



S5 Fig. Gene ontology enrichment analysis of differentially expressed genes (A) and proteins (B) from *Mtb* H37Rv. Bar graphs of significantly enriched GO terms (p -value < 0.05) in the list of differentially expressed genes (A) or proteins (B). For panel A, among the 725 DE genes in ZLM, 663 are protein coding genes with annotated GO terms and were used for the enrichment analysis and for panel B, all 65 DE proteins had GO annotations and were used in the enrichment analysis. The color of the bars is determined by the z-score and indicates whether the given biological process is more likely to be decreased (blue) or increased (red) in the dataset. The scale for the z-score in panel A applies to both bar graphs in panels A and B. A key for the GO terms, their process and the p-value for the enriched term is given to the right of each bar graph. Process refers to the GO term categories labeled above each bar graph which refers to the process belonging to either a cellular component (CC), biological process (BP) or molecular function (MF).