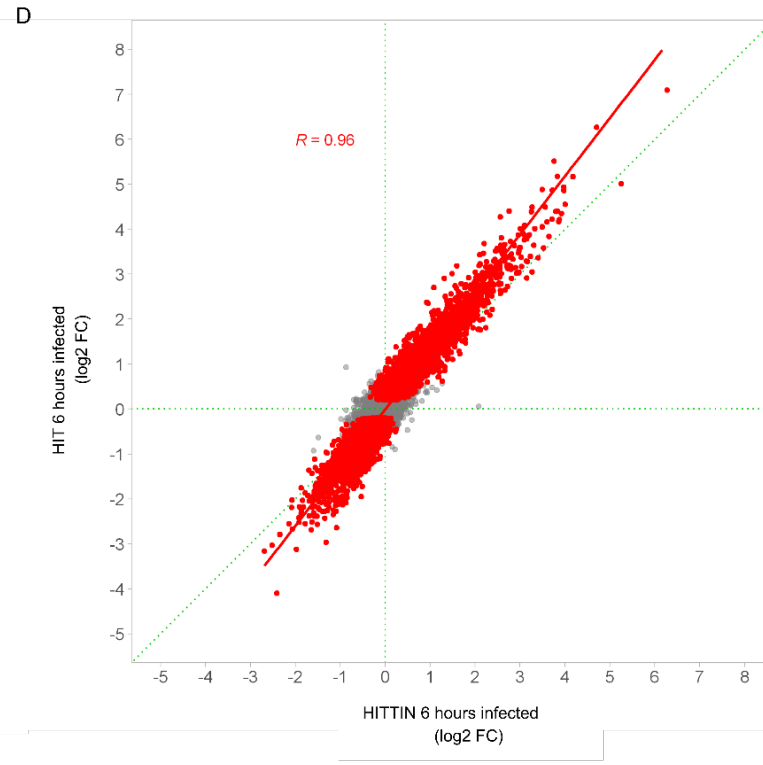
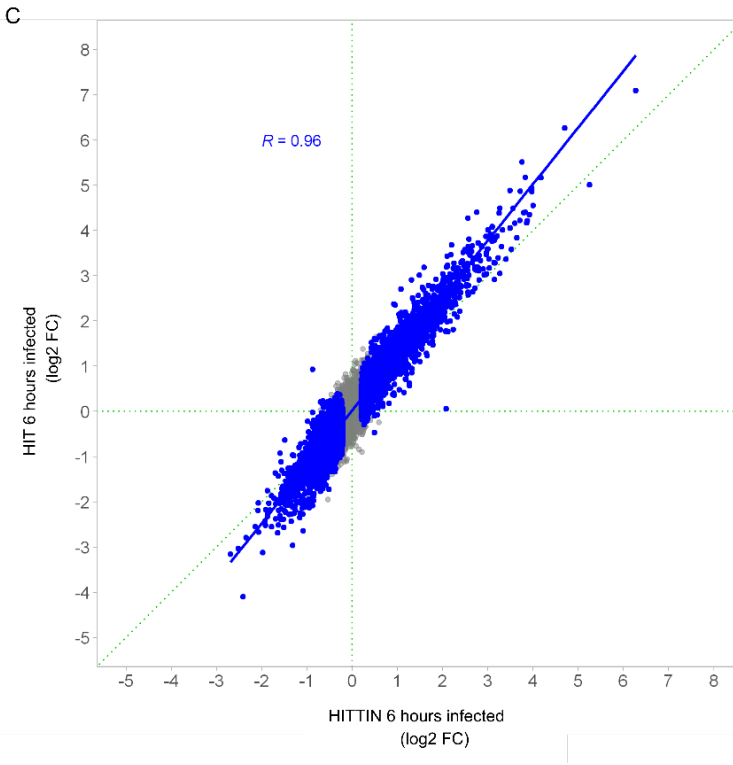
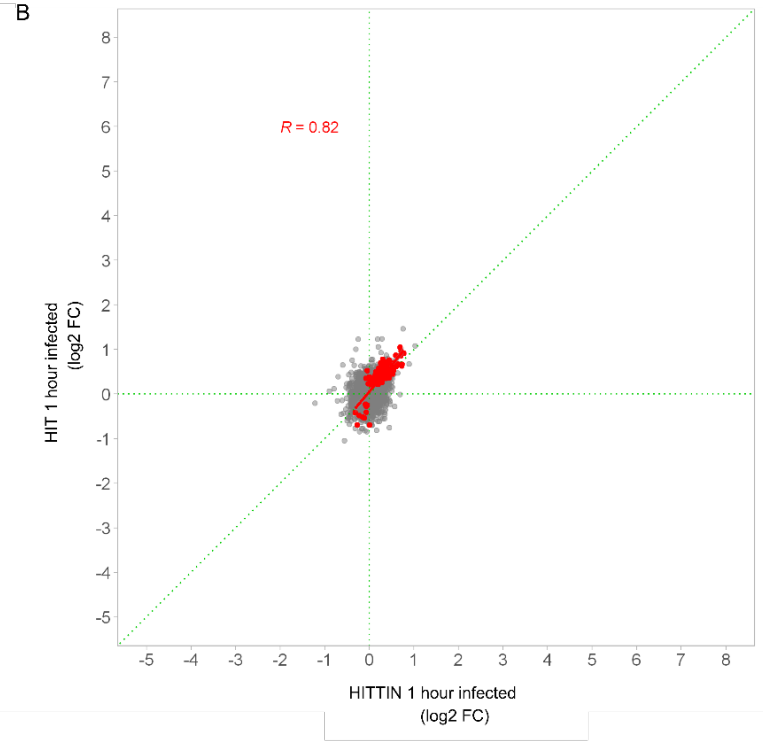
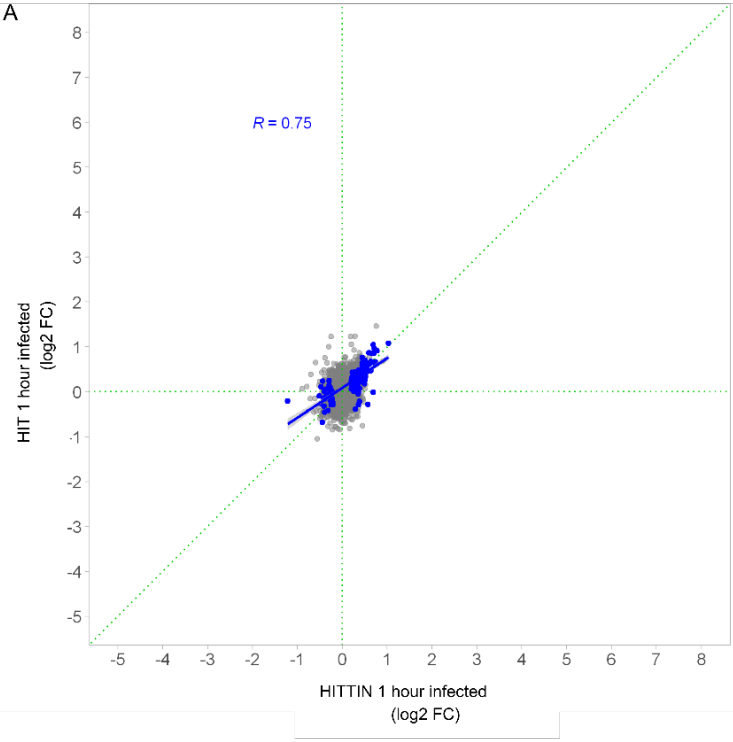


DEGs from the x-axis group

DEGs from the y-axis group



S2 Fig: Correlation plots of \log_2FC gene expression after *Mtb* infection of PMN from HITTIN and HIT

“HITTIN 1h infected” represents the \log_2FC gene expression effect when comparing the 1h *Mtb* infection to the 1h uninfected response in neutrophils (PMN) from HIV-1-positive persistently TB, tuberculin and IGRA negative individuals (PMN_{HITTIN})(x-axis). “HITTIN 6h infected” is the same but for 6h. “HIT 1h infected” represents the \log_2FC gene expression effect when comparing the 1h *Mtb* infection to the 1h uninfected response in PMN from HIV-1-positive, IGRA positive, tuberculin positive individuals (PMN_{HIT})(y-axis). “HIT 6h infected” is the same but for 6h. Scatterplots display the correlation of the \log_2FC gene expression as defined for each group at 1h (**A and B**) or 6h (**C and D**). Each grey dot represents a differentially expressed gene (DEGs). The grey dots show combined DEGs from both groups represented on the x and y axis. Blue coloured dots indicate DEGs from the x-axis group and red dots indicate the y-axis group. Pearson correlation (R value) was calculated for the coloured DEGs. The \log_2FC for each group is plotted with the y-axis as the reference group. Differential gene expression is more pronounced in genes with the highest \log_2FC , with the majority of genes displaying good correlation between phenotype groups.