SUPPLEMENTARY DATA

Supplementary Figure 1. Multiple doses of Bortezomib regulates CTLA-4. Transcript levels of *CTLA-4* are increased with bortezomib, from 0.05 to 10 uM. Normal primary CD4+ T cells were purified as described in Materials and Methods followed by treatment with bortezomib (0.05 μM, dotted line with diamond; 0.1 uM, dash line with square, and 10 μM, dash line with triangle) or untreated (solid line with circle) and concomitant stimulation with PMA/A23187 over a 12 h time course. Total RNA was isolated for qRT-PCR analysis as previously described. Results are the averages of 4 individual normal donors analyzed by qPCR normalized to *B2M* and presented as the fold increase over unstimulated normal cells.

Supplementary Figure 2. *NFAT1* and *FOXP3* expression levels are not augmented by bortezomib. Normal primary CD4+ T cells were purified as described in Materials Methods followed by treatment with 0 μM (solid line with circle), 0.1 μM (dashed line with square) or 10 μM (dotted line with triangle) bortezomib and stimulation with PMA/A23187 over a 12 h time course with 3 h intervals. Total RNA was isolated for qPCR analysis for **(A)** *NFAT1* and **(B)** *FOXP3* expression levels as previously described. Results are the averages of 4 individual normal donors analyzed by qPCR normalized to *B2M* and presented as the fold increase over unstimulated normal cells ± SEM *$p<0.05$, **$p<0.005$.

Supplementary Figure 3. *GATA3* knockdown by siRNA leads to decreased *IL-4* transcription but not *GAPDH* with bortezomib. Samples were prepared as in Figure 6. Transcript levels of **(A)** *IL-4* and **(B)** *GAPDH* were measured by qPCR for samples treated with siCTRL (black bars) or siGATA3 (white bars) as previously described. Results are presented as averages of three independent experiments ± SEM (*p<0.05).

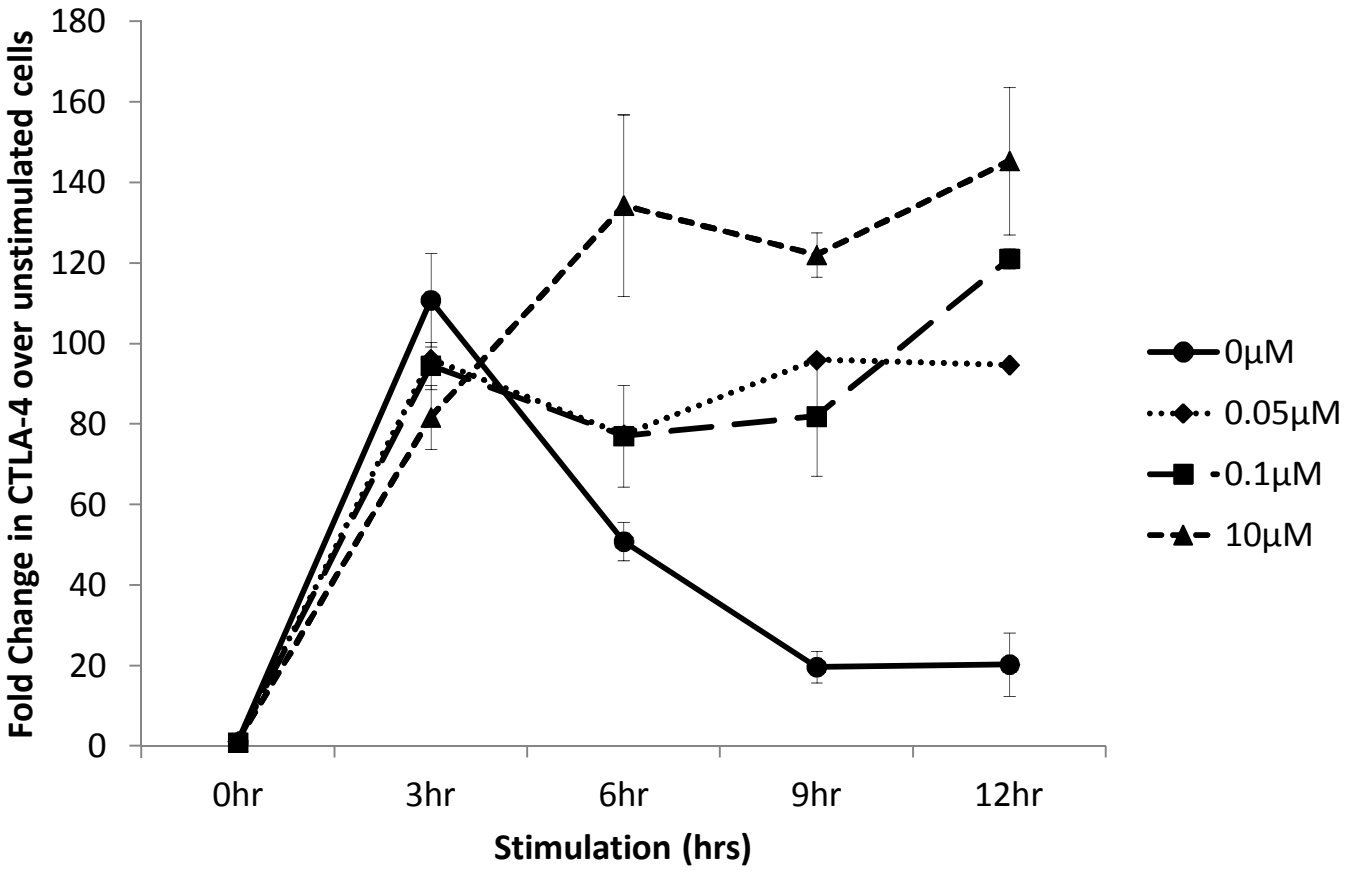
Supplementary Figure 4. Bortezomib treatment and apoptosis in primary CD4+ T cells. Celles were treated with the bortezomib concentration as indicated (green equals 0.1 uM, blue equals 10 uM) and stimulated with PMA/A23187 as described in the Materials and Methods. The cells were stained with Annexin V and analyzed by flow cytometry. Results are representative of three experiments.

Supplementary Table I. PCR Primer Sets

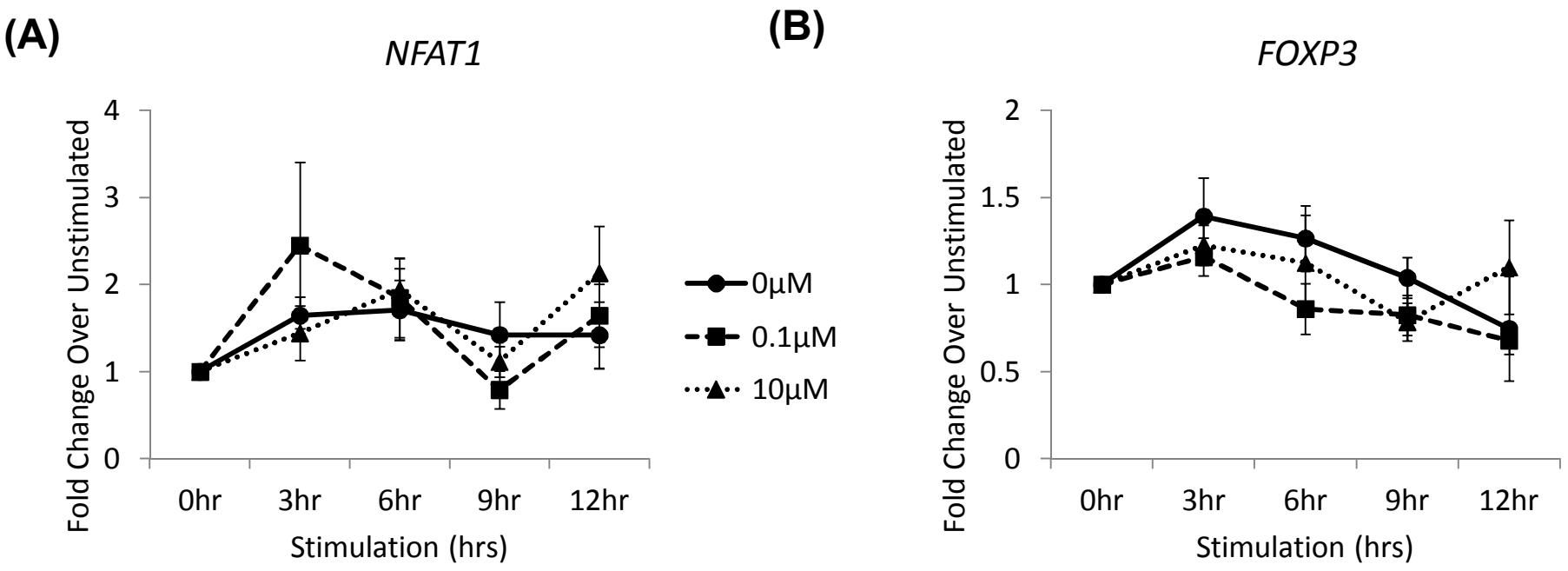
Gene	Forward	Reverse
B2M	**TCTACTTTGAGTGCTGTCTCCATGT**	**AAGTTGCCAGCCCTCCTAGAG**
CTLA-4	**CTACCTGGGCATAGGCAACG**	**CCCCGAACTAACTGCTGCAA**
FoxP3	**ATCCGCCACAACCTGAGTCT**	**GTCCACACAGCCCCCTTCT**
GAPDH	**CCCACTCCTCCACCTTTGAC**	**CATACCAGGAAATGAGCTTGACAA**
GATA3	**TCTGGAGGAGGAATGCCAAT**	**CCGGGTTAAACGAGCTGTTC**

IL-4	**CACAGGCACAAGCAGCTGAT**	**CTCTGGTTGGCTTCCTTCACA**
NFAT1	**TCCTGGAGATACCCTTGGAGC**	**AGTCGATGGTTGCCCTCATG**
ChIP CTLA-4	**GAGGACCCTTGTACTCCAGGAA**	**CGAAAAGACAACCTCAAGCACTC**

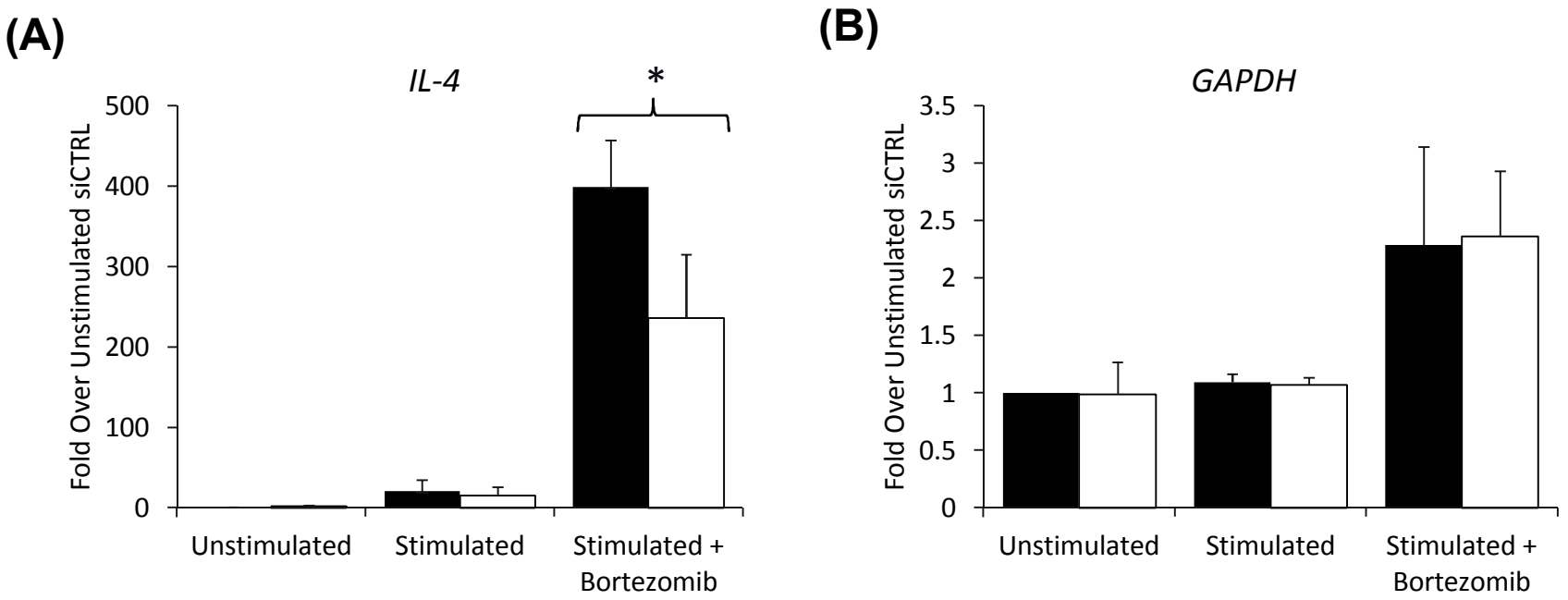
Supplementary Figure 1



Supplementary Figure 2



Supplementary Figure 3



Supplementary Figure 4