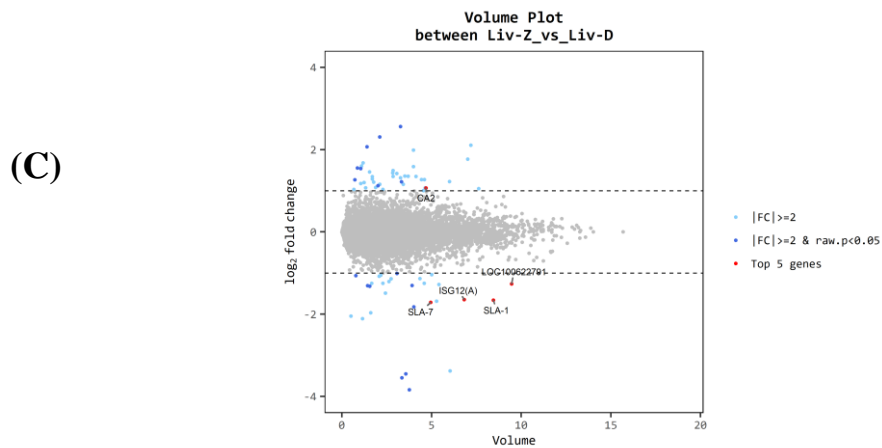
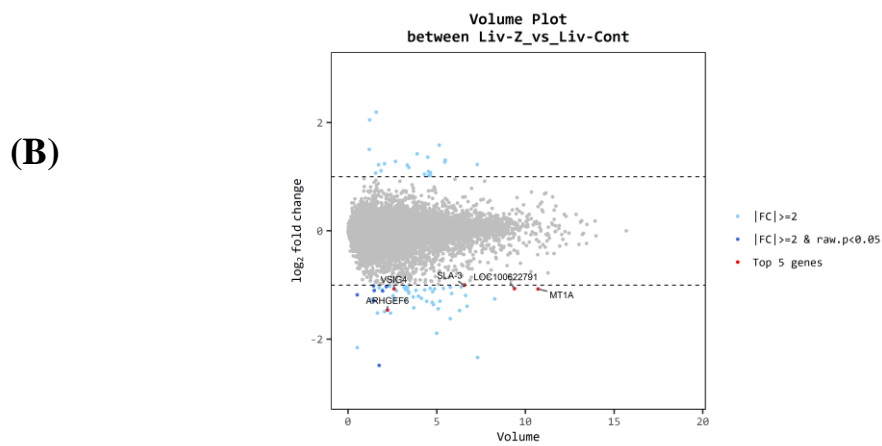
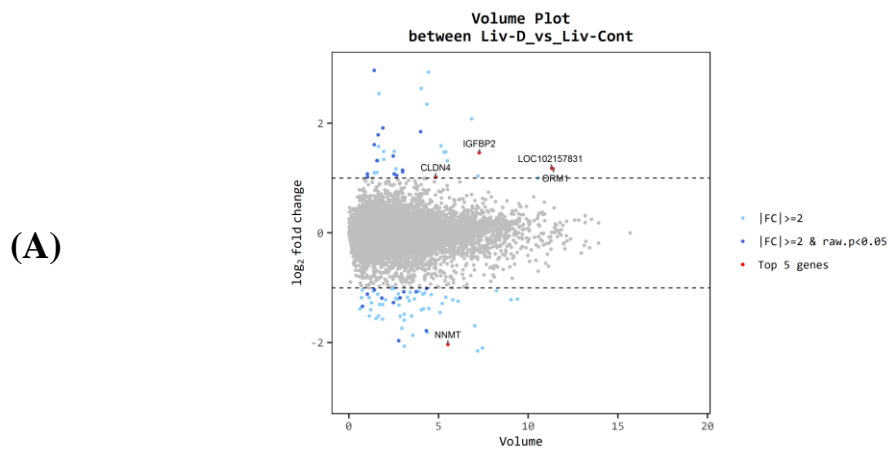


1 **Fig. S1.** Cox-Reid volume plot common dispersion among the control, DON, and ZEN treatment  
 2 groups. (A) control vs. DON (B) control vs. ZEN (C) DON vs. ZEN. The y-axis represents the  $\log_2$   
 3 fold change and the x-axis represents the mean of normalized gene volume.



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25 **Fig. S2.** Hierarchical clustering dendrogram of DEGs. Heatmap derived from two-way hierarchical  
26 clustering of DEGs is displayed according to significant differences in expression levels between  
27 control and DON and ZEN treatment groups. Color gradient from blue to yellow represents  
28 expression values ranging from low to high, respectively.

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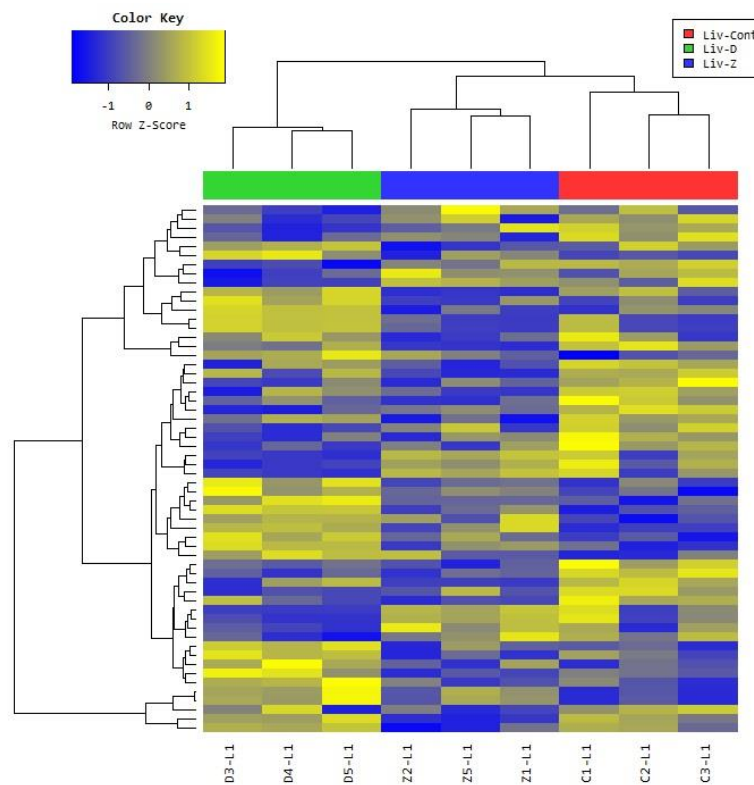
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49 **Fig. S3.** Cox-Reid expression levels of the transcripts between control and mycotoxin treatment  
50 groups. (A) Control vs. DON (B) Control vs. ZEN (C) ZEN vs. DON. In each graph, the y-axis  
51 represents the transcript levels under the mycotoxin treatment and the x-axis represents transcript  
52 levels under the control treatment.

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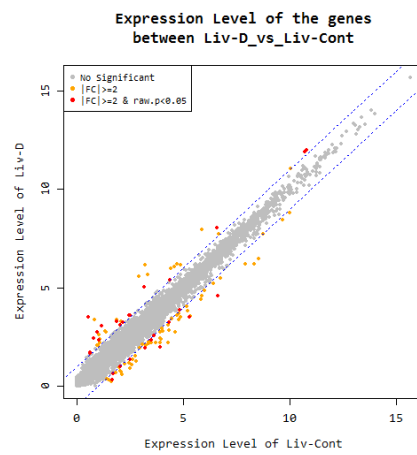
55 (A)

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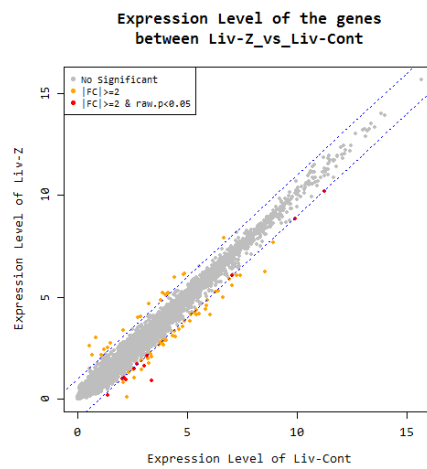
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63 (B)

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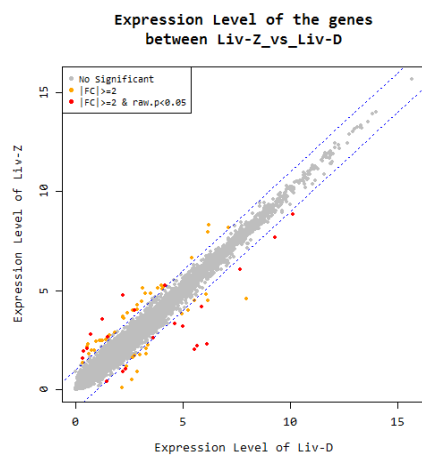
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70 (C)

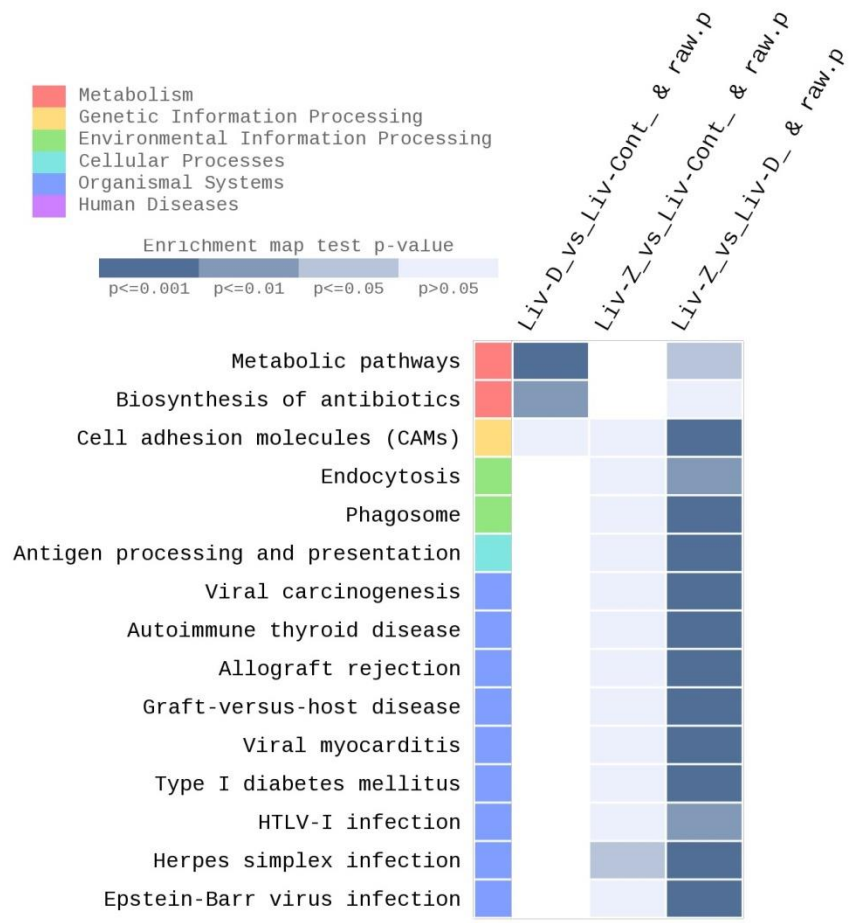
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73 **Fig. S4.** The most significantly enriched KEGG pathways associated with DEGs from both DON and  
 74 ZEN dietary treatment groups.

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98 **Table S1.** Primers used for real-time quantitative PCR validation of DEGs from the DON and ZEN  
 99 treatments and their corresponding accession numbers and product lengths.

S. No	Gene name <sup>1</sup>	Accession Number	Sequence	Product size
1	IGF-I	M31175.1	F: ATCACATCCTCTTCGCATCTC R: CCTGTGGGCTTGTTGAAATAAA	158
2	ORM1	XM_005660371	F: GTACAATGAGTCGGCCAGAT R: CTCAGGGAGCTGTCGTTATAG	133
3	UBD	NM_001160088	F: CTCATGGCCTACTTGGAAAGAT R: CTCCTTGTCAATGCCGTAAGA	151
4	SLA-1	NM_001097431	F: AGGACTATTGGGATGAGGAGAC R: CCCAAGTAGCAGCCAAACA	142
5	HMGCS2	NM_214380	F: CTTGCCCTGGAGGTCTATTTTC R: GTCAGGCACAAGGAGTTGAT	155
6	MT1A	NM_001001266	F: CGTGCAAAGCCTGCAGAT R: CACAGCAGCTGCACTTGT	123
7	NOCT	XM_003129187	F: TAGCCTACCAGCCCGATATAC R: CCATCGGGTCCATTGTTATGT	154
8	TRHDE	XM_003355521	F: GAAGATGTGTGGCTGAAGGA R: CTGTGATACTGGATGGGAACTG	162
9	NNMT	NM_001123146	F: ATCATTGCCACCGACTACAC R: CCGTTCCTTGACTCTGTTC	136
10	ARHGEF6	XM_013991029	F: GGAGCGGTACCTCATGTTATT R: GTCATTGCCTTCCGTTTCATC	139
11	CLDN4	NM_001161637	F: CAACTGCGTGGATGATGAGA R: ATTGTAGAAGTCGCGGATGAC	133
12	PON3	NM_001044604	F: CCTGATACGGGAGATATTTGGG R: TGGCATACTCGGTGCTTATC	145
13	GAPDH	AF017079	F: GTCTGGAGAAACCTGCCAAATA R: CCCAGCATCAAAGGTAGAAGAG	152
14	β- actin	AY550069	F: TCCACGAAACTACCTTCAACTC R: GATCTCCTTCTGCATCCTGTC	131

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101 <sup>1</sup>IGF-I= Insulin-like growth factor I; ORM1= Orosomuroid 1; UBD= Ubiquitin D; SLA-1= Src-Like-Adaptor-1;

102 HMGCS2= Hydroxy-3-methylglutaryl-CoA synthase 2; MT1A= Metallothionein 1A; NOCT= Nocturnin;

103 TRHDE= Thyrotropin-releasing hormone degrading enzyme; NNMT= Nicotinamide N-methyltransferase;

104 ARHGEF6= Rho guanine nucleotide exchange factor 6; CLDN4= Claudin 4; PON3= Paraoxonase 3; GAPDH=

105 Glyceraldehydes 3-phosphate, and β- actin= Beta actin.

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