SUPPLEMENTAL TABLE TITLES AND LEGENDS

Table S1. Related to Figure 1. High-confidence set of *Mtb* secreted proteins.

Mtb culture filtrates separated by SDS-PAGE (Figure S1A) were subjected to LC-MS/MS analysis to identify secreted proteins. These results were manually curated to remove known cytoplasmic or cell-wall contaminants (Målen et al., 2007).

Table S2. Related to Figure 1. Comparison of U937 and 293T co-purifying proteins.

To evaluate the impact of addition of U937 macrophage cell lysates to our PPI scheme (Figure 1A), a subset of bacterial proteins were re-analyzed by AP-MS using 293T lysate alone without inclusion of the U937 lysate. All these interactions were scored by MiST and those with values ≥0.7 are displayed.

Table S3. Related to Figure 1. Full AP-MS dataset.

All host proteins identified from the AP-MS proteomics pipeline described in this study (Figure 1).

Table S4. Related to Figure 1. MiST scoring of AP-MS dataset.

Table S5. Related to Figure 2. Comparison of AP-MS datasets from different pathogens.

Table S6. Related to Figure 2. Functional annotation of high-confidence interacting host proteins.

DAVID v6.8 Uniprot keywords analysis was used to annotate all host proteins with MiST ≥0.7 for the indicated pathogens.

Table S7. Related to Figure 2. Evolutionary analysis of *Mtb*-interacting proteins.

SnIPRE and iHS analysis data.

Table S8. Related to Figure 4. PTMs of host proteins during infection with *Mtb*.

Table S9. Related to Methods. Oligonucleotides, DNA barcodes, and complementation sequences.