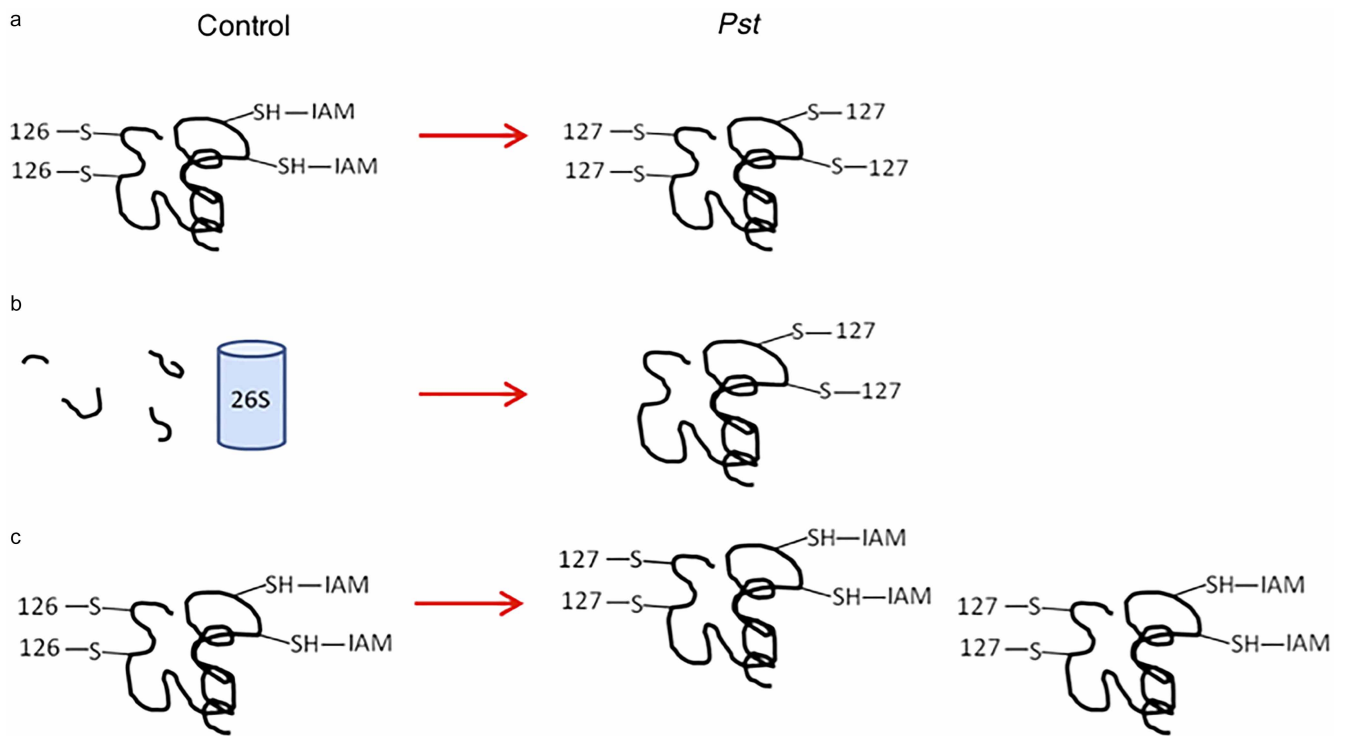Supplementary Figure S1. Criteria used to identify redox proteins under *Pst* infection. A volcano plot of the results of (**a**) *prf3* 4 hai, (**b**) PtoR 4 hai, and (**c**) PtoR 24 hai showing the fold change (*x*-axis) and significance (*p*-value, -log scale on *y*-axis). Each circle represents a peptide identified in at least two biological replicates. The red dashed lines represent the criteria adopted to identify a peptide as being redox-regulated ($p < 0.05$ and FC < 0.8 or FC > 1.2). The blue circles are the peptides determined to be redox responsive.

Supplementary Figure S2. Effect of protein level changes on the analysis of potential redox proteins. (**a**) The protein in the control sample is blocked at two cysteines, and the one in the treated sample has twice the amount of tag. (**b**) Protein degradation could lead to an increase in the treated protein. (**c**) An increase in treated sample can be due to an increase in the protein amount.