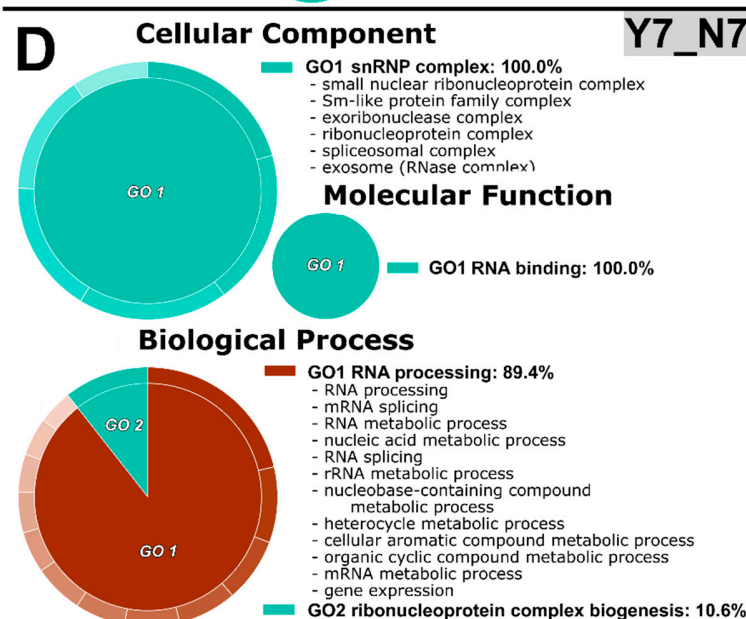
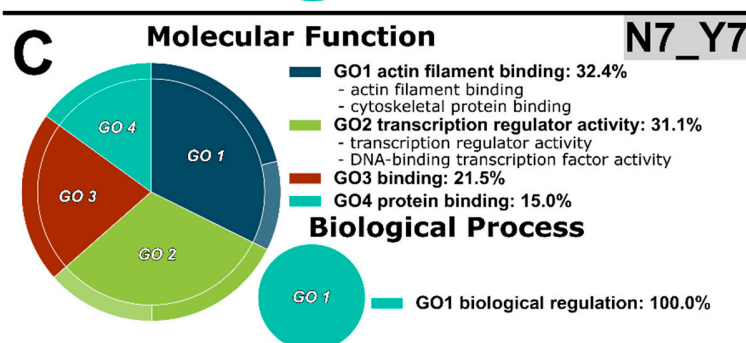
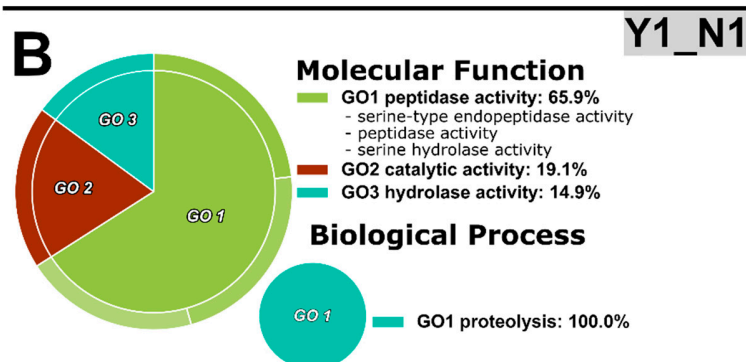
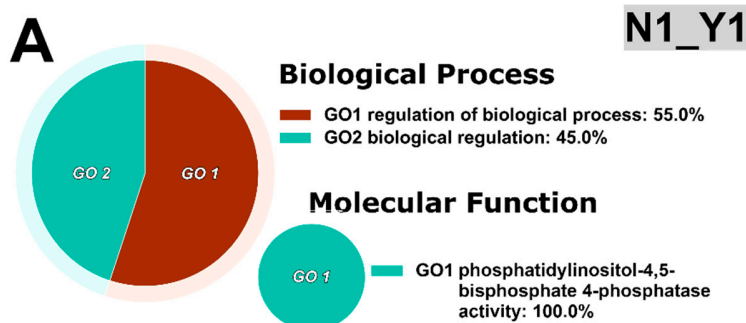
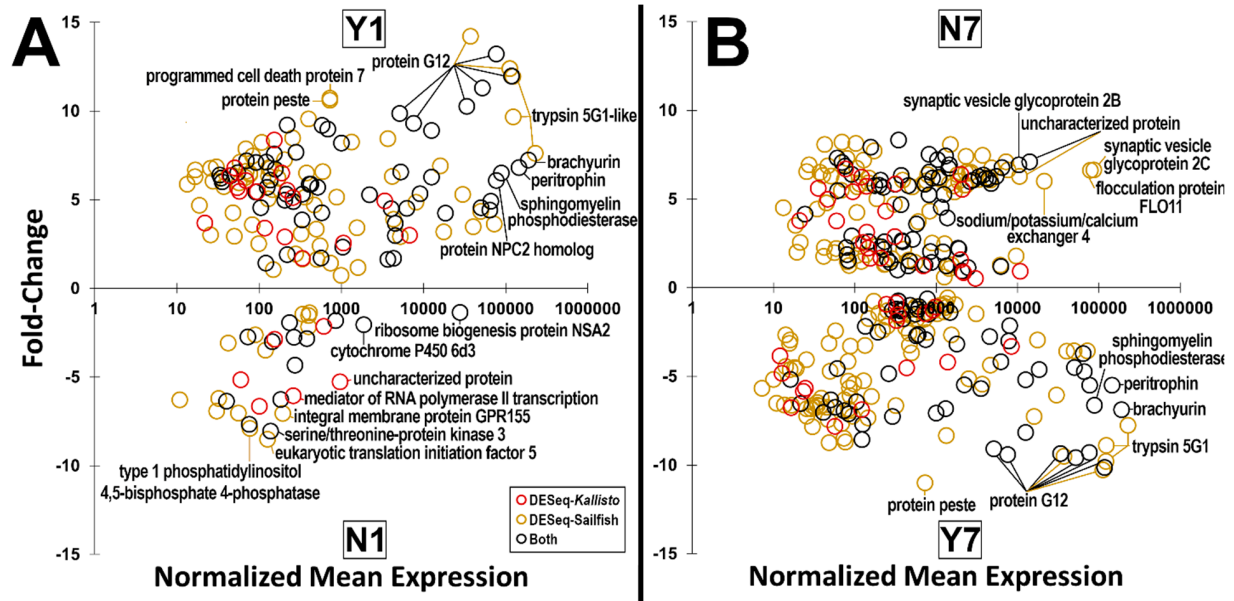


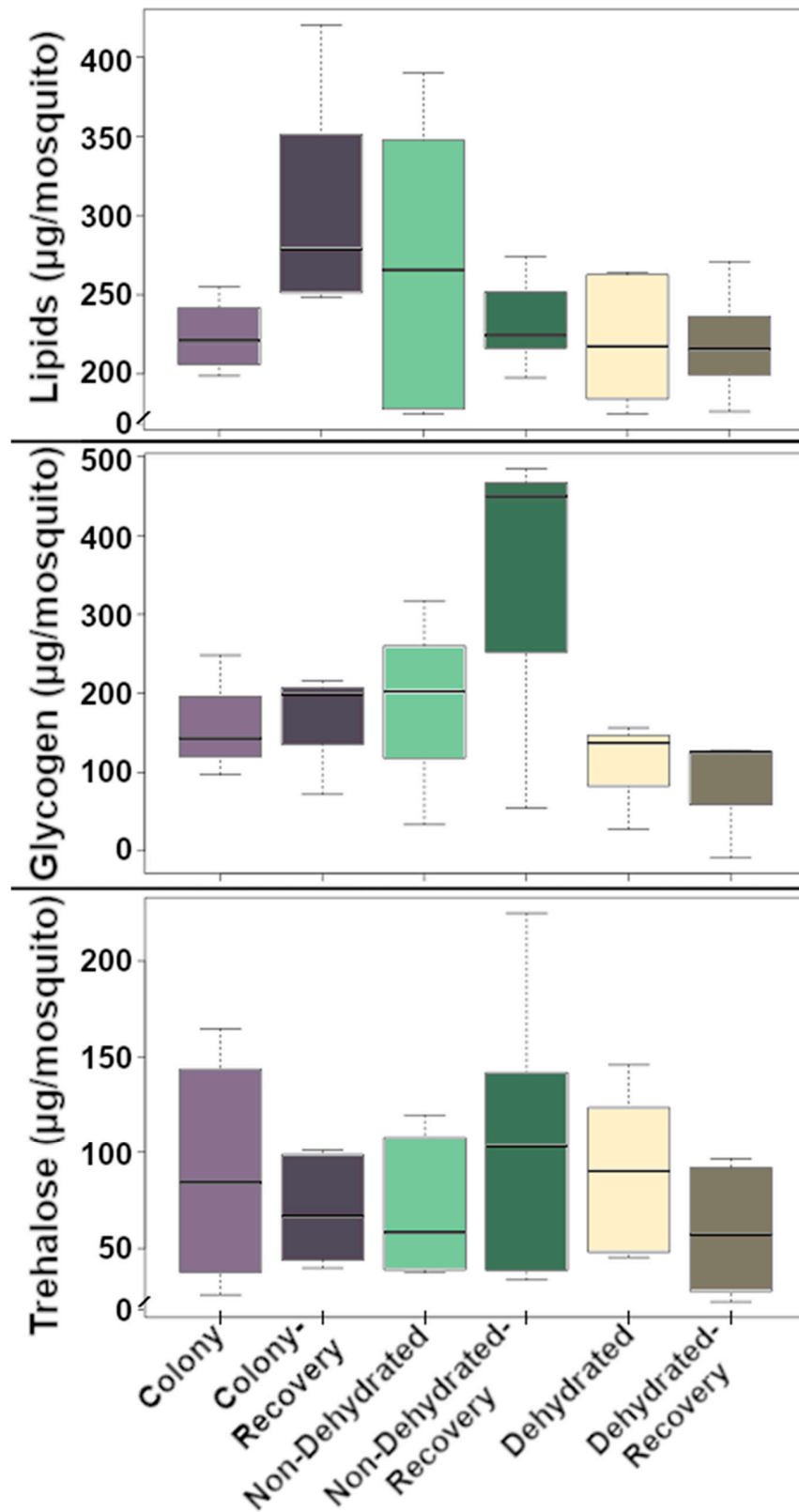
**Supplementary Figure S1:** DESeq2 pipeline comparisons show considerable correlation in shared transcript expression. The Y1 N1 comparison is denoted by circles; Y1 Y7, triangles; N7 N1, squares; N7 Y7, crosses.



**Supplementary Figure S2:** Functional enrichment analyses. A, CirGO-REVIGO representations for the non-bloodfed/non-dehydrated group over the bloodfed/non-dehydrated group (N1\_Y1); B, CirGO-REVIGO representations for the bloodfed/non-dehydrated group over the non-bloodfed/non-dehydrated group (Y1\_N1); C, CirGO-REVIGO representations for the non-bloodfed/dehydrated group over the bloodfed/dehydrated group (N7\_Y7); D, CirGO-REVIGO representations for the bloodfed/dehydrated group over the non-bloodfed/dehydrated group (Y7\_N7). REVIGO groupings are included in Supplementary Table 3 and significant g:Profiler terms are included in Supplementary Table 4 with “intersections” indicating the genes responsible for GO categorization. CLC labels represent significant transcripts identified with the QIAGEN CLC pipeline; DK, the DESeq2-Kallisto pipeline; and DS, the DESeq2-Sailfish pipeline.



**Supplementary Figure S3:** Log2 fold-change comparisons and median-of-ratios normalized mean expression averages across all samples for all differentially expressed genes identified by DESeq2 pipelines. A, comparison between the bloodfed/non-dehydrated group over the non-bloodfed/non-dehydrated group (Y1 N1); B, comparison between the non-bloodfed/dehydrated group over the bloodfed/dehydrated group (N7 Y7). Yellow circles denote genes that were identified through the DESeq-Sailfish pipeline; red circles, DESeq-Kallisto pipeline; and black circles were genes identified by both pipelines, with the highest mean expression pipeline used. Significantly expressed transcripts are included in Supplementary Table 1 and sample-specific normalized mean expression values are included in Supplementary Table 5.



**Supplementary Figure S4:** Macronutrient levels for *A. aegypti* subjected to various treatments.

**Supplementary Table S1:** All significant comparisons (p-value < 0.01, log2 fold-change >1) between groups. Including gene transcripts, nucleotide ID, protein IDs, and relevant protein description. In each Excel worksheet, the initial term (e.g., Y1) represents increased log2 fold-change over the second term (e.g., N1) in a sequence (e.g., Y1 N1 represents Y1 gene expression over N1 expression). CLC, abbreviation for genes identified by the CLC pipeline; DK, DESeq2-Kallisto; DS, DESeq2-Sailfish; FC, log2 fold-change; -p, p-value.

**Supplementary Table S2:** All significant DESeq2-identified transcript comparisons (p-value < 0.01) between groups. Including gene transcripts, highest normalized mean expression across all samples, log2 fold-change, protein ID, and relevant protein description. Each Excel worksheet represents a group comparison. Red fill represents genes identified by the DESeq2-Kallisto pipeline; yellow, DESeq2-Sailfish; black, both DESeq2-pipelines.

**Supplementary Table S3:** All significant REVIGO representatives for GO terms between groups. Including GO term IDs, GO ID names, and REVIGO-assigned representative category. In each Excel worksheet, the initial term (e.g., Y1) represents increased expression over the second term (e.g., N1) in a sequence (e.g., Y1N1 represents Y1 gene expression over N1 expression), the following term (e.g., BP) denotes the GO abbreviation. GO, abbreviation for gene ontology; BP, biological process; CC, cellular component; MF, molecular function.

**Supplementary Table S4:** All significant GO terms and KEGG pathways identified by g:Profiler between groups. Including term names, term IDs, p-value, number of transcript intersections, and identified intersecting gene transcripts. In each Excel worksheet, the initial term (e.g., Y1) represents increased expression over the second term (e.g., N1) in a sequence (e.g., Y1N1 represents Y1 gene expression over N1 expression), the following term (e.g., BP) denotes the GO abbreviation. GO, abbreviation for gene ontology; BP, biological process; CC, cellular component; MF, molecular function; KEGG, Kyoto Encyclopedia of Genes and Genomes pathways.

**Supplementary Table S5:** Normalized gene expression generated by the DESeq2-Sailfish and -Kallisto pipelines for individual samples, including average normalized expression.

**Supplementary Table S6:** BLAST information of proteins associated with an identified ecdysteroid kinase protein (gene ID AAEL012685-RC).