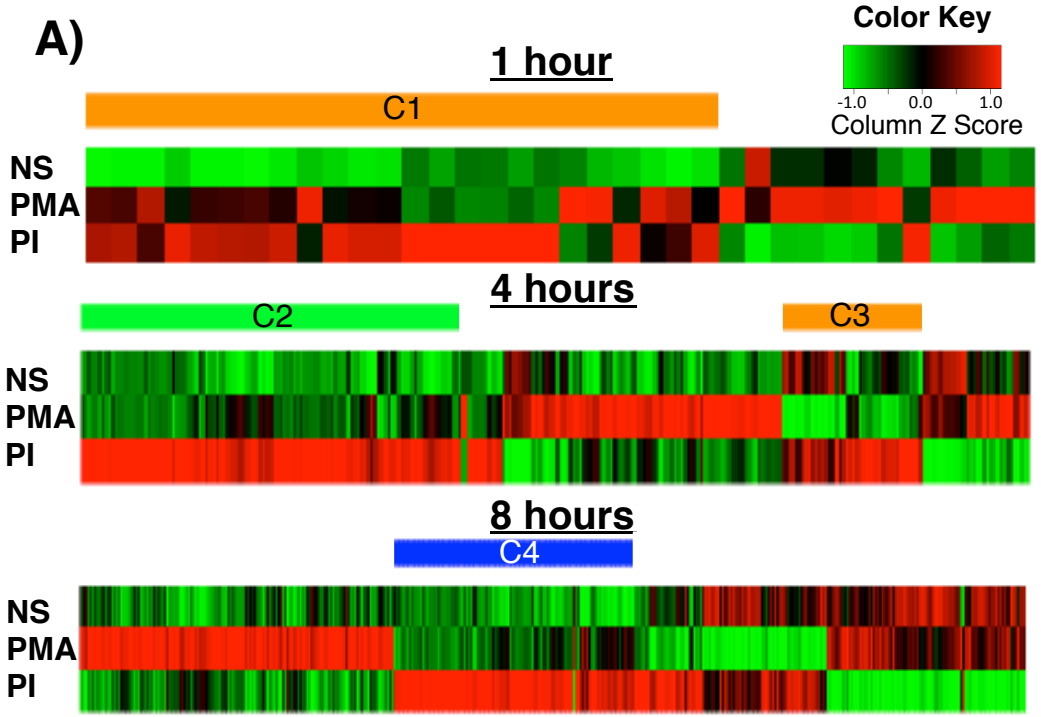
A)

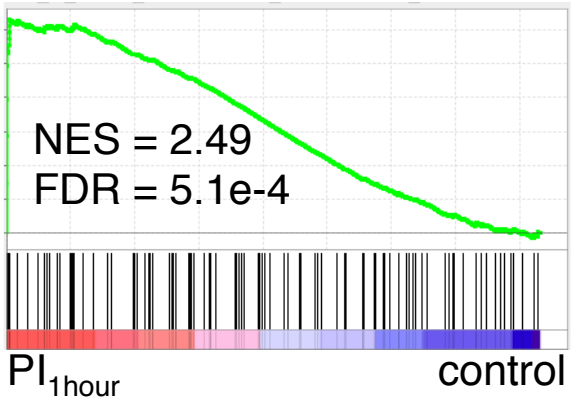


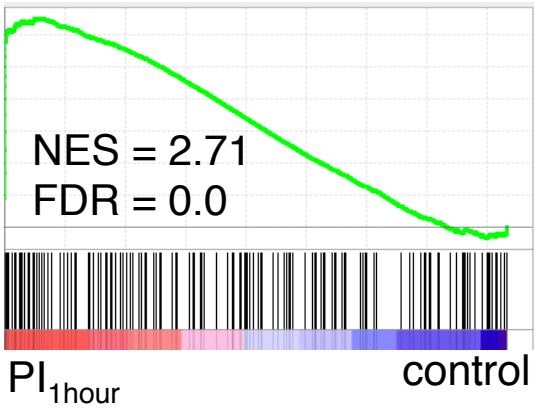
1 Hour			
	Gene Ontology	**Genes**	**ES**
C1	Cell Proliferation	9	2.8
	Reponse to cellular stimuli	6	2.7
	T cell receptor induced transcription	8	2.2

4 Hours			
C2	Apoptosis	14	7.3
	Activation of immune response	5	2.3
C3	Inflammatory Response	12	4.6
	Cytokine Activity	13	4.1
	Motility	14	3.9

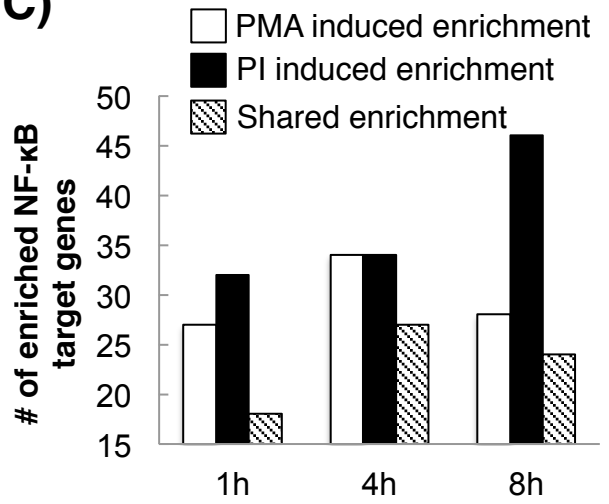
8 hours			
C4	Regulation of Apoptosis	25	4.8
	Cytokine signaling	16	2.5
	NF-kB and MAPK signaling	6	2.5
	Regulation of lymphocyte activation	8	2.2

B)





C)



D)

Gene	FC
CXCL8	3
NFKBIA	2
TNF	7.93
CD69	2.85

Gene	FC
CD83	1.65
RELB	1.69
IL2RA	1.71
IER3	2.08
IRF1	1.55
CD69	2.35
PLAU	5.58
NFKBIA	4.75
BCL2L1	1.72
TRAF1	1.99
FASLG	1.63
TNF	8.37
TAP1	2
CCL20	5.77
CXCL8	14.06
PIM1	2.04
F3	1.66
STAT5A	0.63
LTB	0.57
PRF1	0.38
CCR7	0.55

Gene	FC
STAT5A	0.4
MMP9	0.64
BCL3	0.62
LTB	0.37
PRF1	0.35
CCR7	0.5
CD40LG	0.37
TRAF1	2.25
NFKB2	2.16
NFKBIA	2.47
SOD2	1.54
PLAU	3.19
CXCL8	7.53
CCL20	22.59
TNFRSF9	1.73
CD69	1.91
IER3	2.06
TNF	1.58
TAP1	1.87
NFKB1	1.61
IL2RA	1.62
CD83	1.7
RELB	2.09
BCL2L1	1.58
JUNB	1.52

Figure 1: Transcriptional analysis of T lymphocyte NF-kB activation with and without calcium entry. A) Differential gene expression ($p<0.01$ and LogFC >0.59) and gene ontology for T cells stimulated with PMA, PMA and Ionomycin (PI), and controls cells (not stimulated, NS). Differentially expressed genes between PMA and PI are shown for 1, 4, and 8 hours. Gene ontology for clusters 1 (C1), 2 (C2), 3 (C3), and 4 (C4) are shown as well as the number of up regulated genes and the enrichment score (ES). **B)** Enrichment plots for cells stimulated with PI at 1 hour. T cells stimulated with PI demonstrate significant enrichment for genes downstream of TCR activation (left) and NF-kB activation (right). NF-kB gene set was curated based on human genes with checked binding sites as well as putative target gene sites. **C)** The number of NF-kB target genes, total and shared, enriched at 1, 4, and 8 hours following stimulation with PMA and PI. **D)** Differential expression ($p<0.01$ and LogFC >0.59) of NF-kB target genes between PMA and PI. Control (not stimulated, NS) shown to demonstrate change from baseline. Gene names and fold changes (FC) are shown for each differentially expressed gene.