Supplemental figures

Comparative phosphoproteomics reveals components of host cell invasion and post-transcriptional regulation during *Francisella* infection

Ernesto S. Nakayasu, Rebecca Tempel, Xiaolu A. Cambronne, Vladislav A. Petyuk, Marcus B. Jones, Marina A. Gritsenko, Matthew E. Monroe, Feng Yang, Richard D. Smith, Joshua N. Adkins and Fred Heffron

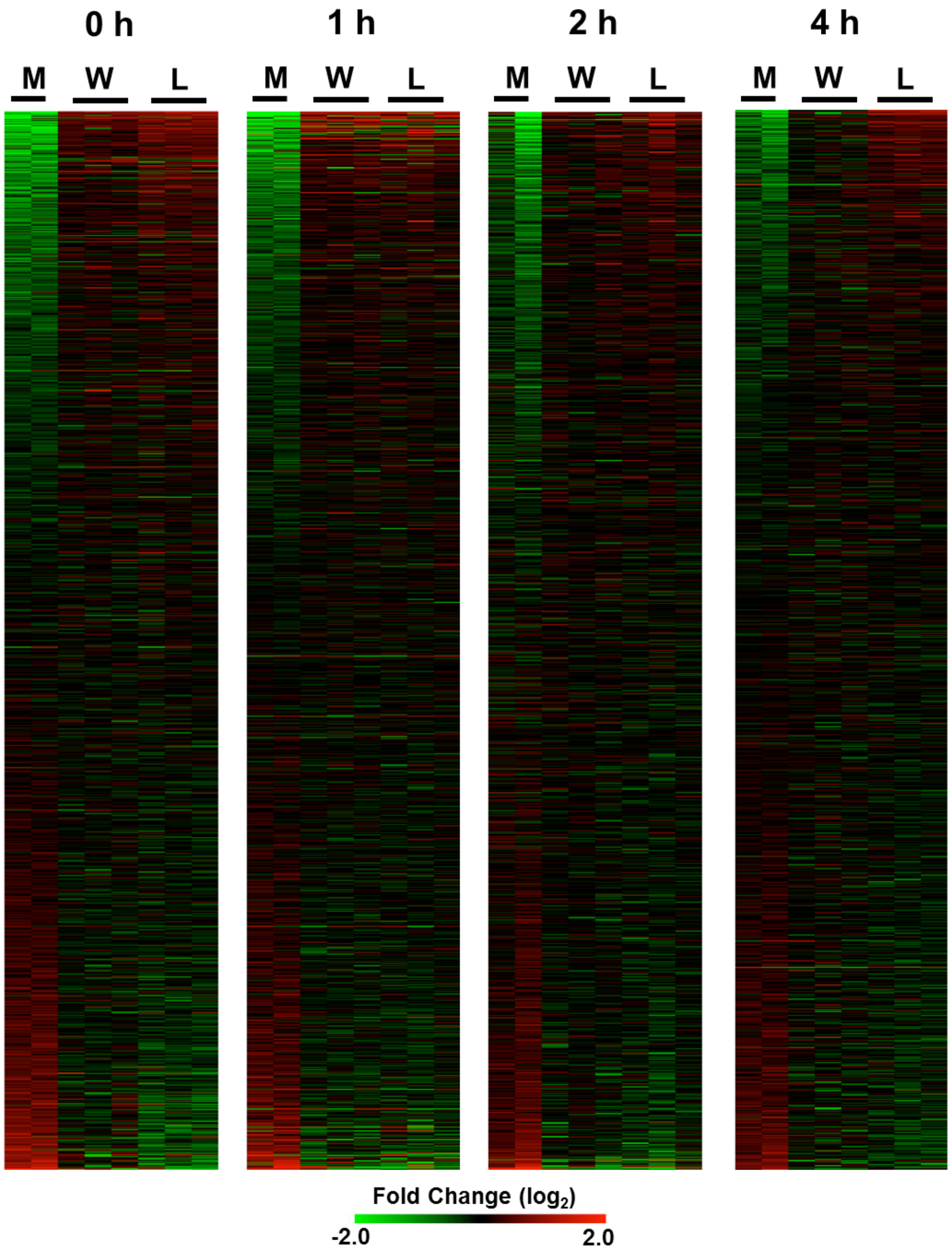

Figure S1. Phosphoproteome of RAW 264.7 infected with *Francisella*. Heatmaps show the abundances of all phosphopeptides in the course of infection. Abbreviations: M, mock-infected; W, wild type-infected; L, *ΔlpcC*-infected.

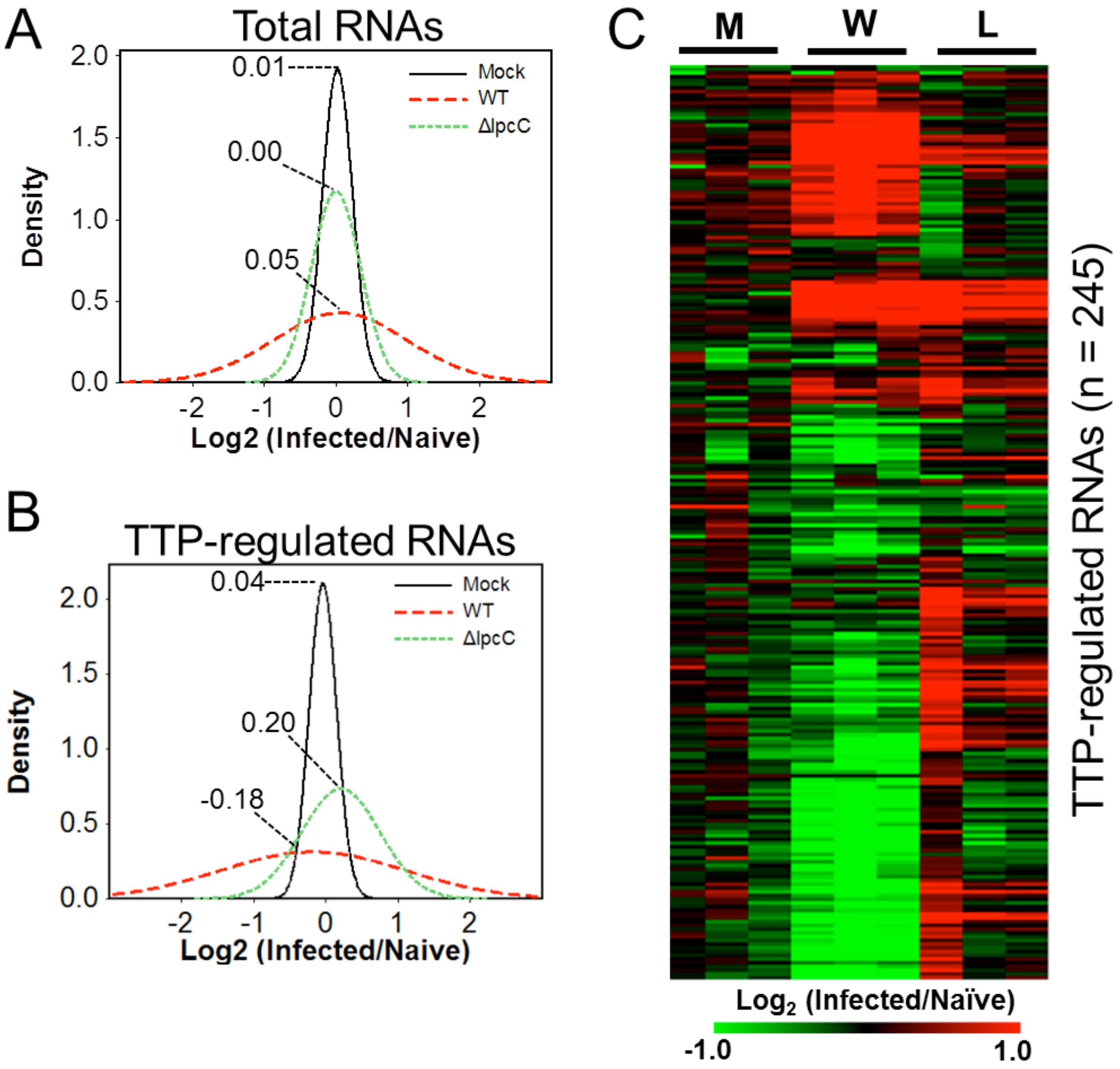

Figure S2. Transcriptomic analysis of spleens from mice infected with *Francisella*. A, Histogram of the abundance of all mRNAs measured in the microarray analysis. B, Histogram of the abundance of mRNAs previously reported to be degraded by tristetraprolin (TTP). C, Heatmap of mRNAs previously reported to be degraded by tristetraprolin (TTP). Abbreviations: M, mock-infected; W, wild type-infected; L, *ΔlpcC*-infected.