

Transcriptomics of chicken cecal tonsils and intestine after infection with low pathogenic avian influenza virus H9N2

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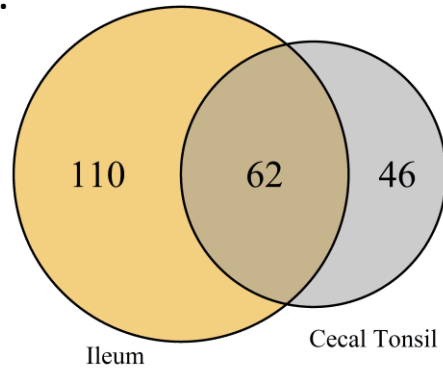
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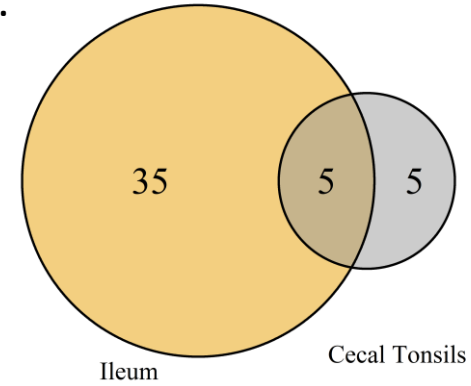
Supplementary figure 2. Venn diagrams showing shared and unique responses to AIV infection in cecal tonsils and ileum. Responses to H9N2 AIV infection in ileum is compared to that in cecal tonsils for upregulated genes at 24 hpi (A) and at 72 hpi (B) and for downregulated genes at 24 hpi (C) and at 72 hpi (D).

A.



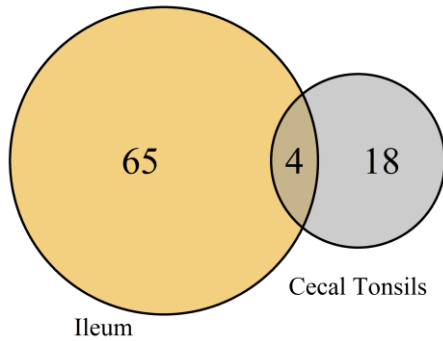
Upregulated genes at 24hpi

B.



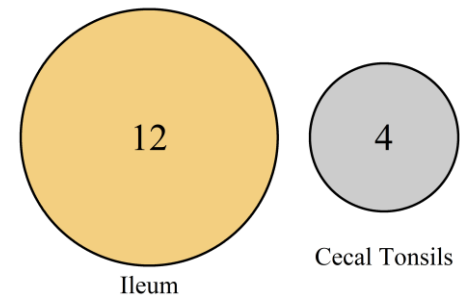
Upregulated genes at 72hpi

C.



Downregulated genes at 24hpi

D.



Downregulated genes at 72hpi

Functional annotation analysis of Reactome pathways using PANTHER

Overrepresentation analysis was performed on PANTHER. The analysis was performed on 110 genes exclusively upregulated in ileum at 24 hpi by filtering genes with a significant p-value of False Discovery Rate (FDR) controlled at 10%.

Reactome pathways	Number of genes in reference list	Number of genes in target list	Expected	Over/under representation (+/-)	Fold enrichment	Raw P-value	FDR
Regulation of gene expression by Hypoxia-inducible Factor (R-GGA-1234158)	3	2	0.02	+	> 100	1.32E-04	6.73E-02
TRAF6 mediated IRF7 activation (R-GGA-933541)	3	2	0.02	+	> 100	1.32E-04	5.05E-02
Formation of the beta-catenin:TCF transactivating complex (R-GGA-201722)	12	3	0.07	+	45.63	4.38E-05	6.68E-02
Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors (R-GGA-8864260)	13	3	0.07	+	42.12	5.54E-05	4.23E-02
SUMO E3 ligases SUMOylate target proteins (R-GGA-3108232)	88	5	0.48	+	10.37	1.34E-04	4.09E-02
SUMOylation (R-GGA-2990846)	90	5	0.49	+	10.14	1.48E-04	3.78E-02