Supplementary Figures Legends

Figure S1. Indvidual plots of Bd load throughout infection trials. In each species, lines are differently colored to highlight individuals that had no detectable infection at time of tissues sampling and were classed as "cleared".

Figure S2. Histogram of *de novo* assembled transcript alignment to the *Xenopus tropicalis* NCBI reference protein dataset. Protein coverage data generated using blastx searches and Trinity-provided perl scripts.

Figure S3. Venn diagrams of species overlap of differentially expressed genes, separating the two congeneric focal species.

Figure S4. Visualization of the hub genes of the SK1 skin module defined by weighted gene coexpression network analysis (WGCNA). Hub genes defined as those included in both the top 100 module membership values and the top 150 network connection strengths.

Figure S5. Visualization of the hub genes of the SP1 spleen module defined by weighted gene coexpression network analysis (WGCNA). Hub genes defined as those included in both the top 100 module membership values and the top 150 network connection strengths.

Figure S6. Visualization of the hub genes of the SP2 spleen module defined by weighted gene coexpression network analysis (WGCNA). Hub genes defined as those included in both the top 100 module membership values and the top 150 network connection strengths.

Figure S7. Examples of inflammatory cytokines found to be differentially expressed in two or more of the studied species. Asterisks denote significance after correction for multiple testing (FDR). White = uninfected (controls), grey = infected. Species ordered by average Bd-infection intensity, from lowest

































