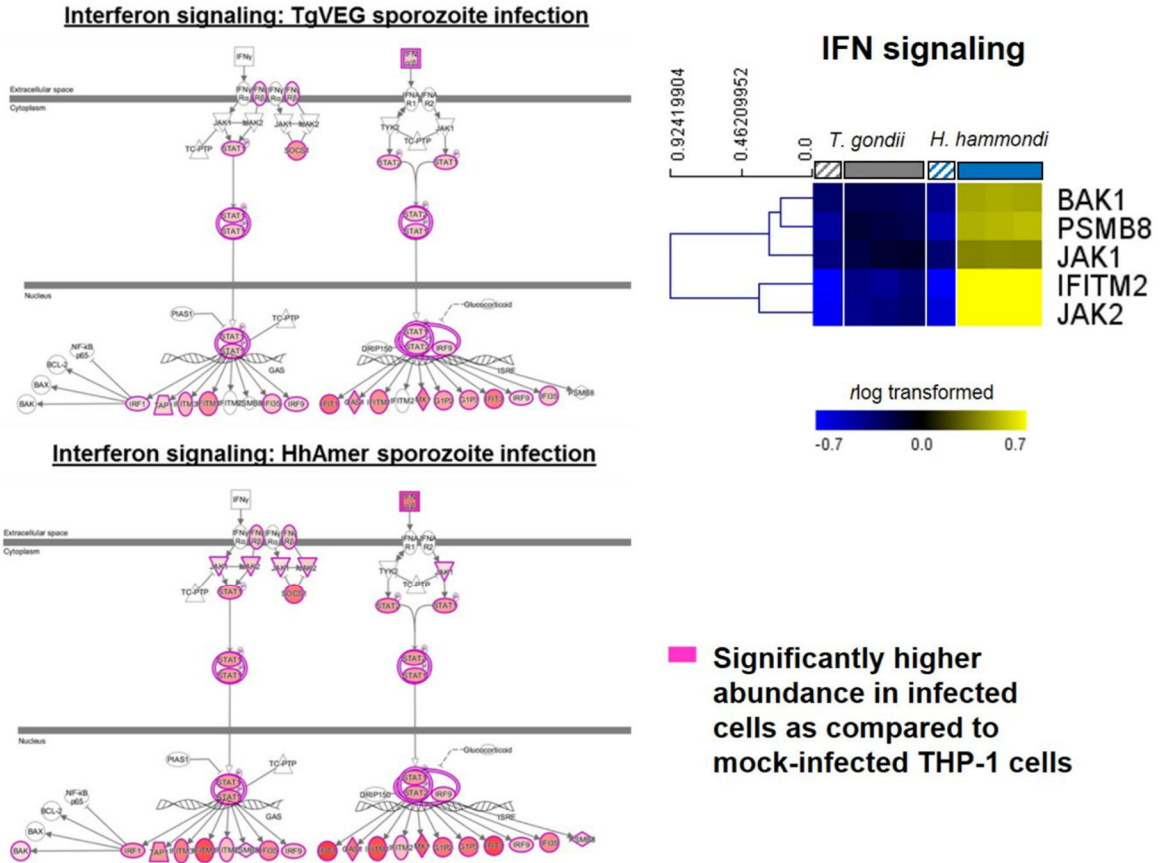


S2A Fig. Top canonical pathways enriched (z scores) in *T. gondii* or *H. hammondi*-infected THP-1 cells compared to mock-infected cells. Log₂ fold-change and DESeq2-derived p_{adj} values of genes with differential transcript abundance (\log_2 fold-change ≥ 2 or ≤ -2 ; $p_{adj} < 0.01$) were analyzed by Ingenuity Pathways Analysis®. **(Top Panel)** Stacked bars show pathways significantly enriched in infected cells compared to mock-treatment ($-\log_{10}(p\text{-value}) > 1.3 = p < 0.05$; z scores ≥ 2 or ≤ -2). Positive z scores represent pathways that were enriched in infected cells and negative z scores represent pathways enriched in uninfected cells. **(Bottom panel)** The majority of pathways enriched in infected or mock-treated cells were shared between *T. gondii* and *H. hammondi* infection. Exceptions for each species are indicated.



S2B Fig. *T. gondii* and *H. hammondi*-infected cells share many similar activated pathways but with significant quantitative differences. (Left panel) THP-1 cells infected with *T. gondii* or *H. hammondi* have significantly higher levels of the majority of transcripts belonging to the Canonical Interferon signaling pathway (from IPA), suggesting that this pathway is targeted by and/or responds to both species. **(Right Panel)** Heatmap of transcript abundance (\log_2 -transformed) from TgVEG and HhAmer-infected THP-1 cells for some members of the Interferon signaling pathway illustrates species-specific transcript abundances. Infected cells shown are represented by the solid boxes while mock-infected cells represented by striped boxes. Data were mean-centered and hierarchically-clustered (Euclidean distance).

IFN- γ response



MYC targets



S2C Fig. Enrichment plots from Gene Set Enrichment Analysis (GSEA) of THP-1 cells infected with *T. gondii* or *H. Hammondii*. Enrichment plots showing GSEA results for *IFN γ response* (top panels) and *MYC targets v1* gene sets (bottom panels) in THP-1 cells after infection with *T. gondii* (Tg) or *H. Hammondii* (Hh). Rank is based on log₂-transformed normalized transcript abundance in infected cells compared to mock. Normalized enrichment scores (NES) are also indicated for each of the plots. The *IFN γ response* gene set was highly positively enriched in response to *T. gondii* and *H. Hammondii* infection while *MYC targets v1* gene set was positively enriched in *T. gondii*-infected cells and negatively enriched in *H. Hammondii*-infected cells.