

Table S1. Differentially expressed genes identified by LRT in DESeq2 with an unadjusted P-value less than 0.05 are found in the "DESeq2_LRT_results" tab. Pairwise Binomial Wald results for this same gene set are included. Genes are identified by their Stringtie accessions and associated NCBI RefSeq annotations. Cells are highlighted for DE genes with FDR < 0.1 for the respective group contrast. The second tab, "DESeq2_BvsR_results", contains full set of genes for Brooding vs. Release Binomial Wald test at the same significance threshold.

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Table S2. Annotation information for expression data derived from the GTF file associated with NCBI accession GCF_000239415.1, plus Gene Ontology info used in enrichment analysis.

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Table S3. Results for Gene Set Enrichment Analysis (GSEA) using GO terms as gene categories. Rows contain results for a single GO term and pairwise contrast between time-points. Additional columns contain GSEA results for each time-point vs. all other time-points combined. GO terms are clusters to account for gene overlap between lists. Second data spreadsheet contains gene list and annotations for each of the significantly enriched GO terms identified by GSEA.

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