SUPPLEMENTAL FIGURES and LEGENDS

Figure S1. The overlap of the two lists of Mtb candidate proteins identified on the protein microarray using two macrophage cell lines, *i. e.*, THP-1 and U937.

Figure S2. The binding model of BfrB and RPS3. The interaction between BfrB (rose red) and RPS3 (green); AAs 164-181 of the BfrB were showed in red, and AAs 1-42 of the RPS3 were displayed in green. AAs, Amino acids

(A) Diagram of the FLAG-tagged BfrB and the mutant of C-terminus truncation.

(B) HEK293T cells transfected with constructs expressing full-length or truncated FLAG-tagged BfrB proteins, lysed after 48 h, and immunoblotted for RPS3 after immunoprecipitation with the FLAG antibody for BfrB in lysates. Experiments were carried out in triplicate.

(C) Total view of the interaction between the RPS3 (pale green) and BfrB (pink).

Figure S3. Immunoblot analysis of IκBα phosphorylation induced by TNF-α (100 ng/mL, 1 h).

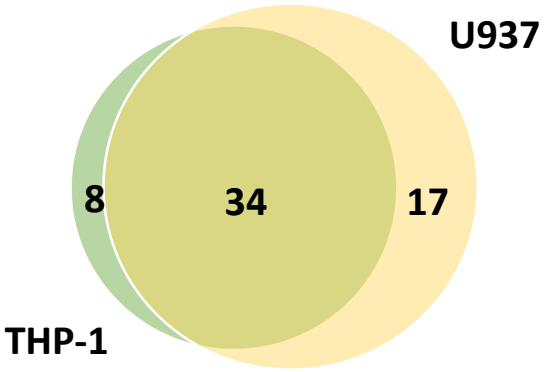
Supplementary Tables and Table Legends

Table S1. The Mtb effectors that have identified host interacting proteins from previous studies.

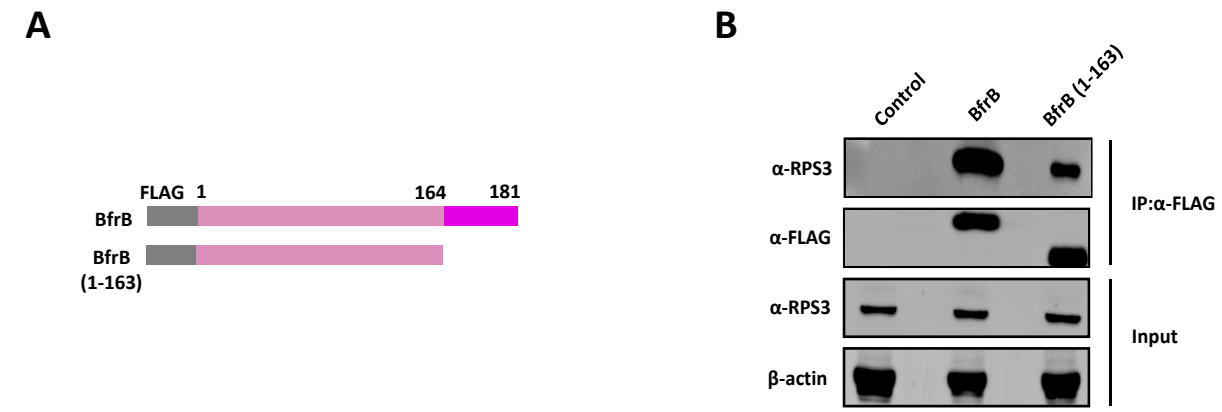
Table S2. The full list of the Mtb proteins that interact with THP-1, U937 cell lysate identified by the strategy of SOPHIE. The cutoff was set as SNR>1.5 and p value $\leqslant 2\times 10^{-5}$.

Table S3. The potential Mtb effectors that overlapped with the list of Mtb membrane proteins and secreted proteins.

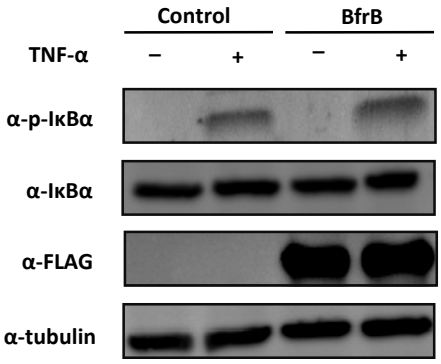
Table S4. The result of LC-MS/MS for the major bands that were enriched by using BfrB as bait.



He *et al.*, Figure S1.



He *et al.*, Figure S2.



He *et al.*, Figure S3.