Supplementary Table S1. Diapause incidence, percent hatch, and percent embryonation results for each biological replicate. “Library use” represents information on replicates used for sequencing at individual time points.

Supplementary Table S3. Genes differentially expressed across all three time periods associated with juvenile hormone metabolism. Homolog descriptions were retrieved from BioMart. Log-fold-change and associated Benjamini-Hochberg corrected p-values are given for each time period. “Other evidence” refers to additional annotation information used to functionally characterize each gene.

Supplementary Table S4. Differentially expressed genes in significantly enriched GO-Slim categories or Kegg pathways. Homolog descriptions and Biotypes were downloaded from BioMart. Log-fold-change and associated Benjamini-Hochberg corrected p-values are listed for each time period, as is the time period in which the category was significantly enriched.

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Supplemental Table 2. Information associated with each gene included in the differential expression analysis. The established homolog and its description and biotype, log-fold-changes and p-values at each data collection time point, and normalized expression values for each library are given.

Download Table S2