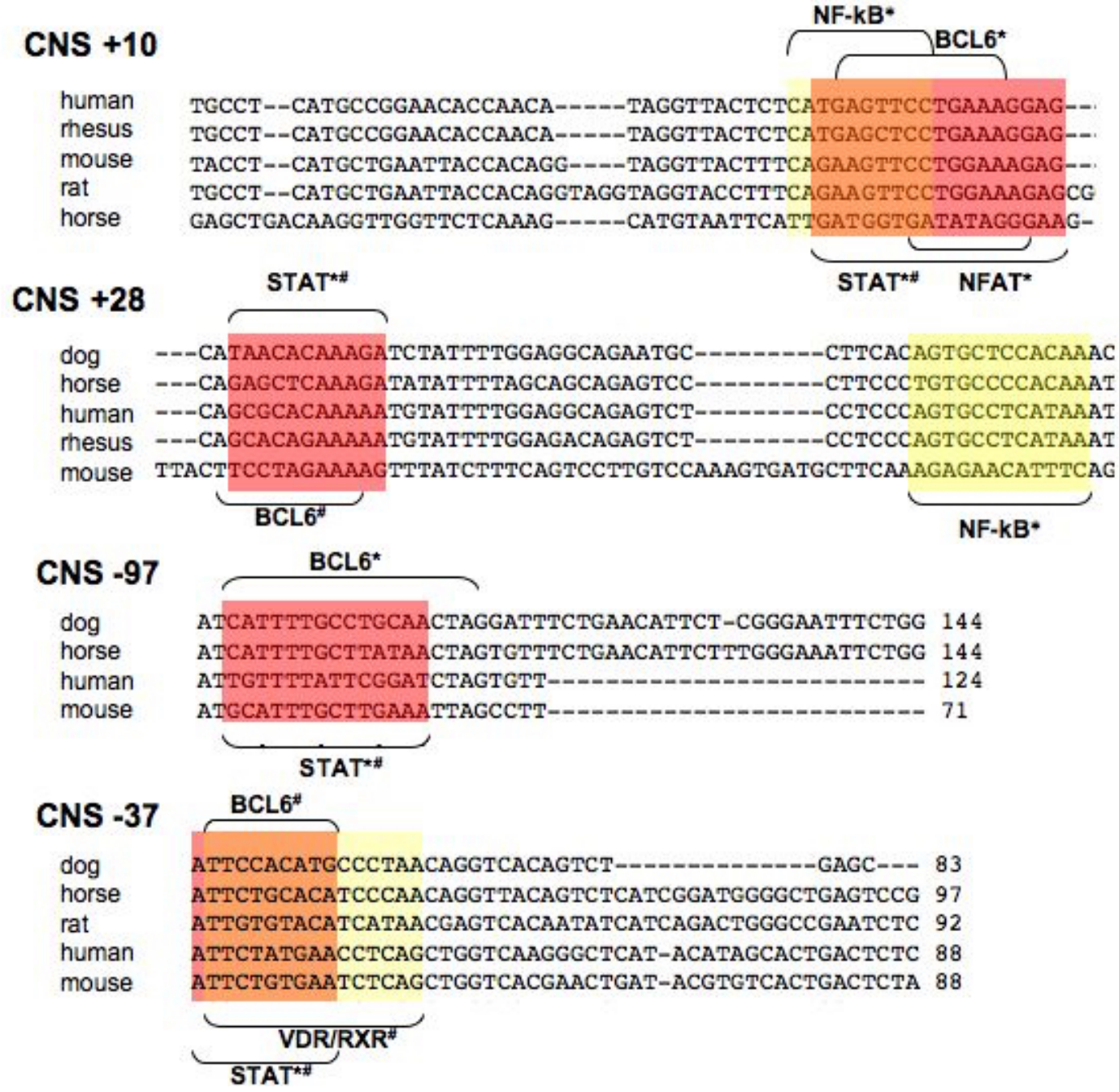
Supplemental Figure 1: Identification of transcription factor binding motifs within *Il17a/f* conserved noncoding sequence elements
Clustal W was used to perform DNA sequence alignments for selected CNS elements cross comparing multiple species. MatInspector identified consensus transcription factor binding sites for the denoted transcription factor families. Individual consensus sequence motifs are indicated by black brackets. Colored boxes identify highly conserved sequences within which consensus transcription factor binding sites are identified.

Supplemental Figure 2: Kinetics of IL-1β-induced NF-kB factor and pY-STAT3 activation
Naïve CD4+ T cells were cultured for 5 days under TH17-polarizing conditions then were either left unstimulated or restimulated with 10ug/mL of cytokine (IL-1β or IL-23 or both) for various times as indicated. Quantification of Tyr705-phosphorylated STAT3 (A), NF-kB p65 (RelA, B), c-Rel (C), and NFkB p50 (D) was performed by immunoblot analysis. Results represent mean +/- SEM of at least three independent experiments. *$p<0.05$ and #$p<0.01$ versus values obtained for IL-23 stimulation alone.

Supplemental Figure 1



Supplemental Figure 2