Supplementary figures for

Enrichment-assisted PhIP-seq discovers a serum antibody peptide signature for active tuberculosis

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This PDF file includes **Figure S1** to **Figure S4**

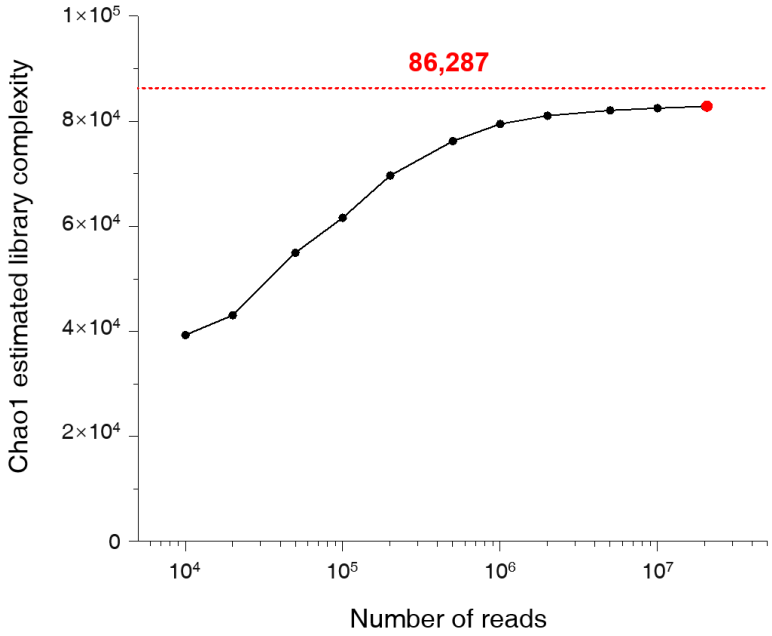

Figure S1. Sequencing-depth and library-complexity assessment of TbMap.

Relationship between sequencing read depth and estimated clone number in TbMap. The curve supports adequate sequencing depth for library characterization and provides additional quality-control evidence for the library summarized in **Figure 1**.

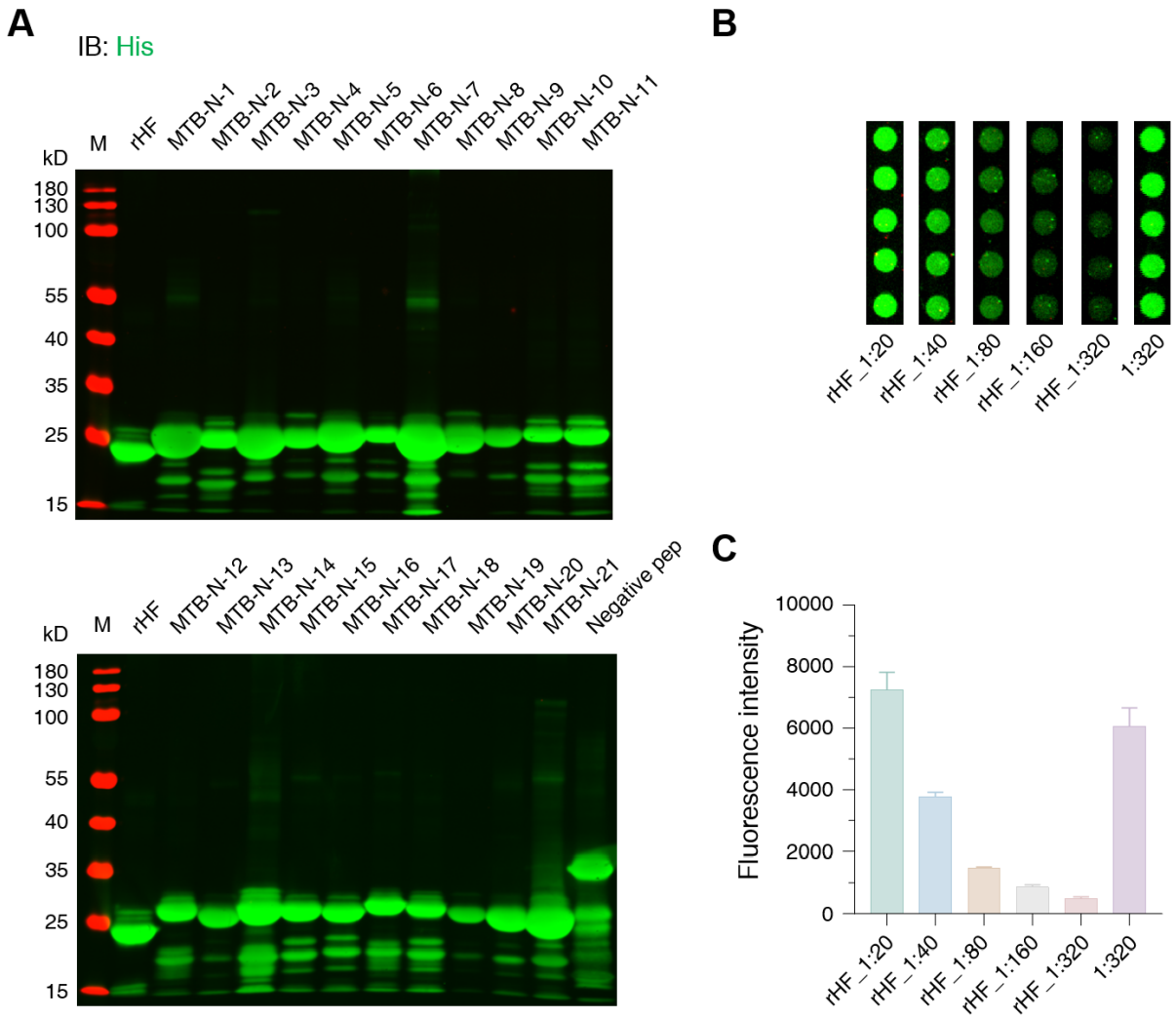

Figure S2. Extended candidate antigen quality control and rHF-background reduction for the peptide microarray assay.

(A) Western blot analysis of purified candidate peptide-rHF fusion proteins and control proteins used in the peptide microarray. (B) Representative microarray images showing rHF-reactive signal after serial rHF-based serum pretreatment or dilution conditions. (C) Quantification of rHF-associated background under the tested conditions. These experiments support antigen-production quality control and assay optimization for the orthogonal peptide microarray validation workflow shown in **Figure 3**.

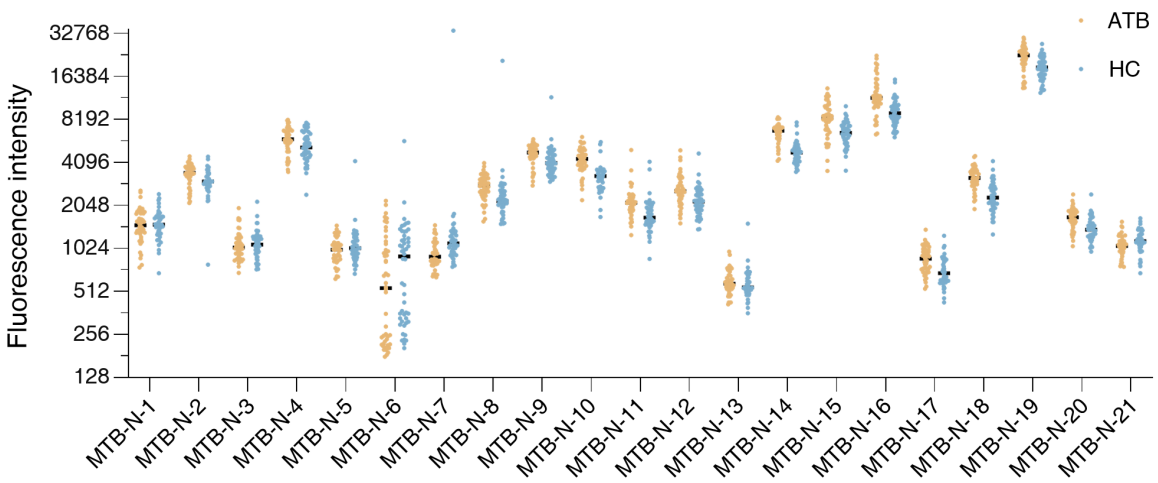

Figure S3. The fluorescence intensity of 21 peptides in the model-development cohort.

combo_ID	n_marker	markers	validation_auc
C9	1	MTB-N-14	0.689
C13	1	MTB-N-18	0.665
C23	2	MTB-N-2 MTB-N-14	0.779
C104	2	MTB-N-14 MTB-N-19	0.730
C359	3	MTB-N-9 MTB-N-10 MTB-N-14	0.886
C194	3	MTB-N-2 MTB-N-14 MTB-N-18	0.787
C1473	4	MTB-N-9 MTB-N-10 MTB-N-14 MTB-N-18	0.885
C1475	4	MTB-N-9 MTB-N-10 MTB-N-14 MTB-N-20	0.896
C4243	5	MTB-N-9 MTB-N-10 MTB-N-14 MTB-N-16 MTB-N-18	0.877
C4219	5	MTB-N-9 MTB-N-10 MTB-N-13 MTB-N-14 MTB-N-18	0.885

Figure S4. The AUC of 10 candidate models in the internal test set cohort.