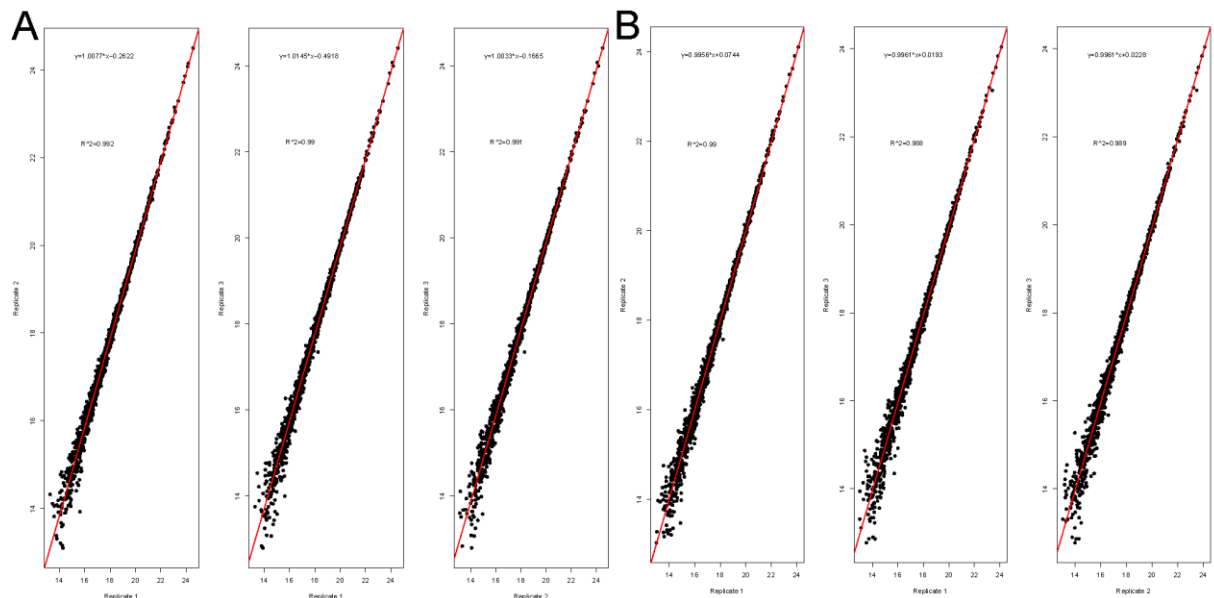


# Identification and Quantification of S-sulfenylation Proteome of *Mycobacterium tuberculosis* under Oxidative Stress

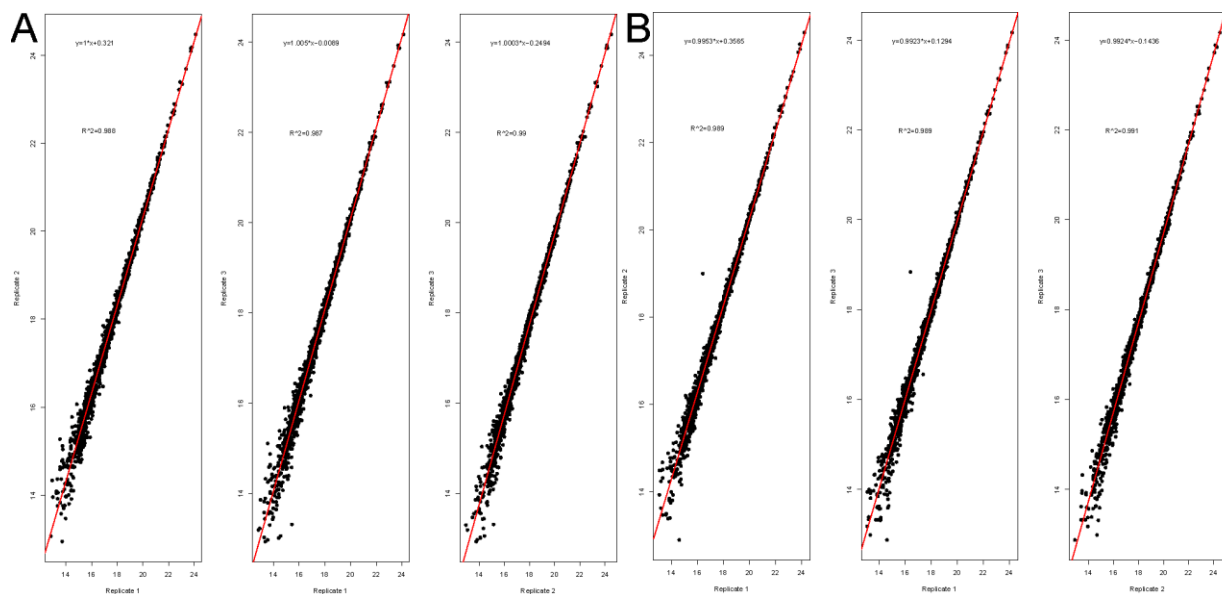
Yun Lu <sup>a</sup>, Hongtong Chen <sup>a</sup>, Penghe Wang <sup>a</sup>, Jing Pang <sup>a</sup>, Xi Lu <sup>a</sup>, Guoqing Li <sup>a</sup>, Xinxin Hu <sup>a</sup>, Xiukun Wang <sup>a</sup>, Xinyi Yang <sup>a</sup>, Congran Li <sup>a</sup>, Yu Lu\*<sup>b</sup>, Xuefu You\*<sup>a</sup>

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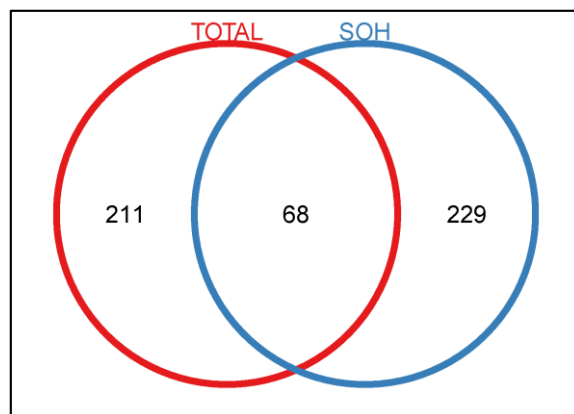
<sup>b</sup> Beijing Key Laboratory of Drug Resistance Tuberculosis Research, Beijing Tuberculosis and Thoracic Tumor Research Institute, and Beijing Chest Hospital, Capital Medical University, Beijing, China



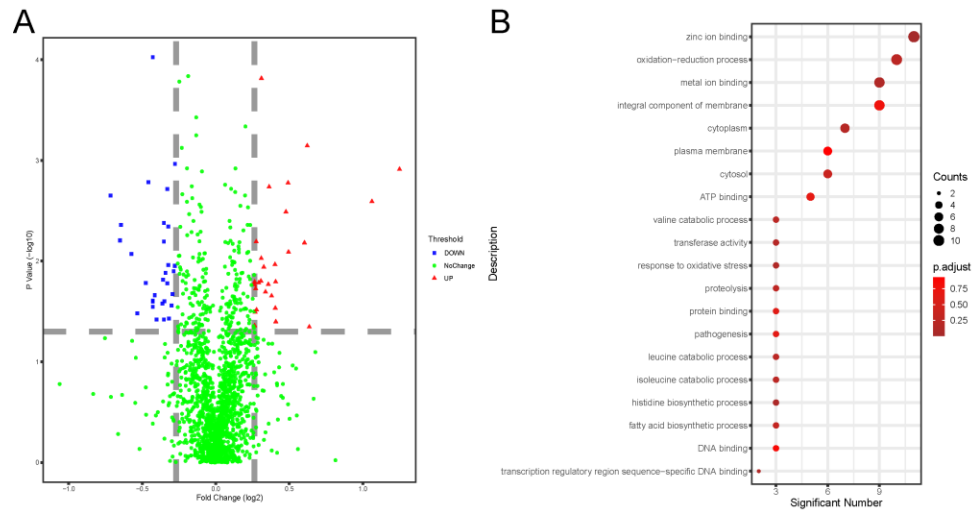
**FIG S1** Linear correlation curves of replicates in control and stressed group of total cysteine modification. A, control group; B, hydrogen peroxide treated group.



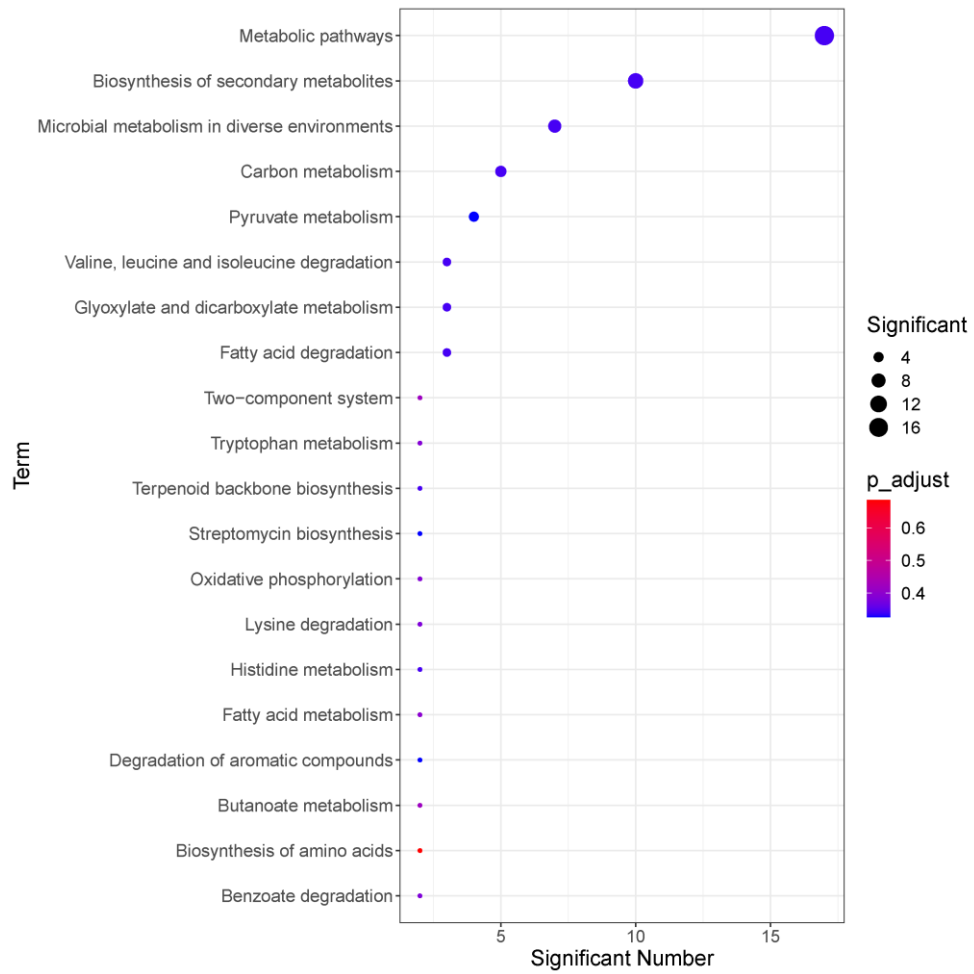
**FIG S2** Linear correlation curves of replicates in control and stressed group of SOH modification. A, control group; B, hydrogen peroxide treated group.



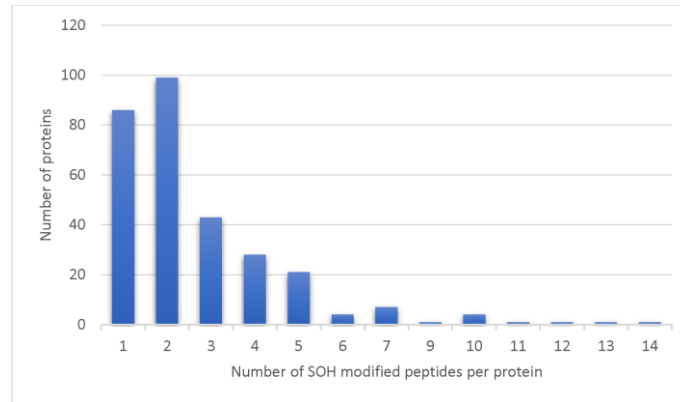
**FIG S3** The venn plot of significant modified proteins ( $p < 0.05$ ) between TC and SOH groups under  $H_2O_2$  pressure.



**FIG S4 A** Volcano plot of total cysteine modified proteins under H<sub>2</sub>O<sub>2</sub> pressure; **B** GO enrichment results of proteins with significantly changed total cysteine modified levels filtered by fold change >1.2 and p <0.05. Significant number means the counts of proteins.



**FIG S5** KEGG pathway enrichment results of proteins with significantly changed total cysteine modified levels filtered by fold change >1.2 and  $p < 0.05$ .



**FIG S6** Number of SOH modified peptides per protein.