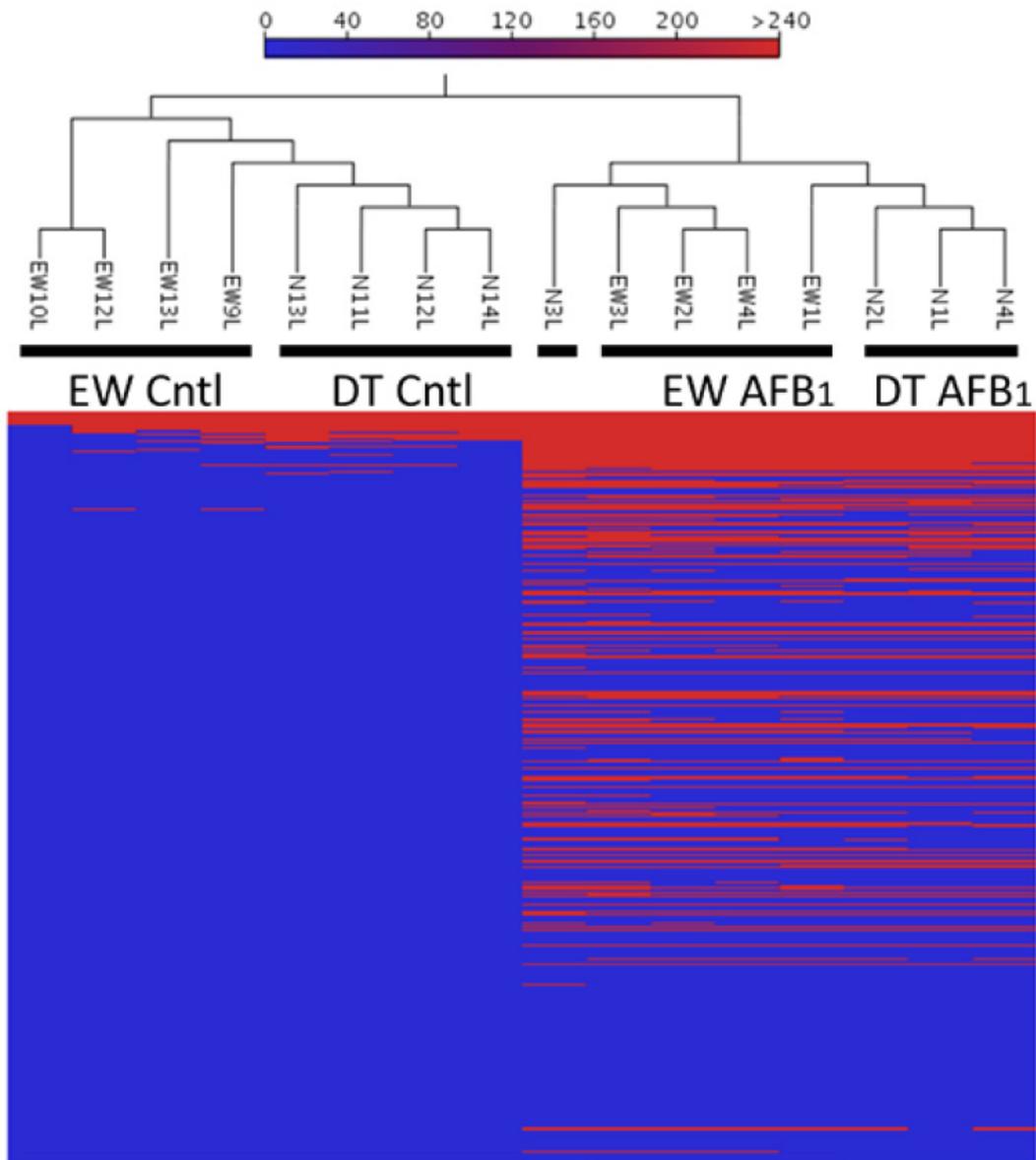
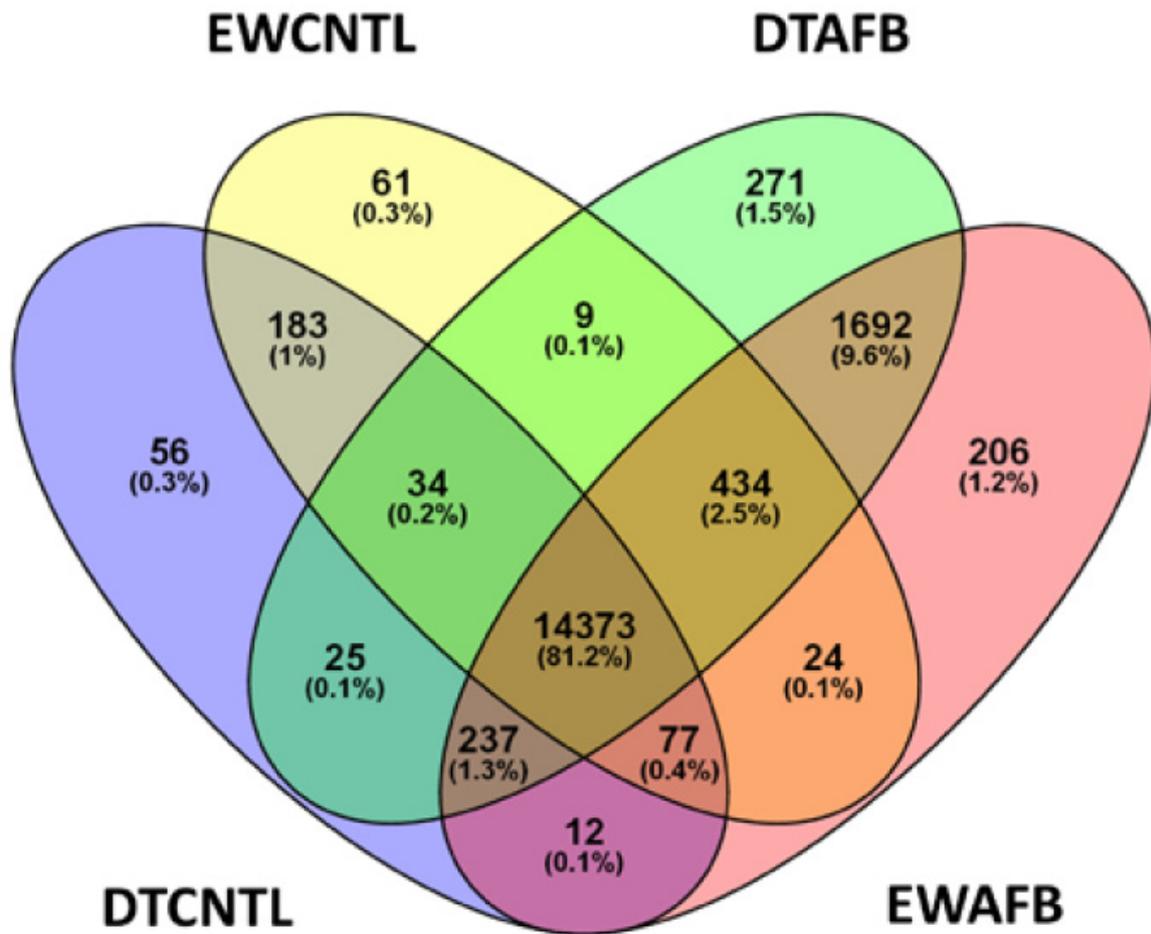


# Supplementary Materials: Comparative Response of the Hepatic Transcriptomes of Domesticated and Wild Turkey to Aflatoxin B<sub>1</sub>

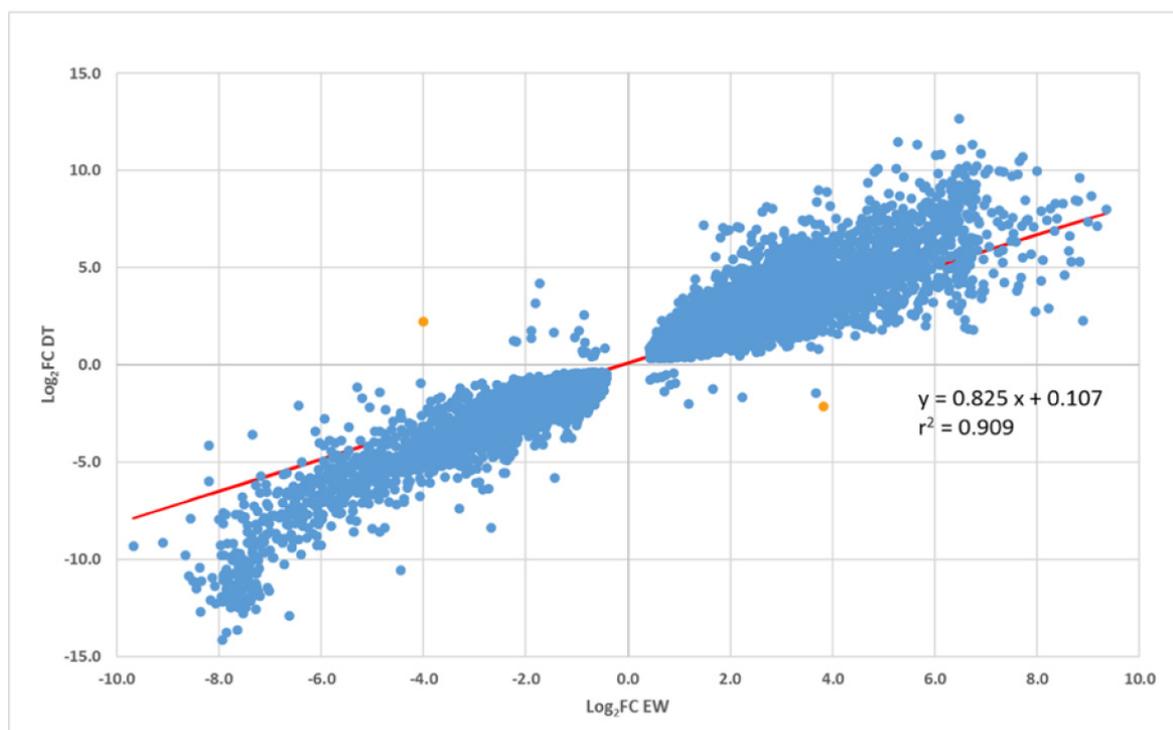
Kent M. Reed, Kristelle M. Mendoza, Juan E. Abrahante and Roger A. Coulombe



**Figure S1.** Hierarchical clustering of samples based on Euclidean distance reiterated relationships shown by PCA. Global gene expression differences among groups are illustrated in the heat map constructed from the 500 co-expressed genes with the greatest experiment-wise differences in averages normalized expression.



**Figure S2.** Distribution of genes expressed in turkey liver by treatment group. Number and percent of genes for which the average number of mapped reads per group was  $\geq 3.0$  are included. EWCNTL = Eastern wild control, DTCNTL = domesticated control, EWAFB = Eastern wild aflatoxin B1 and DTAFB = domesticated aflatoxin B1.



**Figure S3.** Differential fold change in DEGs shared by wild (EW) and domesticated (DT) birds exposed to AFB<sub>1</sub> in comparison to controls. The best-fitting regression line ( $r^2 = 0.909$ ) is indicated in red. Yellow points indicate two genes showing statistically significant differential expression (FDR  $p$ -value < 0.05) with opposite directional change ( $\log_2FC > 2.0$ ).