

Supplementary Figure Legends

Figure S1. Effects of *M. bovis* BCG infection and IFN γ stimulation on nascent and cellular poly-A⁺ RNA for STAT1 and IRF1. THP-1 cells were differentiated, infected with *M. bovis* BCG (as described for *M. tb*) and/or stimulated with IFN γ , and then nascent transcripts were measured using the nuclear run-on assay, or cellular RNA was extracted and poly-A⁺ transcripts were quantified by qRT-PCR. The ratio of the fold-change in the abundance of the poly-A⁺ RNA relative to the fold-change in the level of nascent transcripts is shown for one of two independent experiments that gave similar results.

Figure S2. Effects of *M. tuberculosis* infection and IFN γ stimulation on total and poly-A⁺ nuclear RNA for STAT1 and IRF1. THP-1 cells were differentiated, infected with *M. tb* and/or stimulated with IFN γ , and then total nuclear RNA was extracted and quantified by qRT-PCR using random nonamer or oligo-dT(15) primers for reverse transcription. The ratio of the fold-change in the level of poly-A⁺ nuclear RNA relative to the fold-change in the level of total nuclear RNA is shown for the averages of each from 4-6 replicate experiments.

Figure S3. Effects of *M. tuberculosis* infection and IFN γ stimulation on STAT1 and IRF1 transcript half-life. THP-1 cells were infected with *M. tuberculosis* and/or stimulated with IFN γ , and then treated with actinomycin D for various times. Cellular RNA was extracted and assayed for poly-A⁺ STAT1 and IRF1 transcripts. The half-life of each was calculated. The averages and standard deviations from three or four replicate experiments are shown.

Figure S4. Post-initiation mRNA biogenesis Reactome pathways are down-regulated by *M. tuberculosis* infection. Eighteen pathways were tested. The pathways shown are significantly different for the indicated comparisons (**A-G**) based on a false discovery rate (FDR) criterion of 0.05 for the CERNO test results. The pathway tests were based on the rank order of differential expression for all genes in a pathway (among all transcript measurements of all named genes targeted by the gene expression platform). The top matrix depicts the membership of genes (columns) in pathways (rows) with red squares. The rows and columns of the top matrix are sorted to bring together similar pathway membership patterns. Genes shown are members of one or more pathways that exhibited differential expression for the indicated comparison (one-sided Student's T-test to assess down-regulation, $p < 0.05$ unless otherwise noted). The lower matrix is a heatmap of expression for each of the significantly regulated genes in each of the samples that were compared. The heatmap shows gradations from higher to lower expression as yellow to blue. Gene symbols are shown with the NCBI Gene IDs and the probe (or probe set) identifiers that measured significant differential expression. *M. tuberculosis* is associated with significance for various of the tested pathways as follows: **A**) 16 pathways were down-regulated when comparing *M. tuberculosis*-infected THP-1 cells to uninfected cells; **B**) 17 pathways were down-regulated when THP-1 cells infected with *M. tuberculosis* and stimulated with IFN γ were compared to uninfected, IFN- γ -stimulated THP-1 cells; **C**) four pathways were down-regulated when comparing blood from PTB donors to blood from LTBI donors from London; **D**) eight pathways were down-regulated when comparing blood from PTB donors to blood from LTBI donors from The Gambia (genes shown for t-test p -value < 0.001); **E**) seven pathways were down-regulated when comparing infected (pretreatment) patients to patients after two months of treatment (based on the results of one-sided paired T-tests for increase in expression associated

with treatment); **F**) 15 pathways were down-regulated when comparing infected (pretreatment) patients to patients after twelve months of treatment (based on the results of one-sided paired T-tests for increase in expression associated with treatment); and **G**) 10 pathways were down-regulated when comparing monocyte-derived macrophages (MDM) from LTBI patients to MDM from cured PTB patients.

Figure S1

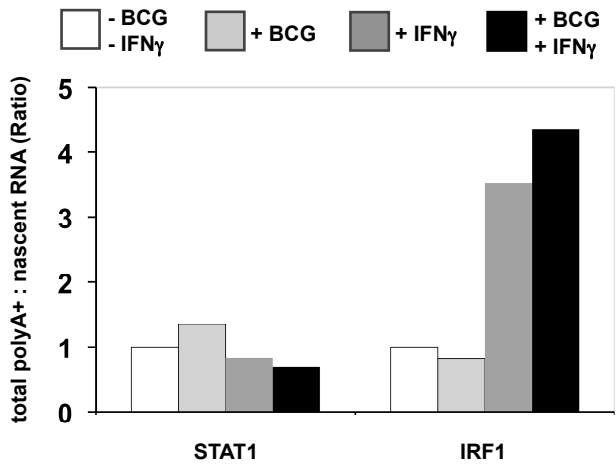


Figure S2

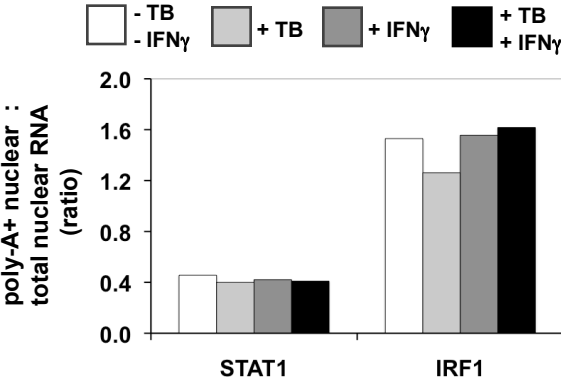


Figure S3

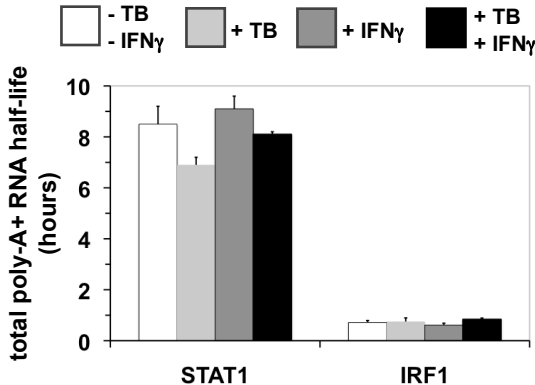
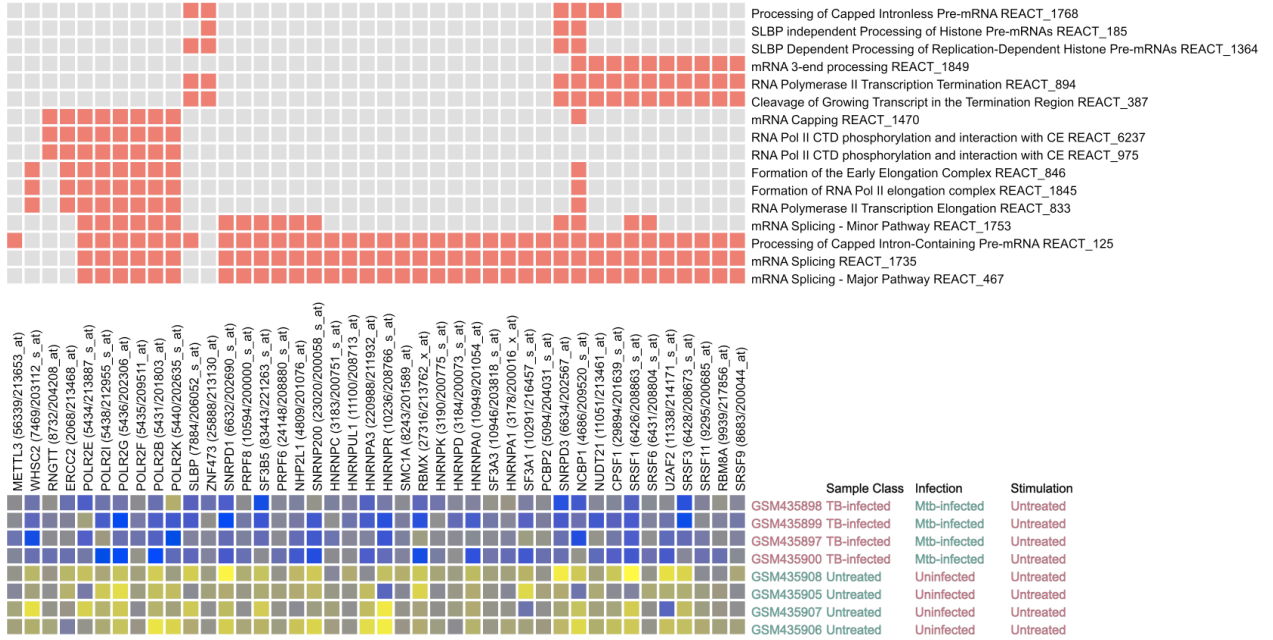
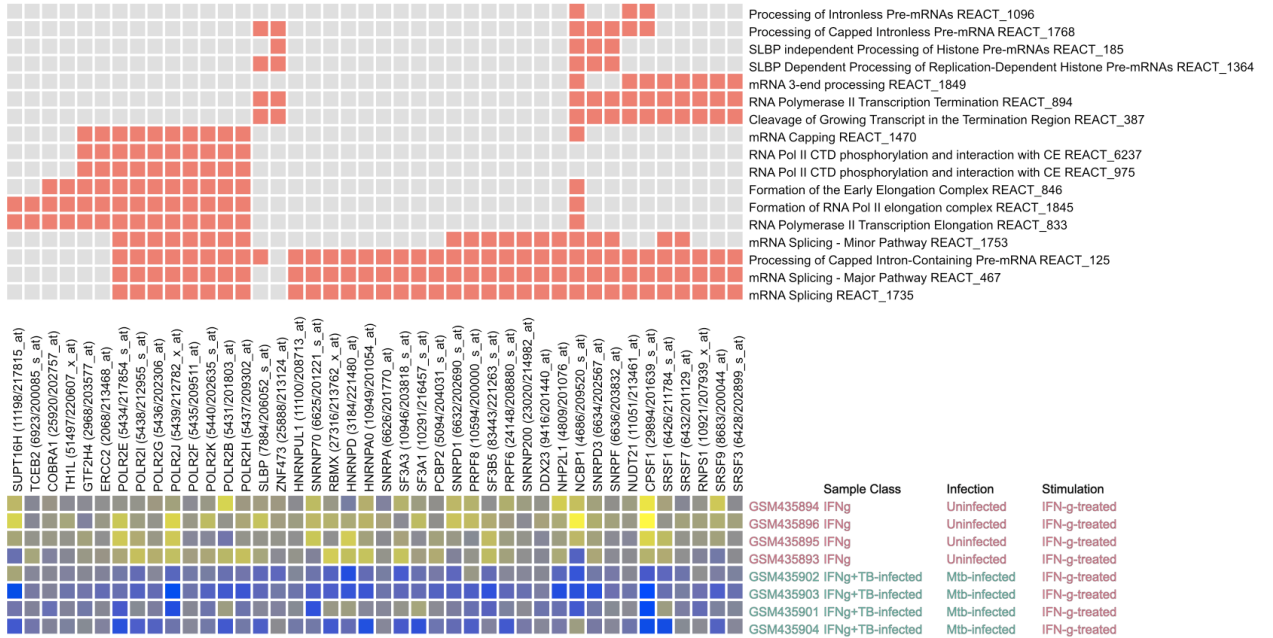


Figure S4

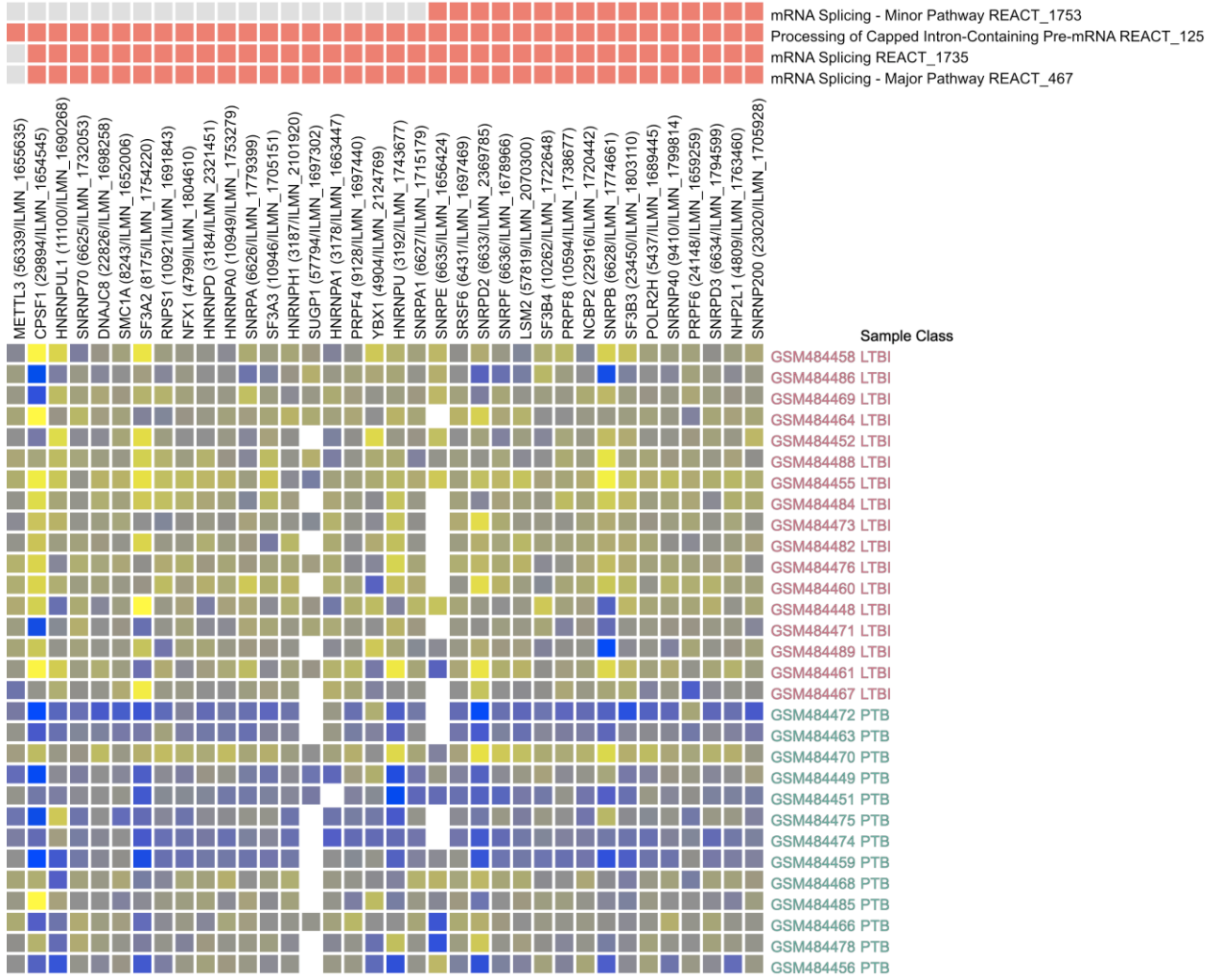
A.



B.



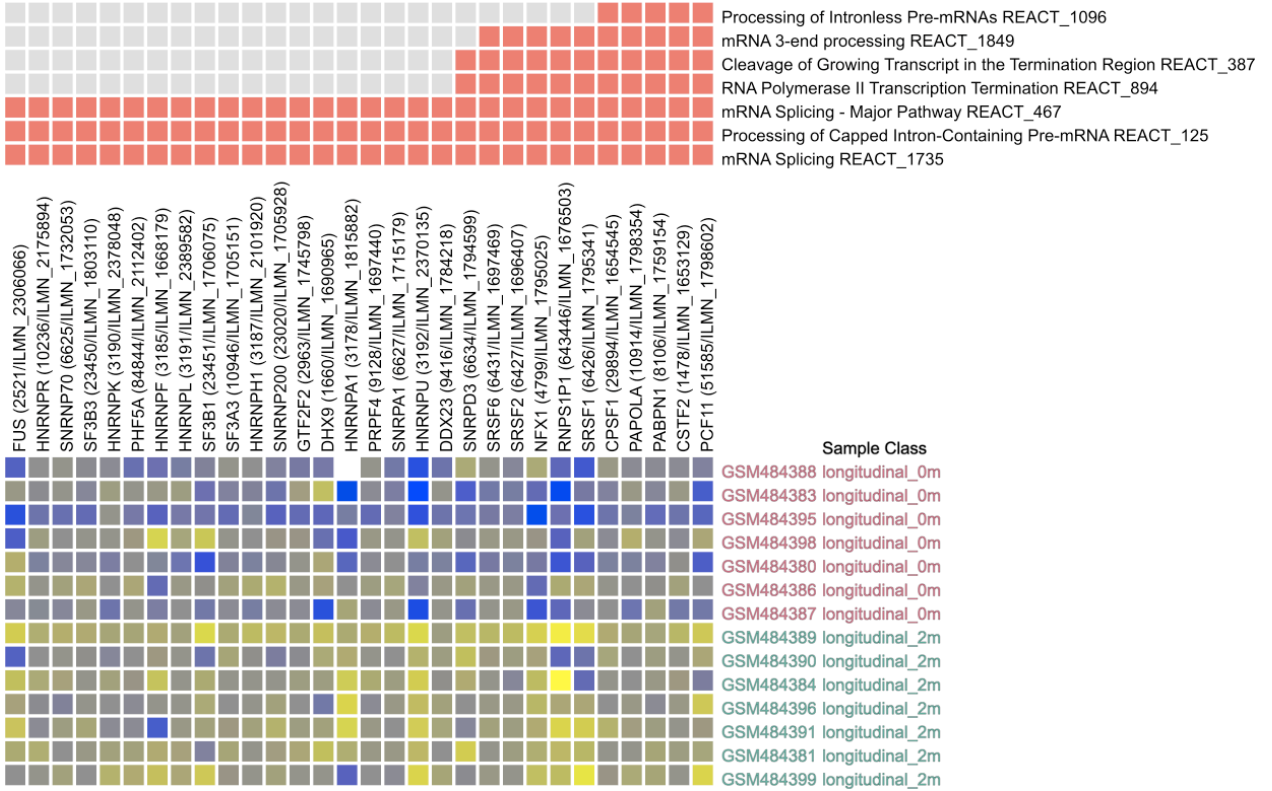
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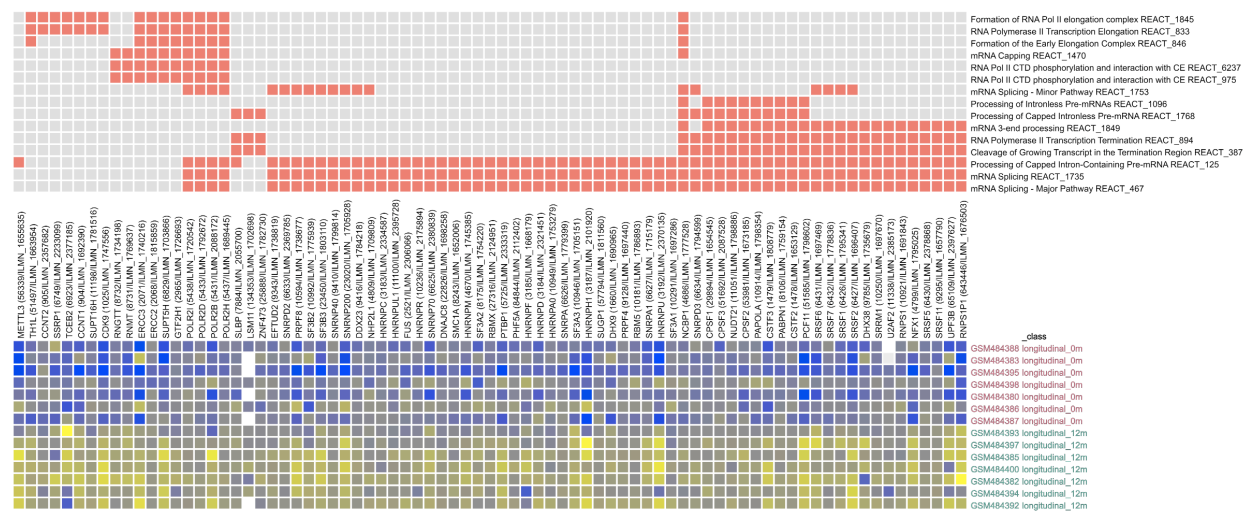
D.



E.



F.



G

