

Table S1. Sample identifiers, treatment group categories, and tadpole morphometrics for all samples used for transcriptomics and metagenomics analyses. Sample IDs in bolded red text came from individual tadpoles that were used in both analyses.

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Table S2. Differentially expressed host genes, their associated GO terms, and associated statistics for comparisons between several treatment group comparisons (sheets 1-4), and lists of significantly enriched GO terms and associated statistics for two treatment group comparisons (sheets 5-6).

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Table S3. Lists of significantly differentially abundant KEGG modules in the microbial metagenome, and associated statistics for comparisons between several treatment group comparisons (sheets 1-2).

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