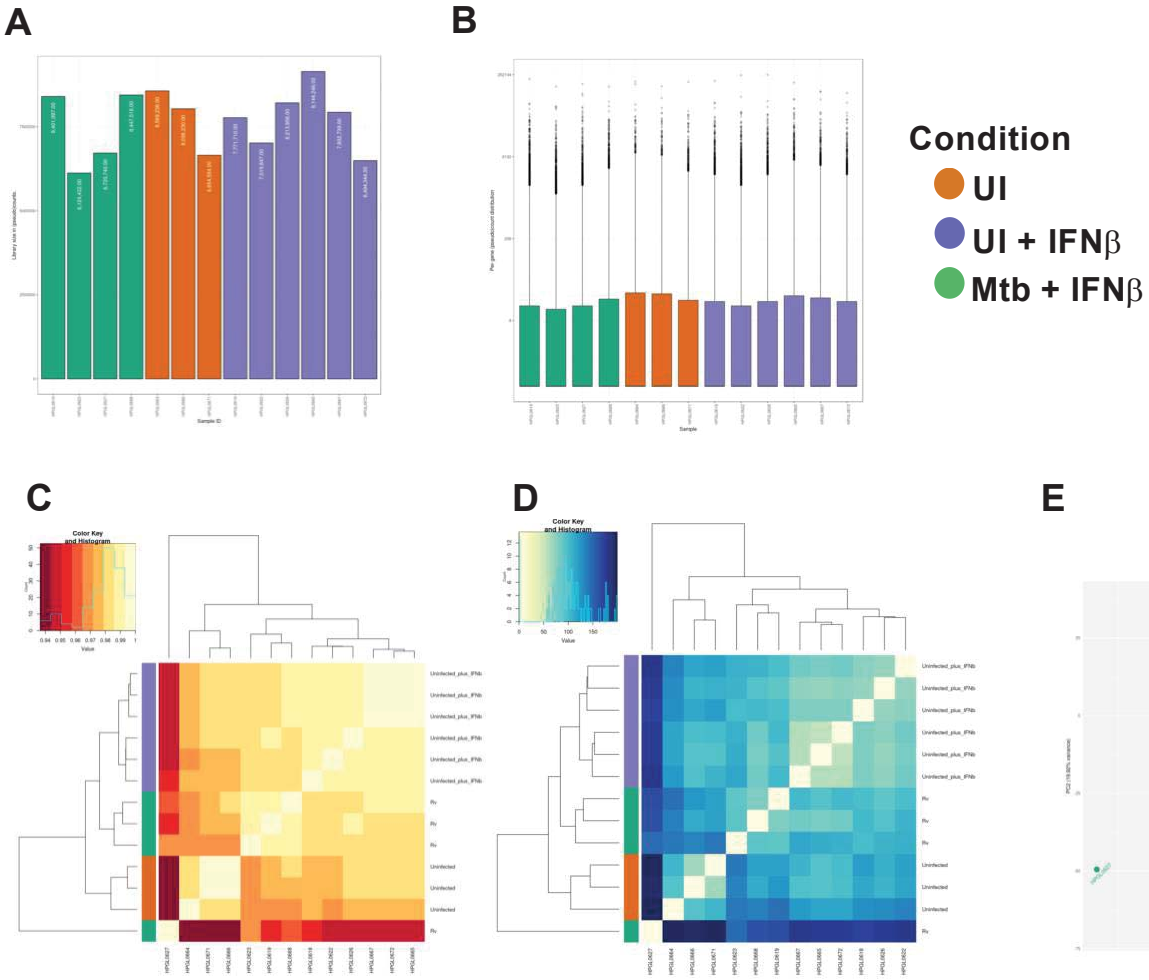
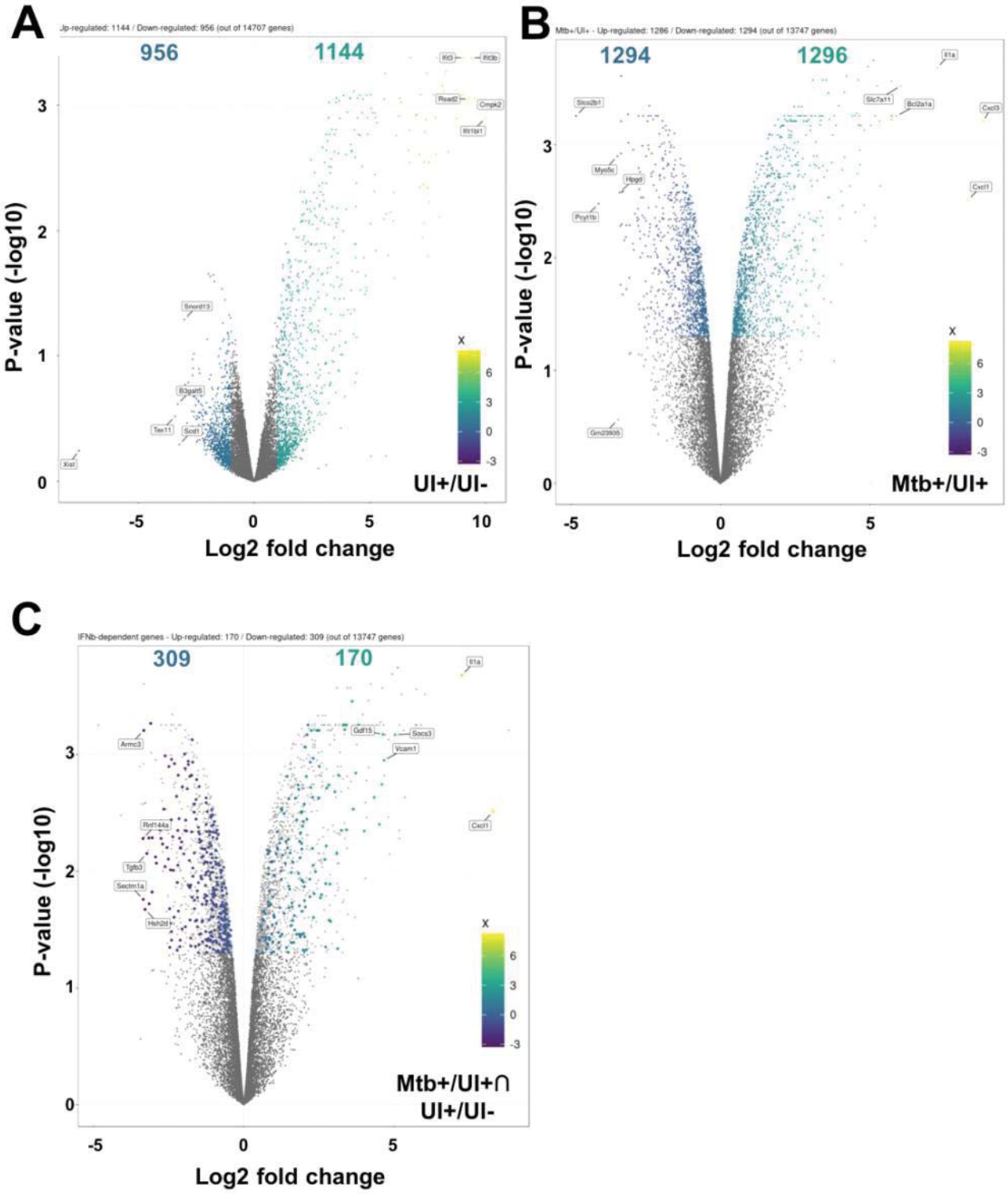


S1 Fig. RNA-seq analysis

(A) Raw RNAseq library sizes, colored according to experimental condition: uninfected (UI), uninfected or Mtb infected cells treated with 50pg/ml IFN-β for 4 hours. (B) Distribution of raw gene counts for each sample. (C) Pearson correlation and (D) Euclidean distance biclustering heatmap. (E) PCA plots of log2-CPM and quantile normalized read counts.

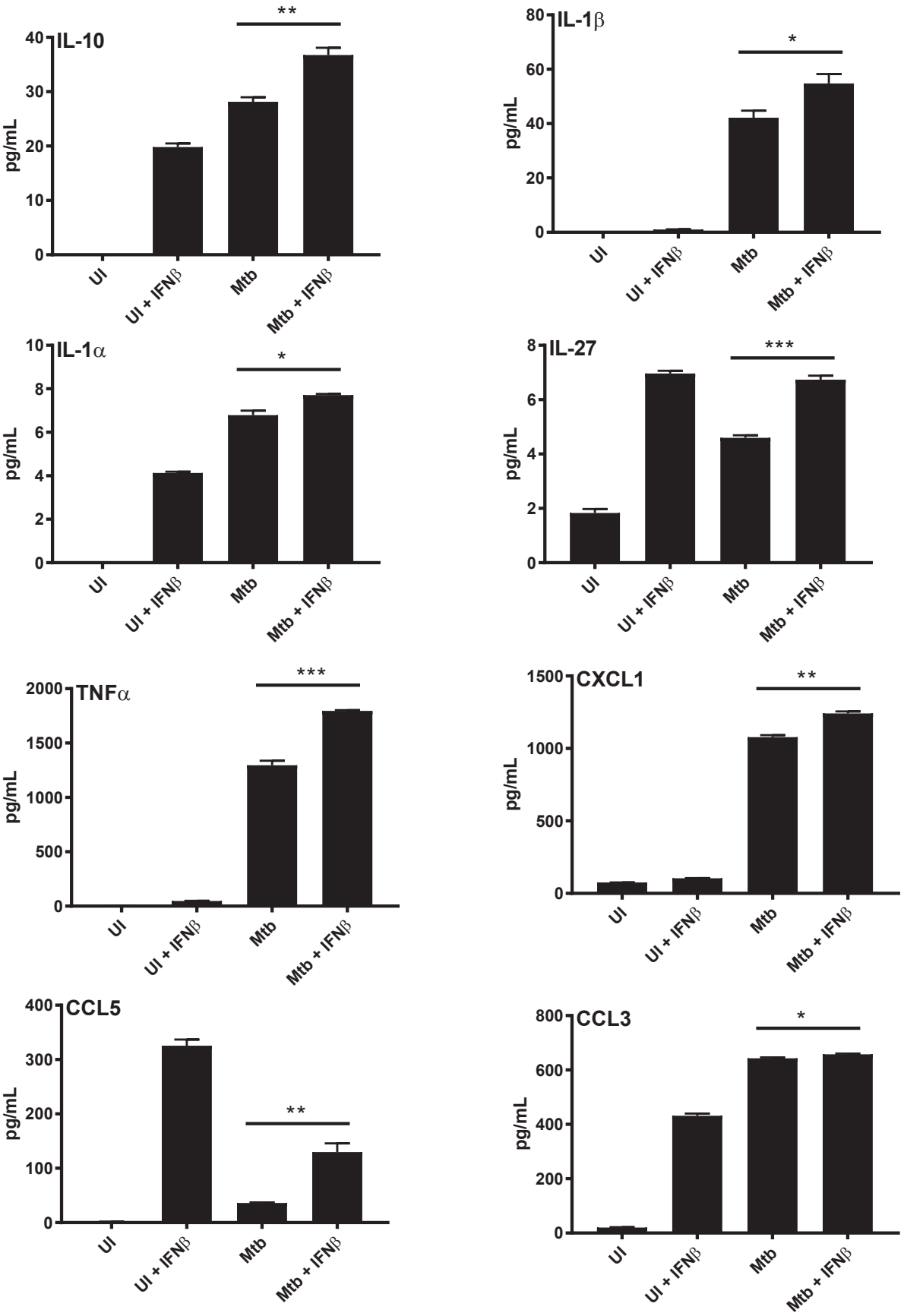
Figure S2



S2 Fig. Volcano plots of deregulated genes as determined by RNA-seq analyses.

P-values to Log2 fold changes were plotted for the deregulated genes of the uninfected plus IFN-β over uninfected minus IFN-β contrast (A), the Mtb-infected over uninfected plus IFN-β contrast (B) and the overlap of both of the contrasts (C).

Figure S3



S3 Fig. Multiplex cytokine/chemokine analysis

Cell culture supernatants were collected at 6 hpi and were analyzed for indicated cytokines or chemokines using a custom ProcartaPlex magnetic bead-based multiplex assay (Thermo Fisher Scientific). Cytokine/chemokine secretion data are representative of a combined three independent experiments and are presented as mean ± S.E.M.