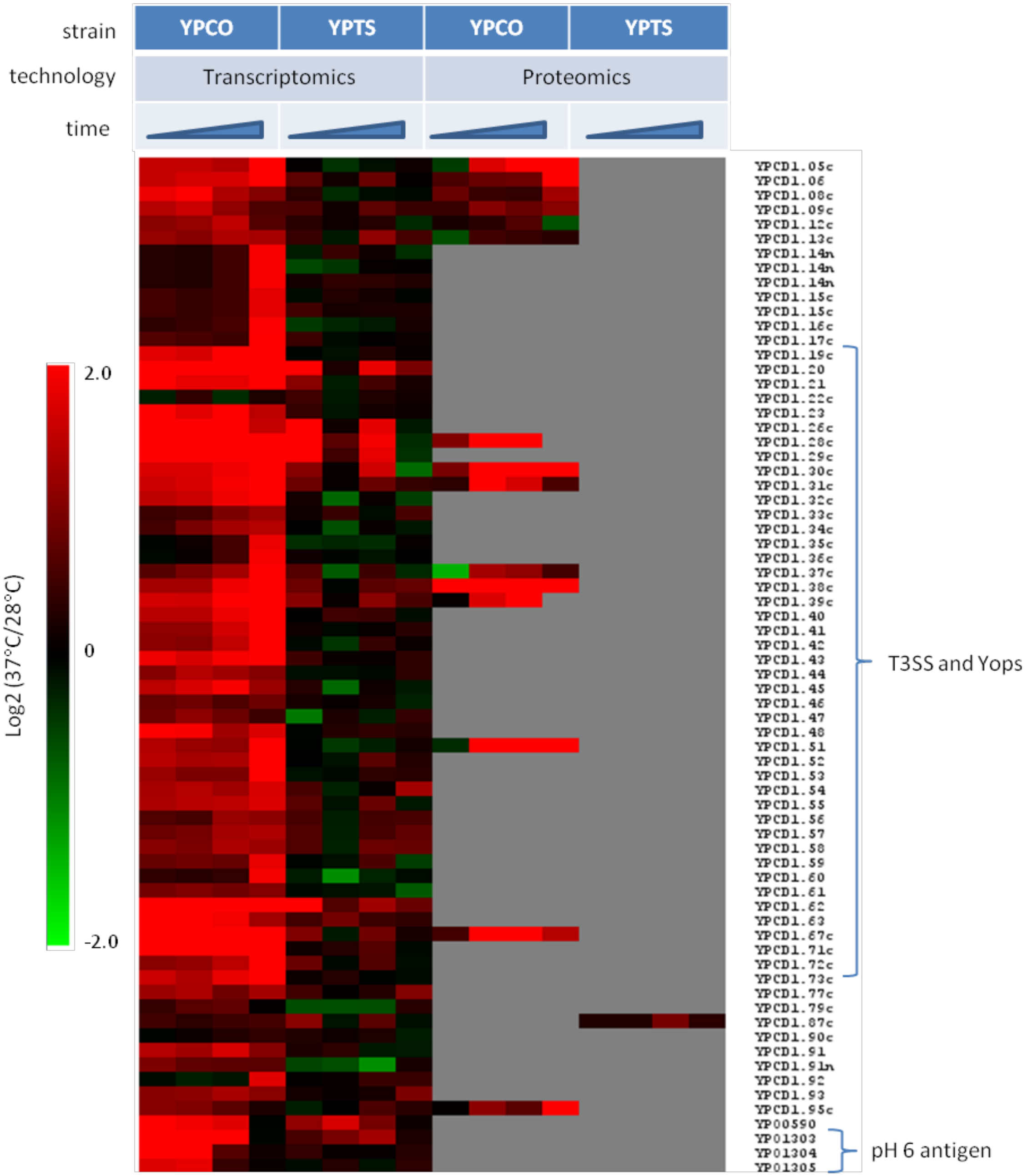
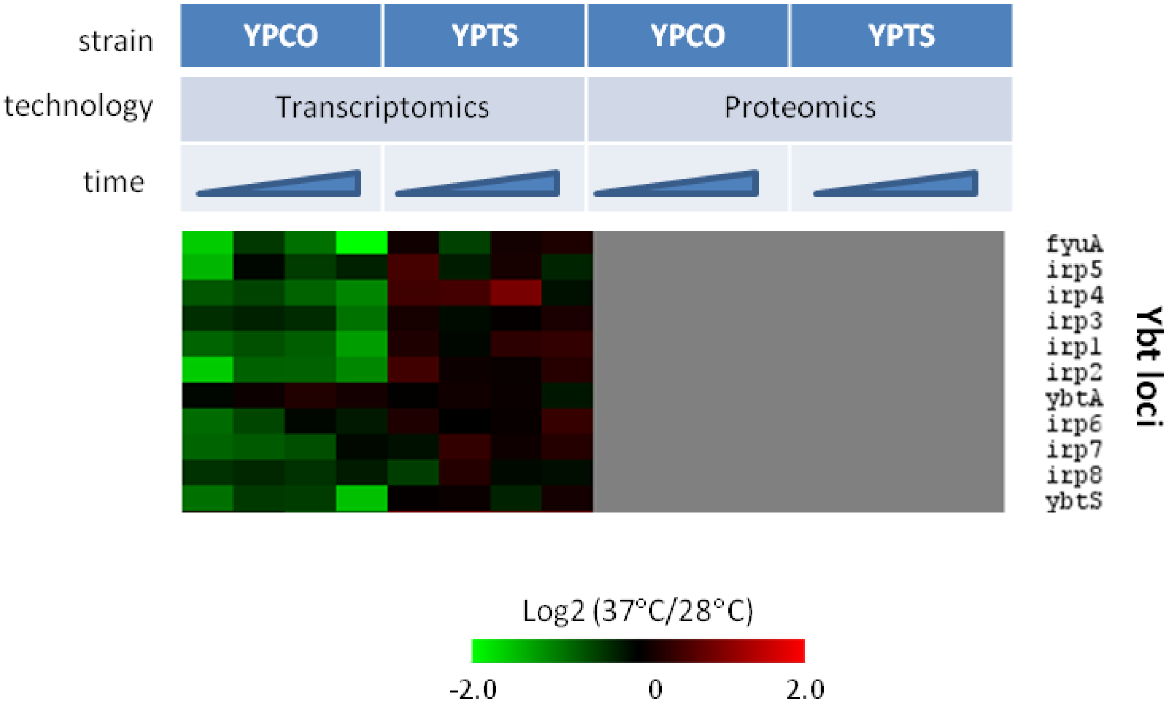
Supplementary Figure 1



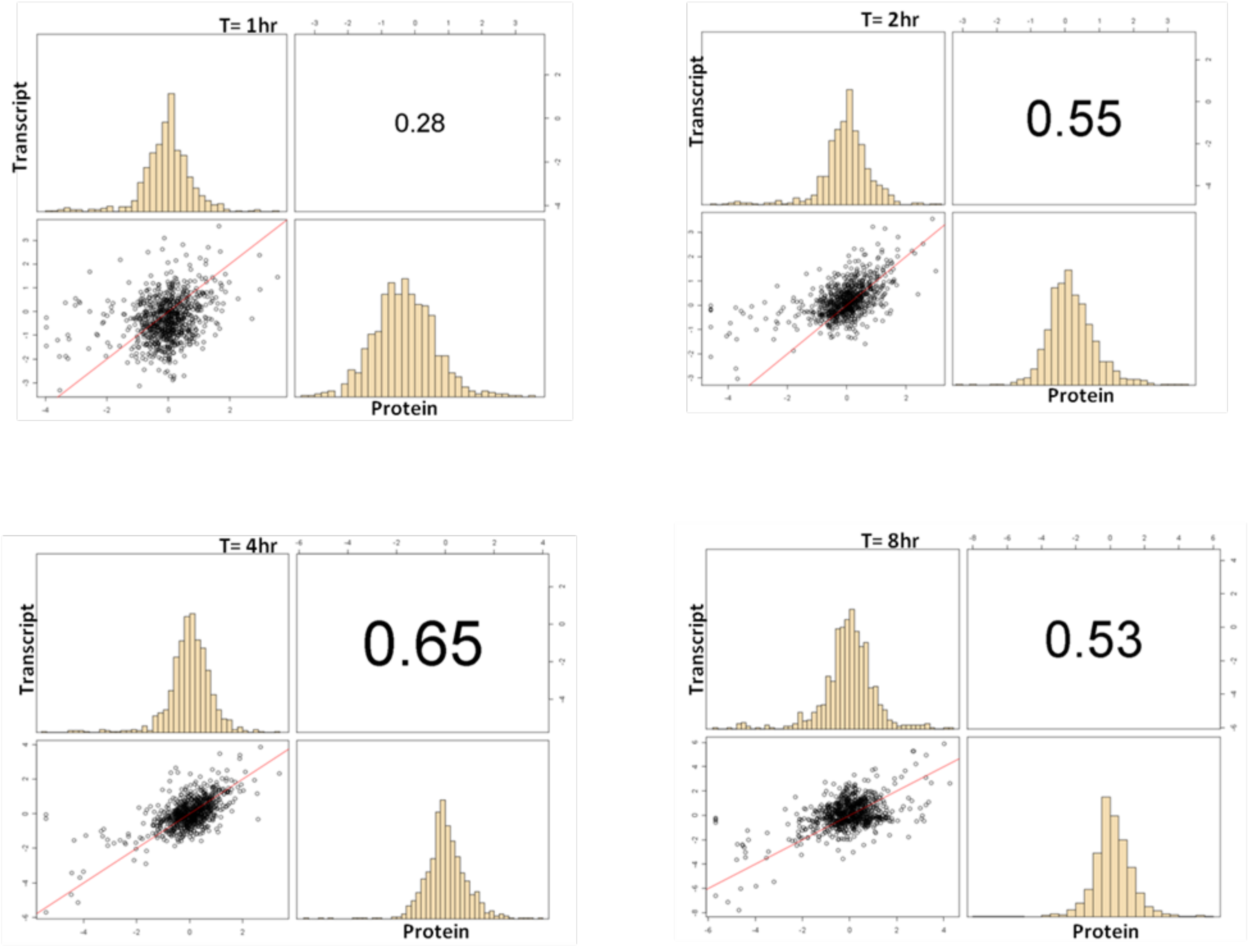
Supplementary Figure 1. Heat map illustration of genes preferentially up-regulated in YPCO relative to YPTS in response to temperature elevation detected by either transcriptomics or proteomics. Time represents sampling points at 1hr, 2hr, 4hr, 8hr. YPCO, *Yersinia pestis* CO92; YPTS, *Yersinia pseudotuberculosis* PB1/+.

Supplementary Figure 2



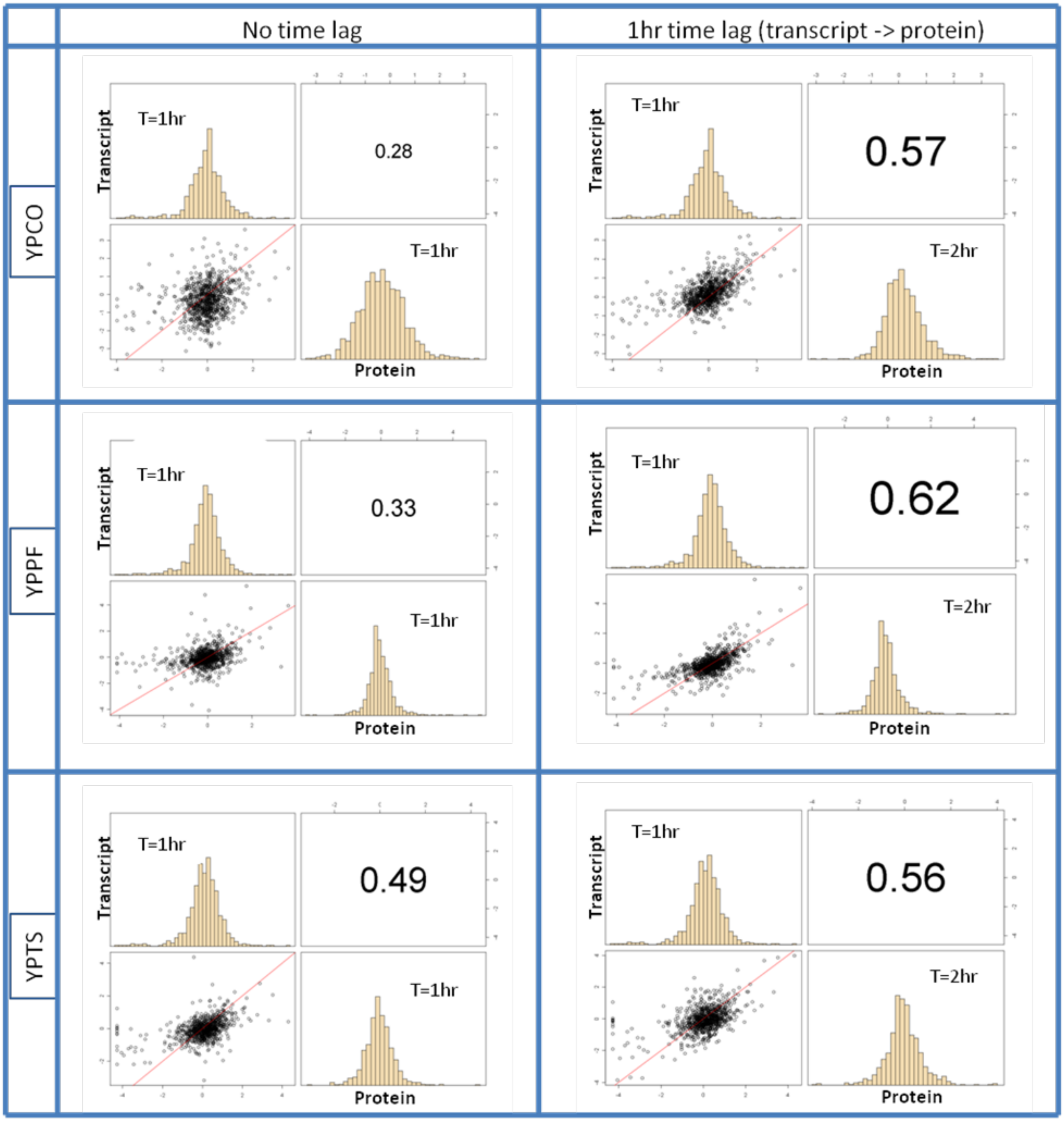
Supplementary Figure 2. Heat map illustration of Ybt loci-members preferentially up-regulated in YPCO relative to YPTS in response to temperature elevation. Time represents sampling points at 1hr, 2hr, 4hr, 8hr. YPCO, *Yersinia pestis* CO92; YPTS, *Yersinia pseudotuberculosis* PB1/+.

Supplementary Figure 3



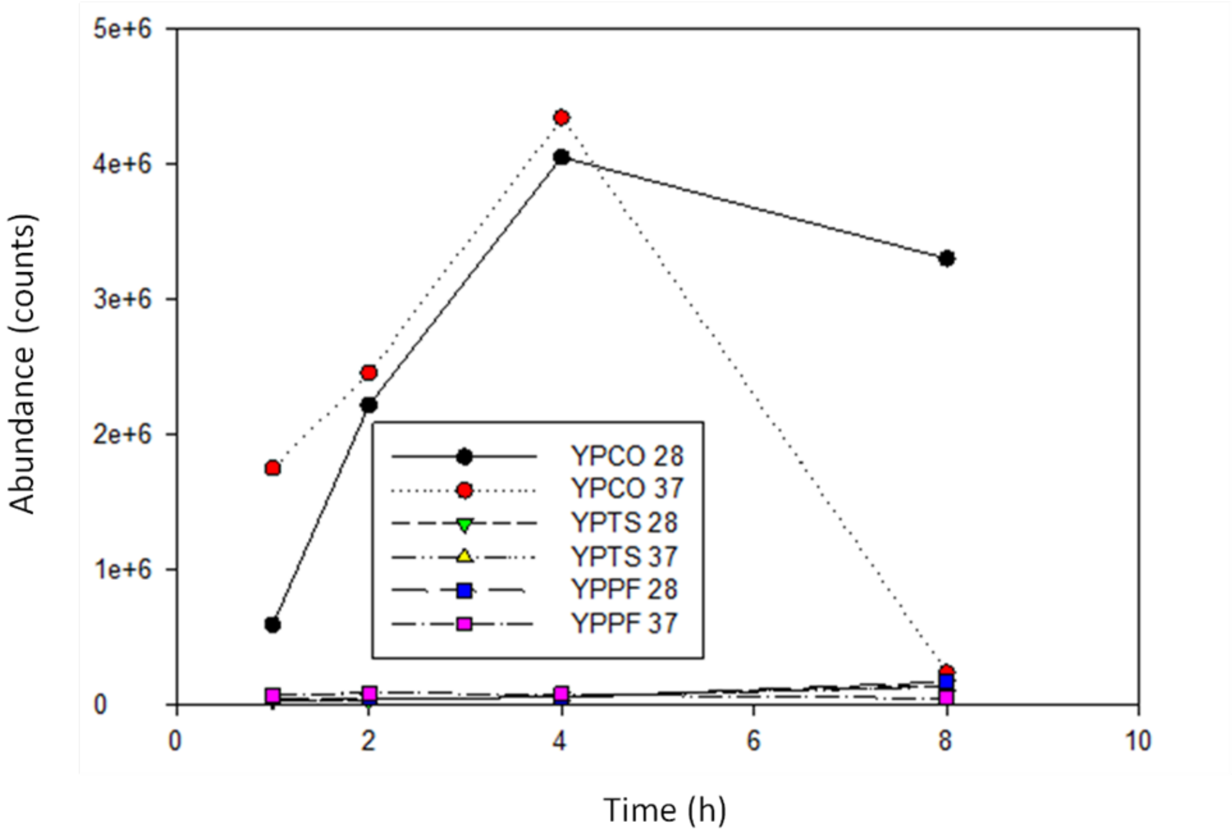
Supplementary Figure 3. Correlation between measured transcript and protein responses to temperature shift at each time point (T = 1hr, T = 2hr, T = 4hr, T = 8hr) for YPCO. YPCO, *Yersinia pestis* CO92.

Supplementary Figure 4



Supplementary Figure 4. Correlation between measured transcript and protein responses to temperature shift compared with and without a 1h time lag in YPCO, YPTS and YPPF. YPCO, *Yersinia pestis* CO92; YPTS, *Yersinia pseudotuberculosis* PB1/+; YPPF, *Yersinia pestis* Pestoides F.

Supplementary Figure 5



Supplementary Figure 5. Glutamic acid abundance measured by GC-MS in YPCO, YPTS and YPPF at flea vector temperature and mammalian host temperature conditions. YPCO, *Yersinia pestis* CO92; YPTS, *Yersinia pseudotuberculosis* PB1/+; YPPF, *Yersinia pestis* Pestoides F. GC-MS, gas chromatography-mass spectrometry.