

Supplemental Information

Transcriptomic Responses of the Honey Bee Brain to Infection with Deformed Wing Virus

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Supplemental Figure Legends:

Figure S1: Principal component analysis of all Mock and DWV infected samples. RNA from Mock infected (blue and maroon) and DWV infected (green) brain samples are shown analyzed using PC1 and PC2. Because a subset of the Mock infected samples (Mock B shown in maroon) segregated with the DWV infected samples, they were removed from further analysis.

Figure S2: Power analysis of differential gene expression. Analysis using the program Scotty [45] showing the percent of genes with various fold-changes in expression and sequencing depth detected at an adjusted $p < 0.05$ for a study design of 5 replicates and 10 million reads per sample.

Figure S3: Most highly expressed genes in each sample as analyzed by DESeq2. A) with reads mapping to DWV included, B) with DWV reads excluded.

List of Supplemental Tables:

Table S1: Complete list of all upregulated genes identified by DESeq2. Genes were identified at $p \leq 0.001$ with OGS 3.2, RefSeq (www.hymenopteragenome.org), and *Drosophila* homologue as determined by g:Profiler (<https://biit.cs.ut.ee/gprofiler/orth>).

Table S2: Complete list of all upregulated genes identified by edgeR. Genes were identified at $p \leq 0.001$ with OGS 3.2, RefSeq (www.hymenopteragenome.org), and *Drosophila* homologue as determined by g:Profiler (<https://biit.cs.ut.ee/gprofiler/orth>).

Table S3: Complete list of all downregulated genes as identified by DESeq2. Genes were identified at $p \leq 0.001$ with OGS 3.2, RefSeq (www.hymenopteragenome.org), and *Drosophila* homologue as determined by g:Profiler (<https://biit.cs.ut.ee/gprofiler/orth>).

Table S4: Complete list of all downregulated genes identified by edgeR. Genes were identified at $p \leq 0.001$ with OGS 3.2, RefSeq (www.hymenopteragenome.org), and *Drosophila* homologue as determined by g:Profiler (<https://biit.cs.ut.ee/gprofiler/orth>).

Table S5: Complete list of Gene Ontology terms and statistical information of upregulated genes. List was produced with g:Profiler.

Table S6: Complete list of Gene Ontology terms and statistical information of downregulated genes. List was produced by g:Profiler.

Table S7: Average aqueous metabolite concentrations in worker bee brains. Rounded averages and sample standard deviations (concentrations in mM, in 0.5 mL NMR buffer) for the profiled

NMR concentrations of worker bee brains. Proline undergoes a strong change with DWV. Other metabolites of interest are suggested by these data, including glutamine, glutamate, taurine and trehalose but further work with larger sample sizes is needed to determine if these metabolites are significant.

Table S8: Average aqueous metabolite concentrations in corresponding bee bodies.

Representative rounded values for average metabolite levels from ca. 40 metabolites which can be profiled in the extracted worker bodies (concentrations in mM, in 0.5 mL NMR buffer).

Although a strong change is observed for acetate, this metabolite is identified by a single peak and can have diverse sources, and confirmatory work is required.