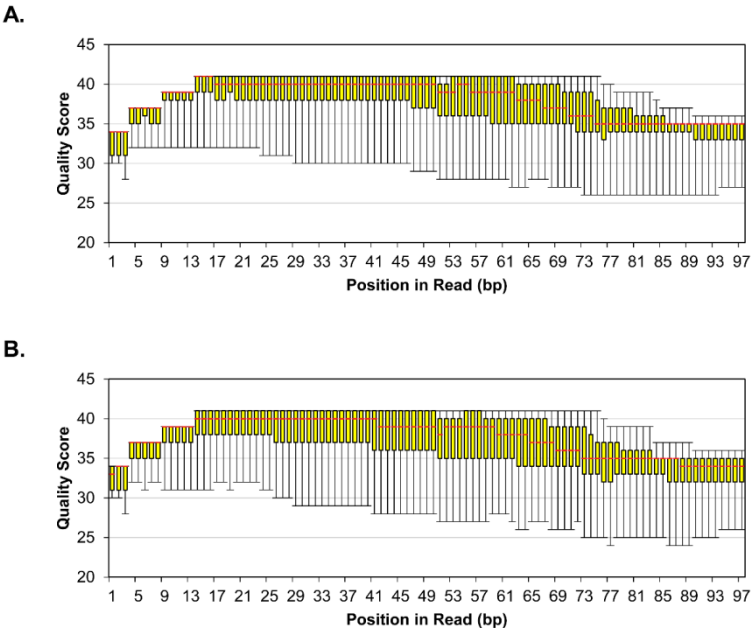
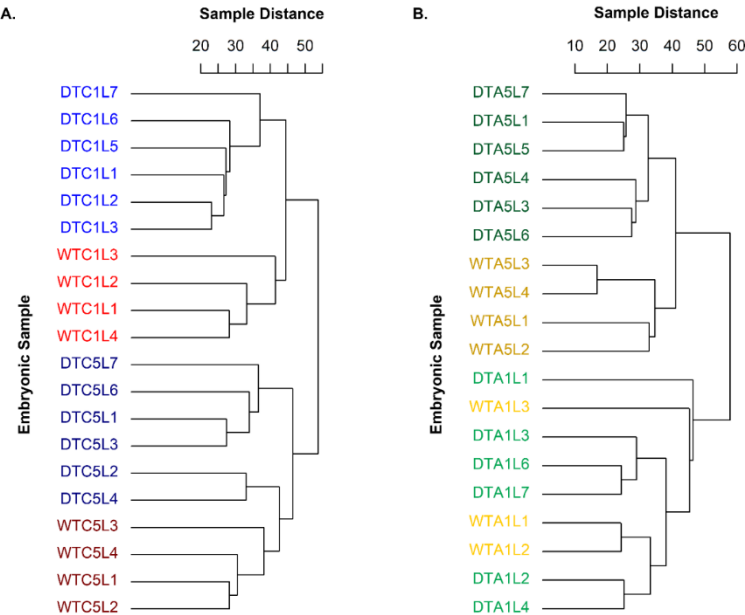


# Supplementary Materials: Hepatic Transcriptome Responses of Domesticated and Wild Turkey Embryos to Aflatoxin B<sub>1</sub>

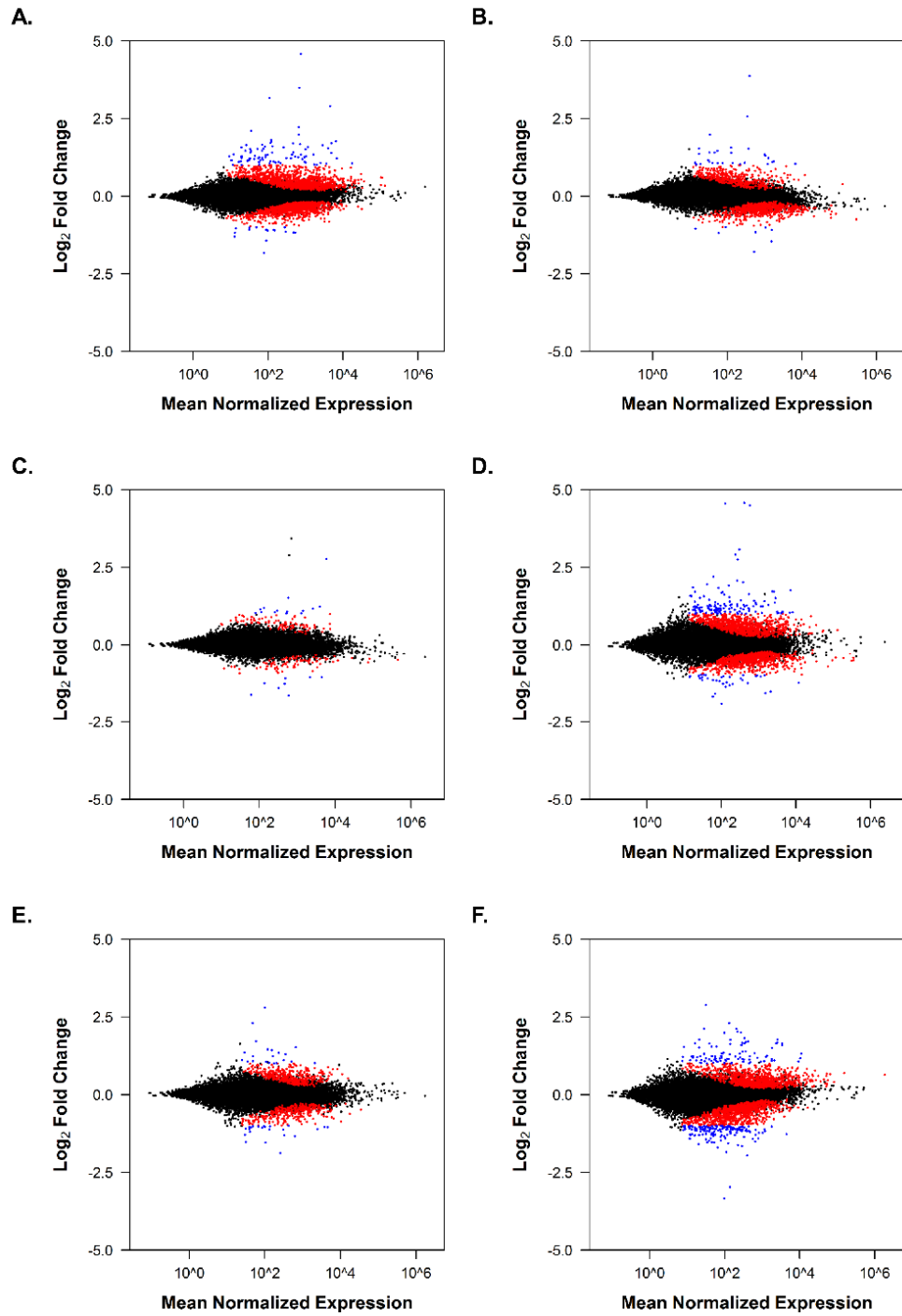
Melissa S. Monson, Carol J. Cardona, Roger A. Coulombe and Kent M. Reed



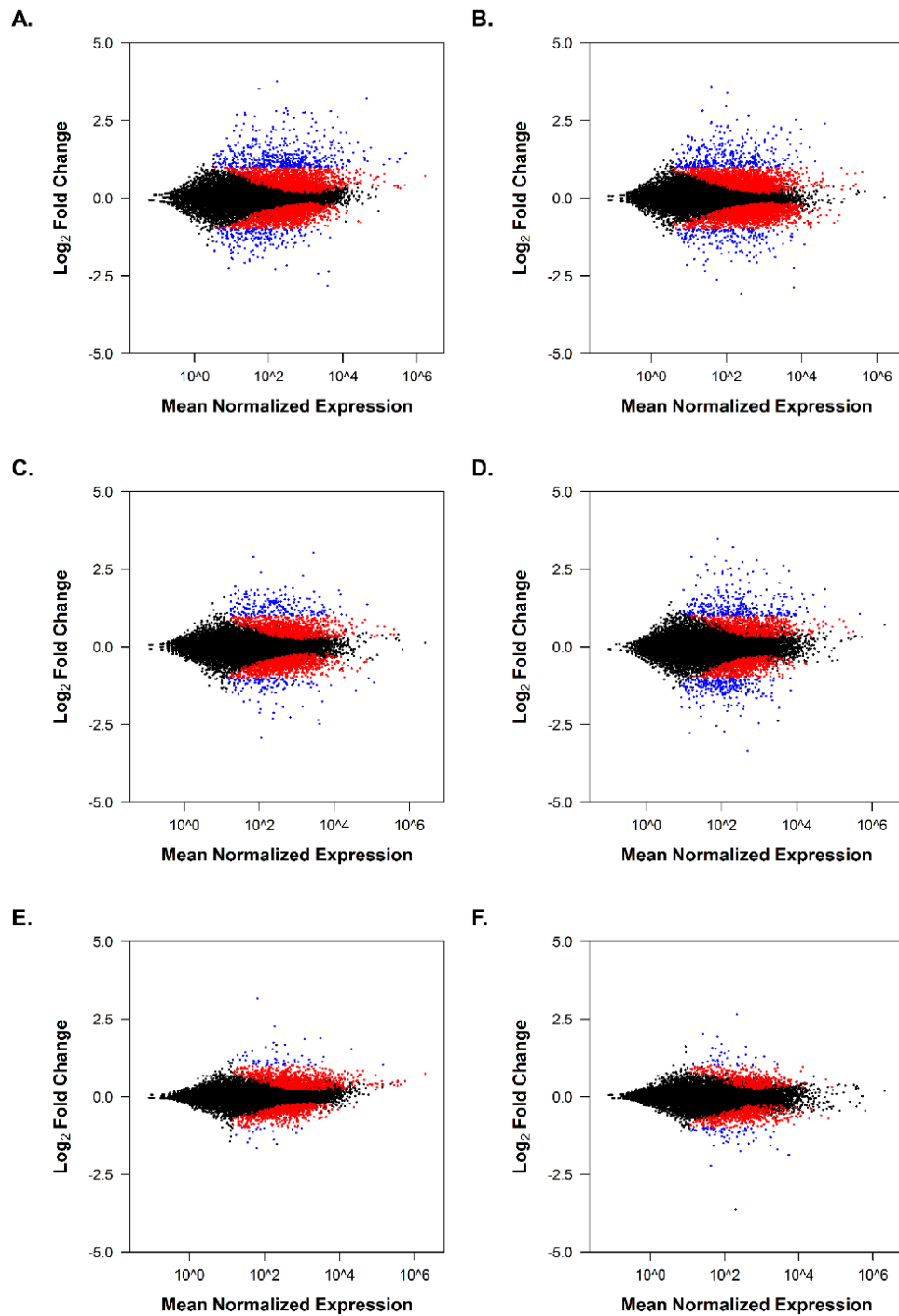
**Figure S1.** Quality scores at each base position for corrected liver RNA-seq datasets. **(A)** Domesticated turkey (DT); **(B)** Wild turkey (WT). Boxplots were based on quality score distributions generated in CLGWB. The median at each position is shown in red.



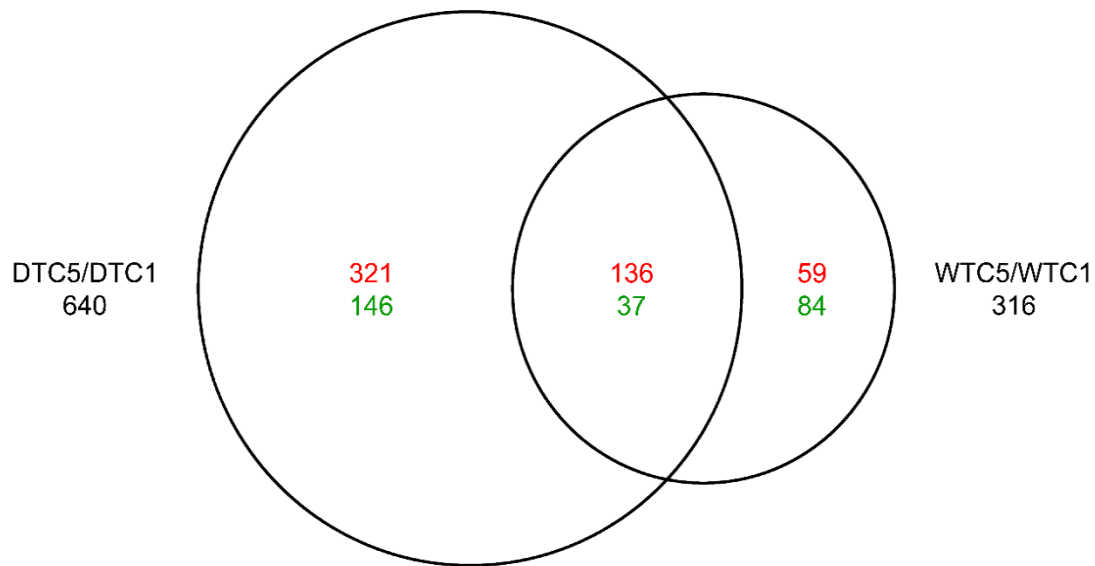
**Figure S2.** Hierarchical clustering of CNTL or AFB samples follows exposure time and turkey time. **(A)** Sample distances in CNTL; **(B)** Sample distances in AFB. Dendrogram was generated in R using regularized log<sub>2</sub> transformed read counts from DESeq2 [30]. Domesticated turkey (DT, green), wild turkey (WT, yellow), aflatoxin B<sub>1</sub> (AFB), aflatoxin B<sub>1</sub> 1 day (A1, lighter), aflatoxin B<sub>1</sub> 5 days (A5, darker), liver sample (L).



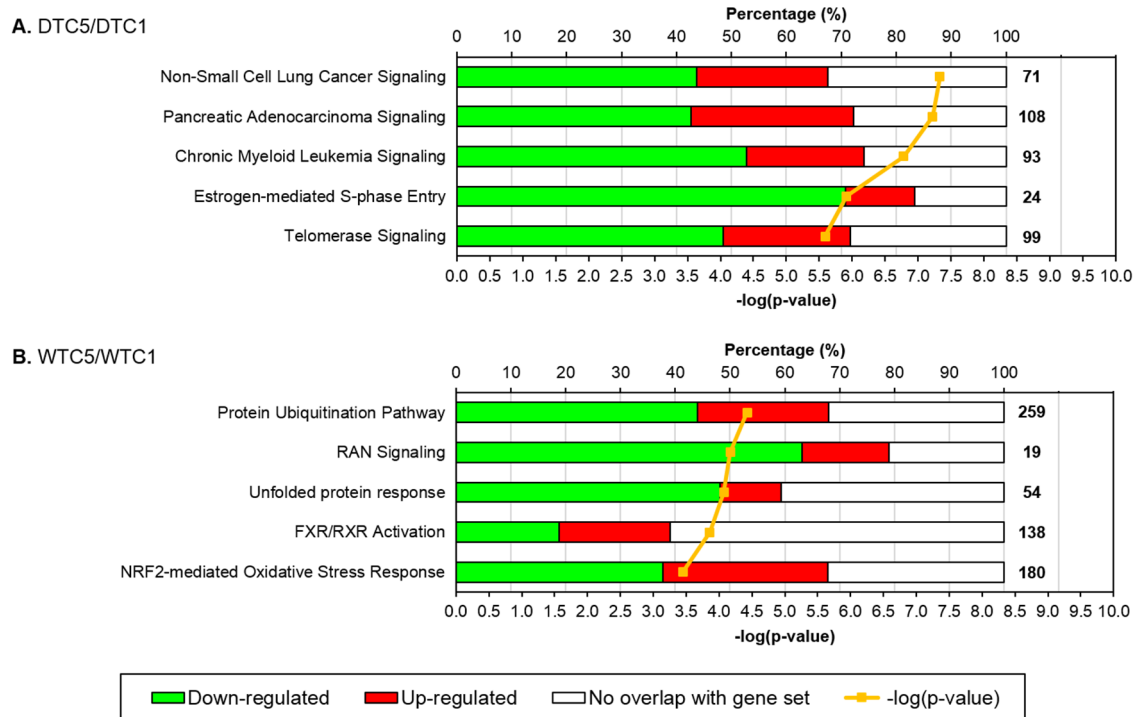
**Figure S3.** Significant DE from AFB exposure in DT and WT. (A) DTA1/DTC1; (B) DTA5/DTC5; (C) WTA1/WTC1; (D) WTA5/WTC5; (E) WTA1/DTA1; (F) WTA5/DTA5. MA plots were created in R using log<sub>2</sub> fold change (log<sub>2</sub>FC) and mean normalized read counts from DESeq2 [30]. Genes with significant differential expression (DE) ( $q$ -values  $\leq 0.05$ ) are red; significant genes with  $|\log_2\text{FC}| \geq 1.0$  are blue. Domesticated turkey (DT), wild turkey (WT), control (CNTL), control 1 day (C1), control 5 days (C5), aflatoxin B<sub>1</sub> (AFB), aflatoxin B<sub>1</sub> 1 day (A1), aflatoxin B<sub>1</sub> 5 days (A5).



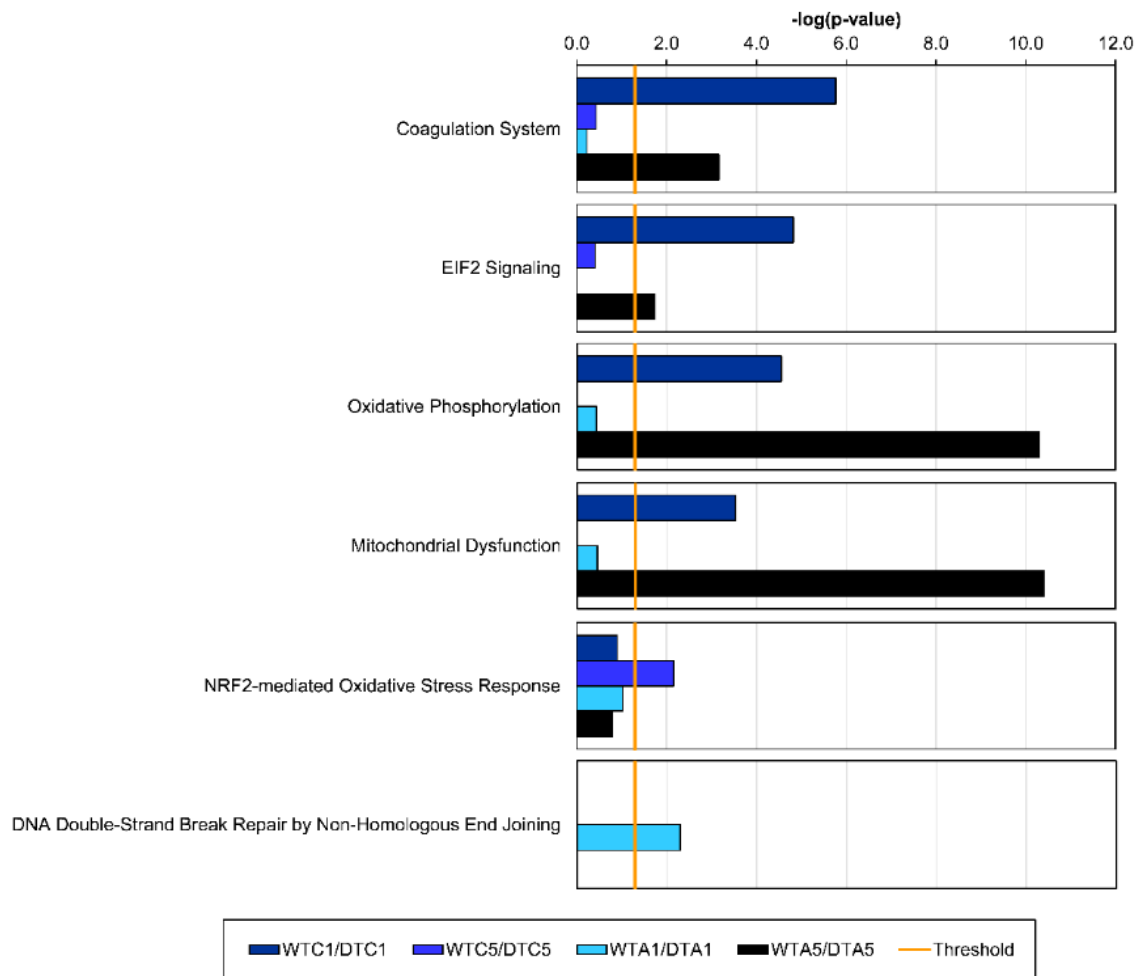
**Figure S4.** Significant DE during development in DT and WT. (A) DTC5/DTC1; (B) DTA5/DTA1; (C) WTC5/WTC1; (D) WTA5/DTA1; (E) WTC1/DTC1; (F) WTC5/DTC5. MA plots were created in R using log<sub>2</sub> fold change (log<sub>2</sub>FC) and mean normalized read counts from DESeq2 [30]. Genes with significant differential expression (DE) ( $q$ -values  $\leq 0.05$ ) are red; significant genes with  $|\log_2FC| \geq 1.0$  are blue. Domesticated turkey (DT), wild turkey (WT), control (CNTL), control 1 day (C1), control 5 days (C5), aflatoxin B<sub>1</sub> (AFB), aflatoxin B<sub>1</sub> 1 day (A1), aflatoxin B<sub>1</sub> 5 days (A5).



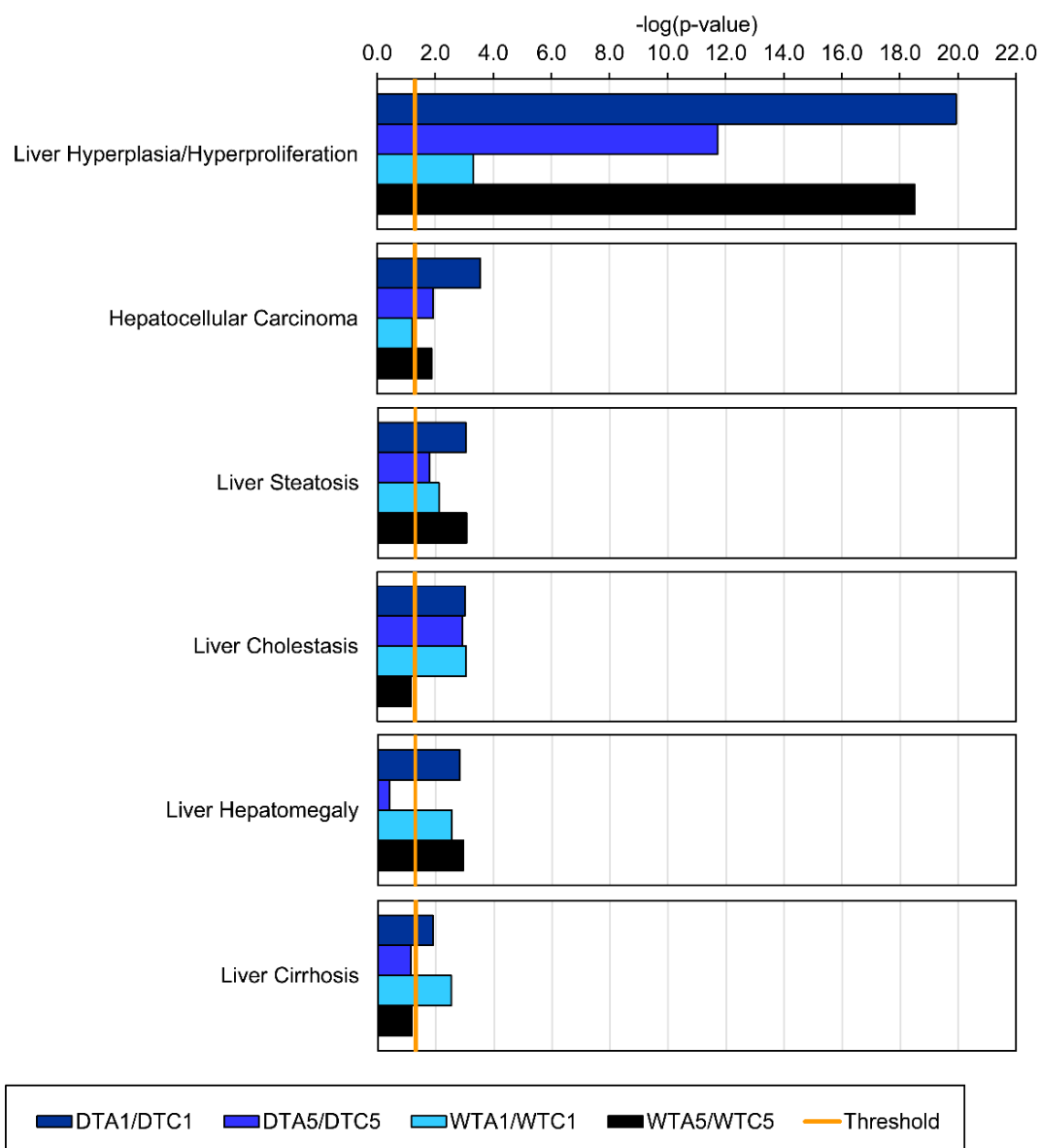
**Figure S5.** Overlap between significant DE in DT and WT during development. The number of shared and unique genes with significant differential expression (DE) ( $q$ -value  $\leq 0.05$ ) and  $|\log_2FC| \geq 1.0$  is indicated for C5 versus C1. Direction of DE is shown (red = up-regulated, green = down-regulated). Domesticated turkey (DT), wild turkey (WT), control 1 day (C1), control 5 days (C5),  $\log_2$  fold change ( $\log_2FC$ ).



**Figure S6.** Expression across highly significant pathways in CNTL groups during development. (A) DTC5/DTC1; (B) WTC5/WTC1. Ingenuity Pathway Analysis (IPA) was used to identify significant effects on canonical pathways ( $-\log(p\text{-value}) > 1.3$ ). Percentage of genes down-regulated (green), up-regulated (red), not represented in MAKER gene set (white) are shown for the 5 most significant pathways ( $-\log(p\text{-values})$  in yellow) in each comparison; both significant and non-significant DE are included. Total number of genes in each pathway are in bold. Domesticated turkey (DT), wild turkey (WT), control (CNTL), control 1 day (C1), control 5 days (C5).



**Figure S7.** Significance of pathway associations vary in WT versus DT comparisons. Ingenuity Pathway Analysis (IPA) assigned *p*-values to canonical pathways based on differential expression (DE). Bar plot provides 6 example pathways with variable significance between the WTC1/DTC1 (dark blue), WTC5/DTC5 (bright blue), WTA1/DTA1 (light blue), and WTA5/DTA5 (black) comparisons. Pathway associations must have a  $-\log(p\text{-value}) > 1.3$  (threshold line, yellow) to be considered significant. Domesticated turkey (DT), wild turkey (WT), control 1 day (C1), control 5 days (C5), aflatoxin B<sub>1</sub> 1 day (A1), aflatoxin B<sub>1</sub> 5 days (A5).



**Figure S8.** Significance of hepatotoxicity associations in AFB versus CNTL comparisons. Ingenuity Pathway Analysis (IPA) assigned  $p$ -values to toxicological functions based on differential expression (DE). Bar plot provides the 6 most significant hepatotoxic outcomes across the DTA1/DTC1 (dark blue), DTA5/DTC5 (bright blue), WTA1/WTC1 (light blue), and WTA5/WTC5 (black) comparisons. Functional associations must have a  $-\log(p\text{-value}) > 1.3$  (threshold line, yellow) to be considered significant. Domesticated turkey (DT), wild turkey (WT), control (CNTL), control 1 day (C1), control 5 days (C5), aflatoxin B<sub>1</sub> (AFB), aflatoxin B<sub>1</sub> 1 day (A1), aflatoxin B<sub>1</sub> 5 days (A5).

**Table S1.** Post hoc comparisons of mean egg, embryo and liver weights.

Group	Mean	St Dev	Group	Mean	St Dev	<i>p</i> -Value
<i>Egg Weights</i>						
DTA1	81.13	±8.49	DTC1	79.56	±5.62	1.00
DTA5	82.16	±5.56	DTC5	76.60	±5.71	0.68
DTC5	76.60	±5.71	DTC1	79.56	±5.62	0.98
DTA5	82.16	±5.56	DTA1	81.13	±8.49	1.00
WTA1	74.70	±4.51	WTC1	66.77	±8.75	0.69
WTA5	60.18	±3.68	WTC5	66.30	±10.52	0.84
WTC5	66.30	±10.52	WTC1	66.77	±8.75	1.00
WTA5	60.18	±3.68	WTA1	74.70	±4.51	0.081
WTA1	74.70	±4.51	DTA1	81.13	±8.49	0.78
WTA5	60.18	±3.68	DTA5	82.16	±5.56	<0.001
WTC1	66.77	±8.75	DTC1	79.56	±5.62	0.051
WTC5	66.30	±10.52	DTC5	76.60	±5.71	0.18
<i>Embryo Weights</i>						
DTA1	17.67	±0.49	DTC1	16.58	±0.97	0.94
DTA5	32.60	±2.86	DTC5	30.70	±1.93	0.53
DTC5	30.70	±1.93	DTC1	16.58	±0.97	< 0.001
DTA5	32.60	±2.86	DTA1	17.67	±0.49	< 0.001
WTA1	19.08	±1.17	WTC1	18.71	±1.09	1.00
WTA5	24.83	±0.46	WTC5	29.59	±4.46	0.023
WTC5	29.59	±4.46	WTC1	18.71	±1.09	< 0.001
WTA5	24.83	±0.46	WTA1	19.08	±1.17	0.0078
WTA1	19.08	±1.17	DTA1	17.67	±0.49	0.94
WTA5	24.83	±0.46	DTA5	32.60	±2.86	< 0.001
WTC1	18.71	±1.09	DTC1	16.58	±0.97	0.58
WTC5	29.59	±4.46	DTC5	30.70	±1.93	0.97
<i>Liver Weights</i>						
DTA1	0.28	±0.03	DTC1	0.26	±0.03	1.00
DTA5	0.53	±0.22	DTC5	0.65	±0.13	0.047
DTC5	0.65	±0.13	DTC1	0.26	±0.03	<0.001
DTA5	0.53	±0.22	DTA1	0.28	±0.03	<0.001
WTA1	0.33	±0.04	WTC1	0.34	±0.04	1.00
WTA5	0.46	±0.06	WTC5	0.64	±0.07	0.016
WTC5	0.64	±0.07	WTC1	0.34	±0.04	<0.001
WTA5	0.46	±0.06	WTA1	0.33	±0.04	0.20
WTA1	0.33	±0.04	DTA1	0.28	±0.03	0.92
WTA5	0.46	±0.06	DTA5	0.53	±0.22	0.68
WTC1	0.34	±0.04	DTC1	0.26	±0.03	0.54
WTC5	0.64	±0.07	DTC5	0.65	±0.13	1.00
<i>Relative Liver Weights</i>						
DTA1	1.56	±0.17	DTC1	1.56	±0.12	1.00
DTA5	1.64	±0.22	DTC5	2.12	±0.37	0.0086
DTC5	2.12	±0.37	DTC1	1.56	±0.12	0.0015
DTA5	1.64	±0.22	DTA1	1.56	±0.17	1.00
WTA1	1.74	±0.26	WTC1	1.81	±0.20	1.00
WTA5	1.87	±0.25	WTC5	2.21	±0.34	0.41
WTC5	2.21	±0.34	WTC1	1.81	±0.20	0.24
WTA5	1.87	±0.25	WTA1	1.74	±0.26	0.99
WTA1	1.74	±0.26	DTA1	1.56	±0.17	0.93
WTA5	1.87	±0.25	DTA5	1.64	±0.22	0.71
WTC1	1.81	±0.20	DTC1	1.56	±0.12	0.61
WTC5	2.21	±0.34	DTC5	2.12	±0.37	1.00

Non-significant *p*-values (≥0.05) from multiple comparisons tests are shown in grey. Domesticated turkey (DT), wild turkey (WT), control 1 day (C1), control 5 days (C5), aflatoxin B<sub>1</sub> 1 day (A1), aflatoxin B<sub>1</sub> 5 days (A5).

**Table S3.** Distribution and expression of the MAKER gene set across the turkey genome (UMD 5.0).

Chromosome	Size (Mb)	Total Genes	BLAST Annotated Genes	Gene Density <sup>1</sup>	Genes Expressed in		
					DT	WT	Both
1	190.7	2228	2109	41.0%	2155	2160	2174
2	109.7	1395	1295	44.0%	1354	1352	1365
3	93.2	879	813	43.5%	847	841	853
4	70.7	874	813	50.8%	848	844	854
5	59.0	1024	939	47.7%	996	997	1001
6	50.7	699	630	47.9%	660	652	662
7	36.3	584	543	49.6%	565	562	569
8	34.7	569	529	48.5%	551	548	554
9	19.1	379	348	46.9%	369	369	371
10	29.2	620	570	52.3%	609	602	611
11	23.7	524	473	50.3%	502	501	505
12	19.6	447	415	54.5%	430	434	436
13	19.1	409	388	49.1%	403	401	404
14	19.5	358	330	47.4%	349	347	353
15	17.5	400	366	38.6%	385	384	390
16	14.9	462	435	51.4%	449	449	453
17	13.1	394	372	53.8%	386	385	388
18	0.3	32	31	82.7%	31	30	31
19	10.3	315	288	55.3%	299	299	300
20	10.7	325	309	48.8%	313	315	316
21	9.7	359	342	57.1%	346	346	350
22	13.7	390	362	43.3%	376	378	381
23	6.7	291	274	52.7%	276	276	281
24	4.1	119	112	58.0%	117	117	118
25	5.6	230	221	44.0%	225	224	225
26	6.4	198	173	43.0%	192	189	192
27	1.4	106	105	58.3%	102	104	104
28	5.0	261	249	58.1%	253	249	255
29	4.3	240	231	58.4%	231	230	234
30	4.6	287	277	57.9%	281	279	281
W	0.3	2	2	83.6%	2	2	2
Z	68.5	772	739	40.1%	753	743	755
Unassigned	177.0	2093	2034	3.2%	1638	1602	1672
Total Genome	1149.2	18,265	17,117	39.4%	17,293	17,211	17,440

Domesticated turkey (DT), wild turkey (WT). <sup>1</sup> Total length of genes (including introns and UTRs) per chromosome/chromosome size.



**Table S6.** Significant DE genes involved in NRF2-mediated responses in AFB versus CNTL groups.

Gene ID	Gene	DTA1/DTC1		DTA5/DTC5		WTA1/WTC1		WTA5/WTC5	
		Log2FC	q-Value	Log2FC	q-Value	Log2FC	q-Value	Log2FC	q-Value
Upstream Cytoplasmic									
T_ALT_S_009346	ACTA2	0.50	1.05 × 10 <sup>-2</sup>	0.05	9.24 × 10 <sup>-1</sup>	0.13	9.69 × 10 <sup>-1</sup>	0.22	5.13 × 10 <sup>-1</sup>
T_ALT_S_010243	ACT5	-0.03	8.66 × 10 <sup>-1</sup>	-0.01	9.62 × 10 <sup>-1</sup>	0.04	9.92 × 10 <sup>-1</sup>	0.43	5.97 × 10 <sup>-3</sup>
T_ALT_S_006365	X10IF2AK3	-0.37	3.08 × 10 <sup>-3</sup>	-0.06	8.11 × 10 <sup>-1</sup>	-0.22	6.14 × 10 <sup>-1</sup>	-0.04	9.06 × 10 <sup>-1</sup>
T_ALT_S_010902	MAP2K3	0.57	1.64 × 10 <sup>-3</sup>	0.05	9.03 × 10 <sup>-1</sup>	0.24	8.44 × 10 <sup>-1</sup>	0.34	2.37 × 10 <sup>-1</sup>
T_ALT_S_010558	MAP2K5	-0.27	1.15 × 10 <sup>-2</sup>	0.01	9.67 × 10 <sup>-1</sup>	-0.24	6.09 × 10 <sup>-1</sup>	-0.12	6.12 × 10 <sup>-1</sup>
T_ALT_S_011089	MAPK1	-0.20	1.77 × 10 <sup>-2</sup>	0.06	6.87 × 10 <sup>-1</sup>	-0.15	7.67 × 10 <sup>-1</sup>	-0.25	2.44 × 10 <sup>-2</sup>
T_ALT_S_015036	MAPK14 <sup>1</sup>	-0.23	4.07 × 10 <sup>-2</sup>	-0.17	2.21 × 10 <sup>-1</sup>	-0.03	9.90 × 10 <sup>-1</sup>	-0.26	6.29 × 10 <sup>-2</sup>
T_ALT_S_015037	MAPK14 <sup>1</sup>	0.94	5.73 × 10 <sup>-13</sup>	-0.07	7.93 × 10 <sup>-1</sup>	0.45	3.05 × 10 <sup>-1</sup>	0.70	3.96 × 10 <sup>-4</sup>
T_ALT_S_009331	MAPK8	-0.37	1.59 × 10 <sup>-3</sup>	-0.30	2.56 × 10 <sup>-2</sup>	-0.11	9.41 × 10 <sup>-1</sup>	-0.18	3.14 × 10 <sup>-1</sup>
T_ALT_S_010038	PIK3CA	-0.54	1.84 × 10 <sup>-3</sup>	-0.29	2.81 × 10 <sup>-1</sup>	-0.27	6.42 × 10 <sup>-1</sup>	-0.30	1.50 × 10 <sup>-1</sup>
T_ALT_S_014476	PIK3CD	-0.33	4.13 × 10 <sup>-2</sup>	0.20	3.18 × 10 <sup>-1</sup>	0.36	6.12 × 10 <sup>-1</sup>	0.20	5.08 × 10 <sup>-1</sup>
T_ALT_S_006672	PIK3R1 <sup>1</sup>	-0.05	8.48 × 10 <sup>-1</sup>	-0.53	1.79 × 10 <sup>-2</sup>	-0.26	6.21 × 10 <sup>-1</sup>	-0.67	6.42 × 10 <sup>-3</sup>
T_ALT_S_006673	PIK3R1 <sup>1</sup>	-0.09	7.56 × 10 <sup>-1</sup>	-0.67	2.14 × 10 <sup>-2</sup>	-0.06	9.89 × 10 <sup>-1</sup>	-0.31	3.35 × 10 <sup>-1</sup>
T_ALT_S_011518	PRKCD	0.12	5.36 × 10 <sup>-1</sup>	-0.46	4.06 × 10 <sup>-2</sup>	-0.05	9.92 × 10 <sup>-1</sup>	-0.40	1.16 × 10 <sup>-1</sup>
T_ALT_S_002624	PRKCX10	-0.71	8.70 × 10 <sup>-3</sup>	0.31	4.30 × 10 <sup>-1</sup>	0.15	9.63 × 10 <sup>-1</sup>	-0.44	2.47 × 10 <sup>-1</sup>
T_ALT_S_004522	PRKCH <sup>1</sup>	0.50	1.42 × 10 <sup>-1</sup>	0.41	2.16 × 10 <sup>-1</sup>	-0.28	8.22 × 10 <sup>-1</sup>	1.27	3.87 × 10 <sup>-5</sup>
T_ALT_S_004523	PRKCH <sup>1</sup>	0.27	NA	0.38	3.25 × 10 <sup>-1</sup>	0.02	NA	1.39	4.58 × 10 <sup>-5</sup>
T_ALT_S_010069	PRKCI	-0.27	1.01 × 10 <sup>-2</sup>	0.07	7.63 × 10 <sup>-1</sup>	-0.01	9.97 × 10 <sup>-1</sup>	-0.02	9.47 × 10 <sup>-1</sup>
T_ALT_S_004239	PRKD1	-0.21	2.82 × 10 <sup>-1</sup>	0.20	2.85 × 10 <sup>-1</sup>	-0.11	9.69 × 10 <sup>-1</sup>	-0.41	4.01 × 10 <sup>-2</sup>
Nuclear									
T_ALT_S_002034	ATM	-0.25	2.01 × 10 <sup>-2</sup>	-0.26	2.63 × 10 <sup>-2</sup>	-0.09	9.38 × 10 <sup>-1</sup>	-0.06	7.25 × 10 <sup>-1</sup>
T_ALT_S_001339	BACH1	-0.51	3.24 × 10 <sup>-3</sup>	-0.36	3.18 × 10 <sup>-2</sup>	-0.30	4.15 × 10 <sup>-1</sup>	-0.63	1.12 × 10 <sup>-4</sup>
T_ALT_S_014852	CDC34	-0.33	9.37 × 10 <sup>-2</sup>	-0.64	8.97 × 10 <sup>-4</sup>	0.05	9.93 × 10 <sup>-1</sup>	0.04	8.76 × 10 <sup>-1</sup>
T_ALT_S_010676	CRX10BBP	0.45	2.35 × 10 <sup>-5</sup>	0.07	6.94 × 10 <sup>-1</sup>	-0.18	9.21 × 10 <sup>-1</sup>	0.67	9.17 × 10 <sup>-3</sup>
T_ALT_S_009069	DNAJB4	-0.24	4.29 × 10 <sup>-2</sup>	-0.20	1.46 × 10 <sup>-1</sup>	-0.06	9.89 × 10 <sup>-1</sup>	-0.08	7.75 × 10 <sup>-1</sup>
T_ALT_S_007316	DNAJB6	-0.35	3.03 × 10 <sup>-2</sup>	-0.25	1.06 × 10 <sup>-1</sup>	-0.12	9.49 × 10 <sup>-1</sup>	-0.22	4.65 × 10 <sup>-1</sup>
T_ALT_S_009102	DNAJC9	-0.35	2.39 × 10 <sup>-2</sup>	0.01	9.81 × 10 <sup>-1</sup>	-0.27	6.24 × 10 <sup>-1</sup>	-0.47	5.08 × 10 <sup>-2</sup>
T_ALT_S_000577	X10P300	-0.04	8.35 × 10 <sup>-1</sup>	-0.14	4.30 × 10 <sup>-1</sup>	0.13	8.84 × 10 <sup>-1</sup>	-0.36	3.48 × 10 <sup>-2</sup>
T_ALT_S_001124	GSK3B	0.15	2.86 × 10 <sup>-1</sup>	0.23	2.25 × 10 <sup>-1</sup>	0.04	9.93 × 10 <sup>-1</sup>	0.33	4.84 × 10 <sup>-2</sup>
T_ALT_S_008102	NFX102L2	0.58	1.84 × 10 <sup>-7</sup>	0.33	3.70 × 10 <sup>-2</sup>	0.52	1.09 × 10 <sup>-3</sup>	0.21	1.44 × 10 <sup>-1</sup>
T_ALT_S_002690	PRKD3	-0.04	8.59 × 10 <sup>-1</sup>	0.06	8.68 × 10 <sup>-1</sup>	0.06	9.84 × 10 <sup>-1</sup>	-0.41	4.26 × 10 <sup>-2</sup>
T_ALT_S_008084	UBX102X 103	-0.23	1.83 × 10 <sup>-1</sup>	-0.10	6.92 × 10 <sup>-1</sup>	0.03	9.93 × 10 <sup>-1</sup>	-0.59	1.34 × 10 <sup>-2</sup>

Table S6. *Cont.*

<i>Downstream Cytoplasmic</i>									
T_ALT_S_008999	<i>AKR1A1</i>	0.34	$3.18 \times 10^{-2}$	0.07	$7.76 \times 10^{-1}$	0.25	$8.07 \times 10^{-1}$	0.69	$5.58 \times 10^{-5}$
T_ALT_S_014672	<i>AKR7A2</i>	0.47	$1.15 \times 10^{-2}$	0.14	$4.91 \times 10^{-1}$	0.34	$5.55 \times 10^{-1}$	0.18	$3.37 \times 10^{-1}$
T_ALT_S_008024	<i>AOX1</i>	0.28	$3.65 \times 10^{-2}$	0.00	$9.96 \times 10^{-1}$	-0.02	$9.95 \times 10^{-1}$	-0.04	$8.86 \times 10^{-1}$
T_ALT_S_003995	<i>CAT</i>	-0.18	$3.15 \times 10^{-1}$	-0.44	$3.49 \times 10^{-4}$	-0.18	$8.54 \times 10^{-1}$	-0.30	$1.58 \times 10^{-1}$
T_ALT_S_010665	<i>DNAJA3</i>	0.40	$1.15 \times 10^{-3}$	-0.03	$8.79 \times 10^{-1}$	0.07	$9.78 \times 10^{-1}$	0.21	$1.66 \times 10^{-1}$
T_ALT_S_009842	<i>DNAJB11</i>	-0.32	$7.44 \times 10^{-3}$	-0.08	NA	-0.39	$2.36 \times 10^{-1}$	0.31	$1.15 \times 10^{-1}$
T_ALT_S_008078	<i>DNAJC10</i>	-0.39	$1.01 \times 10^{-3}$	-0.02	$9.65 \times 10^{-1}$	-0.05	$9.91 \times 10^{-1}$	0.18	$4.09 \times 10^{-1}$
T_ALT_S_014426	<i>DNAJC11</i>	0.26	$4.81 \times 10^{-2}$	-0.06	$7.63 \times 10^{-1}$	-0.20	$8.47 \times 10^{-1}$	0.20	$3.88 \times 10^{-1}$
T_ALT_S_007708	<i>DNAJC13</i>	0.03	$8.56 \times 10^{-1}$	-0.40	$6.56 \times 10^{-3}$	0.07	$9.80 \times 10^{-1}$	0.08	$7.48 \times 10^{-1}$
T_ALT_S_014061	<i>DNAJC18</i>	-0.02	$8.95 \times 10^{-1}$	-0.02	$9.44 \times 10^{-1}$	-0.24	$5.93 \times 10^{-1}$	-0.42	$1.81 \times 10^{-2}$
T_ALT_S_002734	<i>X10PHX1</i>	0.63	$5.74 \times 10^{-4}$	-0.06	$8.95 \times 10^{-1}$	0.03	$9.93 \times 10^{-1}$	0.57	$2.36 \times 10^{-3}$
T_ALT_S_003948	<i>FTH1</i>	0.10	$6.77 \times 10^{-1}$	0.38	$4.52 \times 10^{-2}$	-0.10	$9.41 \times 10^{-1}$	0.12	$7.29 \times 10^{-1}$
T_ALT_S_003347	<i>GSTA3</i> <sup>1</sup>	1.60	$1.47 \times 10^{-10}$	0.74	$1.79 \times 10^{-2}$	0.48	$3.63 \times 10^{-1}$	0.52	$2.34 \times 10^{-1}$
T_ALT_S_003348	<i>GSTA3</i> <sup>1</sup>	1.52	$2.87 \times 10^{-9}$	0.85	$4.31 \times 10^{-3}$	0.39	$5.52 \times 10^{-1}$	0.23	$6.61 \times 10^{-1}$
T_ALT_S_003346	<i>GSTA3</i> <sup>1</sup>	1.11	$9.74 \times 10^{-5}$	0.40	$2.66 \times 10^{-1}$	0.36	$5.83 \times 10^{-1}$	0.80	$4.76 \times 10^{-2}$
T_ALT_S_003345	<i>GSTA4</i>	0.82	$8.65 \times 10^{-7}$	0.47	$2.82 \times 10^{-2}$	0.35	$6.56 \times 10^{-1}$	0.42	$4.09 \times 10^{-2}$
T_ALT_S_001023	<i>GSTK1</i>	0.07	$6.99 \times 10^{-1}$	-0.31	$2.39 \times 10^{-2}$	-0.26	$5.83 \times 10^{-1}$	-0.11	$6.34 \times 10^{-1}$
T_ALT_S_009475	<i>GSTO1</i>	0.13	$5.87 \times 10^{-1}$	0.06	$8.65 \times 10^{-1}$	-0.28	$3.27 \times 10^{-1}$	1.07	$4.63 \times 10^{-3}$
T_ALT_S_011992	<i>HX10RPUD1</i>	-0.25	$3.76 \times 10^{-1}$	0.69	$3.75 \times 10^{-4}$	-0.20	$9.21 \times 10^{-1}$	-0.26	$3.11 \times 10^{-1}$
T_ALT_S_000662	<i>HMOX1</i>	0.29	$1.91 \times 10^{-1}$	-0.14	$7.31 \times 10^{-1}$	0.32	$3.84 \times 10^{-1}$	0.85	$1.48 \times 10^{-9}$
T_ALT_S_005601	<i>MGST2</i>	0.84	$6.76 \times 10^{-7}$	0.14	$6.23 \times 10^{-1}$	0.41	$2.18 \times 10^{-1}$	0.37	$8.19 \times 10^{-2}$
T_ALT_S_008700	<i>MGST3</i>	0.56	$9.79 \times 10^{-5}$	0.10	$7.83 \times 10^{-1}$	0.33	$2.55 \times 10^{-1}$	0.73	$4.64 \times 10^{-4}$
T_ALT_S_012166	<i>NQO1</i>	0.63	$2.64 \times 10^{-6}$	0.03	$8.87 \times 10^{-1}$	0.57	$1.81 \times 10^{-3}$	0.02	$9.39 \times 10^{-1}$
T_ALT_S_004785	<i>NQO2</i>	0.24	$2.42 \times 10^{-1}$	0.63	$1.94 \times 10^{-4}$	0.00	1.00	0.73	$6.78 \times 10^{-6}$
T_ALT_S_009000	<i>PRDX1</i>	0.49	$2.13 \times 10^{-3}$	0.10	$6.39 \times 10^{-1}$	0.10	$9.69 \times 10^{-1}$	0.66	$1.03 \times 10^{-4}$
T_ALT_S_016734	<i>STIP1</i>	-0.03	$8.93 \times 10^{-1}$	-0.19	$2.64 \times 10^{-1}$	-0.14	$8.98 \times 10^{-1}$	0.36	$9.48 \times 10^{-3}$
T_ALT_S_007072	<i>TXN</i>	0.09	$5.73 \times 10^{-1}$	-0.62	$2.26 \times 10^{-3}$	-0.05	$9.80 \times 10^{-1}$	-0.07	$6.80 \times 10^{-1}$
T_ALT_S_000674	<i>TXNRD1</i> <sup>1</sup>	0.61	$1.32 \times 10^{-2}$	0.15	$7.63 \times 10^{-1}$	0.54	$2.55 \times 10^{-1}$	0.45	$2.82 \times 10^{-1}$
T_ALT_S_011677	<i>TXNRD1</i> <sup>1</sup>	-0.30	$2.07 \times 10^{-3}$	0.00	$9.99 \times 10^{-1}$	0.00	$9.99 \times 10^{-1}$	-0.16	$3.06 \times 10^{-1}$
T_ALT_S_007907	<i>UGT1A1</i>	0.62	$2.35 \times 10^{-5}$	0.06	$8.19 \times 10^{-1}$	0.15	$9.05 \times 10^{-1}$	0.34	$8.16 \times 10^{-3}$
<i>Extracellular/Plasma Membrane</i>									
T_ALT_S_009396	<i>MRP2</i>	0.16	$3.07 \times 10^{-1}$	-0.32	$3.68 \times 10^{-2}$	0.24	$4.82 \times 10^{-1}$	0.24	$2.59 \times 10^{-1}$
T_ALT_S_006174	<i>SOD3</i>	0.33	$3.12 \times 10^{-1}$	0.17	$7.08 \times 10^{-1}$	0.07	$9.92 \times 10^{-1}$	0.58	$2.25 \times 10^{-2}$

Genes were identified using Ingenuity Pathway Analysis (IPA). Log<sub>2</sub> fold change (Log<sub>2</sub>FC) and FD-adjusted *p*-values (*q*-values) were determined in DESeq2 [30]. Differential expression (DE), domesticated turkey (DT), wild turkey (WT), control (CNTL), control 1 day (C1), control 5 days (C5), aflatoxin B<sub>1</sub> (AFB), aflatoxin B<sub>1</sub> 1 day (A1), aflatoxin B<sub>1</sub> 5 days (A5), no statistics due to low read counts (NA). <sup>1</sup> Multiple genes in the MAKER gene set had significant DE and annotated to the same reference.