

Blue-winged Teal Differential Expression Analyses

Amanda Dolinski & Jared J. Homola

These analyses examine differential gene expression in ileum and bursa tissues for LPAIV-infected blue-winged teals. Analyses for both tissues were conducted at the transcript and gene level. The analyses were conducted for the following comparisons:

1. Uninfected control teals at 1 and 14 DPI
2. LPAIV-infected and uninfected control teals at 1, 3, 5, and 14 DPI
3. LPAIV-infected teals at different DPI: 1 vs 3, 3 vs 5, and 5 vs 14
4. Virus Shed Level at 1, 3, and 5 DPI

The overall approach was to:

1. Filter lowly expressed transcripts by requiring expression of >0.5 counts per million in at least 25% of the birds.
2. Require a false discovery rate (FDR) corrected alpha value of 0.1 and a required log fold count difference (LFC) of 1.0 to establish differential expression.
3. Sex, age at inoculation, weight at 55 days old, and sample sequencing pool were included as covariates in each analysis.
4. Putative gene names were assigned to genes and transcripts based on existing SwissProt annotations of the blue-winged teal reference transcriptome (Dolinski, Homola, et al., 2020).
5. We performed enrichment analyses to identify over-represented gene ontology (GO) terms. GO enrichment was performed with the R package “topGO” (Alexa and Rahnenfuhrer, 2020) using the elimination algorithm and Fisher statistic to determine significance using a maximum p-value of 0.01.

Table of Contents:

Pg.

Combine Control Groups – Gene.....	1
Combine Control Groups – Transcript.....	3
LPAIV-infected and Control by DPI – Ileum – Gene.....	6
LPAIV-infected and Control by DPI – Ileum – Trans.....	16
LPAIV-infected and Control by DPI – Bursa – Gene.....	31
LPAIV-infected and Control by DPI – Bursa – Trans.....	35
Shed Level Early Infection (LvMvH) – Ileum – Gene.....	38
Shed Level Early Infection (LvMvH) – Ileum – Trans.....	43
Shed Level Early Infection (LvMvH) – Bursa – Gene.....	52

Shed Level Early Infection (LvMvH) – Bursa – Trans.....	57
Shed Level Late Infection (LvMvH) – Ileum – Gene.....	63
Shed Level Late Infection (LvMvH) – Ileum – Trans.....	71
Shed Level Late Infection (LvMvH) – Bursa – Gene.....	88
Shed Level Late Infection (LvMvH) – Bursa – Trans.....	90

Combine control groups - Gene

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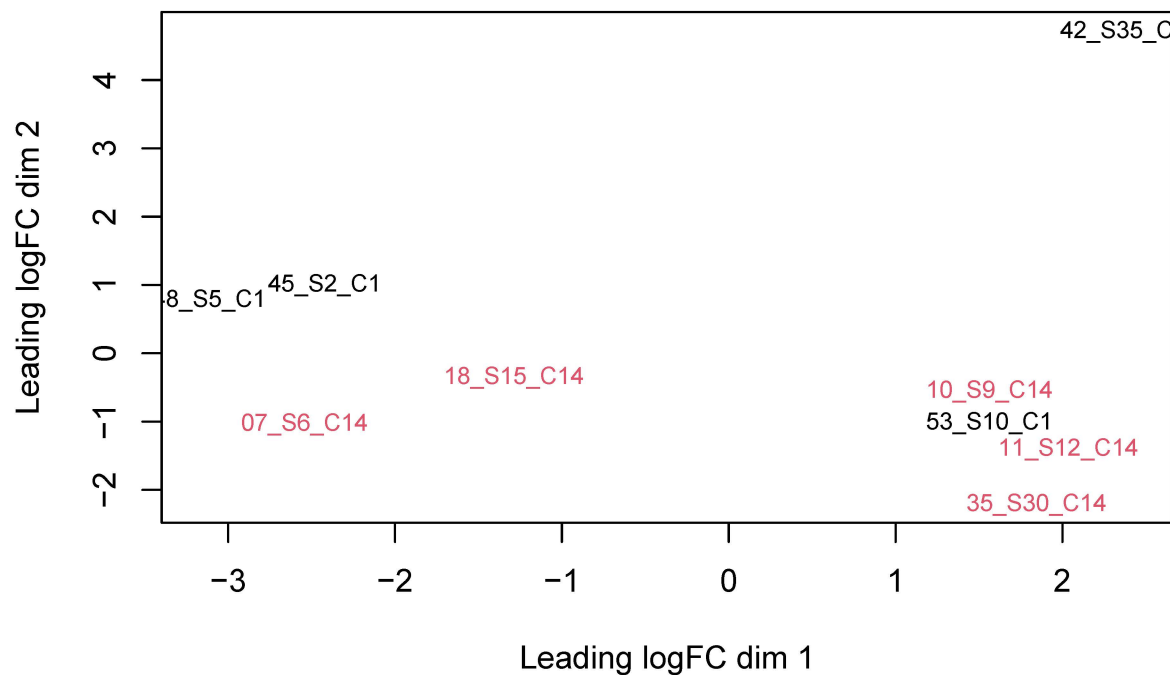
21 March, 2021

This analysis asks whether it is appropriate to combine the day 1 and day 14 control groups for the analysis between LPAIV-infected and uninfected control blue-winged teals. This is for the gene-level data.

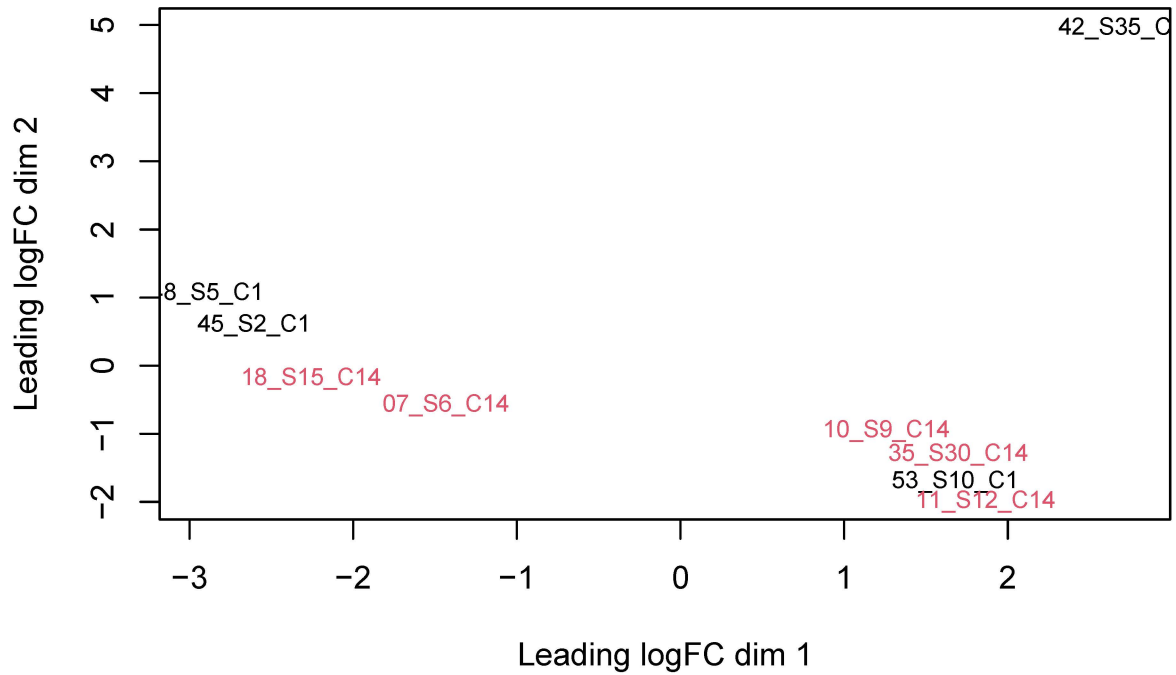
Plot MDS

Multidimensional scaling (MDS) plots are an ordination technique that lets us examine sample clustering based on overall gene expression levels.

Control comparison – Bursa



Control comparison – Ileum



Differential expression analysis

Table 1: Count of DE bursa genes. For a gene to be considered differentially expressed, we require a p-value of 0.1 with a false discovery rate correction and a log fold change difference of 1.0.

	C1vC14
Down	0
NotSig	75290
Up	0

Table 2: Count of DE ileum genes. For a gene to be considered differentially expressed, we require a p-value of 0.1 with a false discovery rate correction and a log fold change difference of 1.0.

	C1vC14
Down	0
NotSig	56961
Up	0

Combine control groups - Transcript

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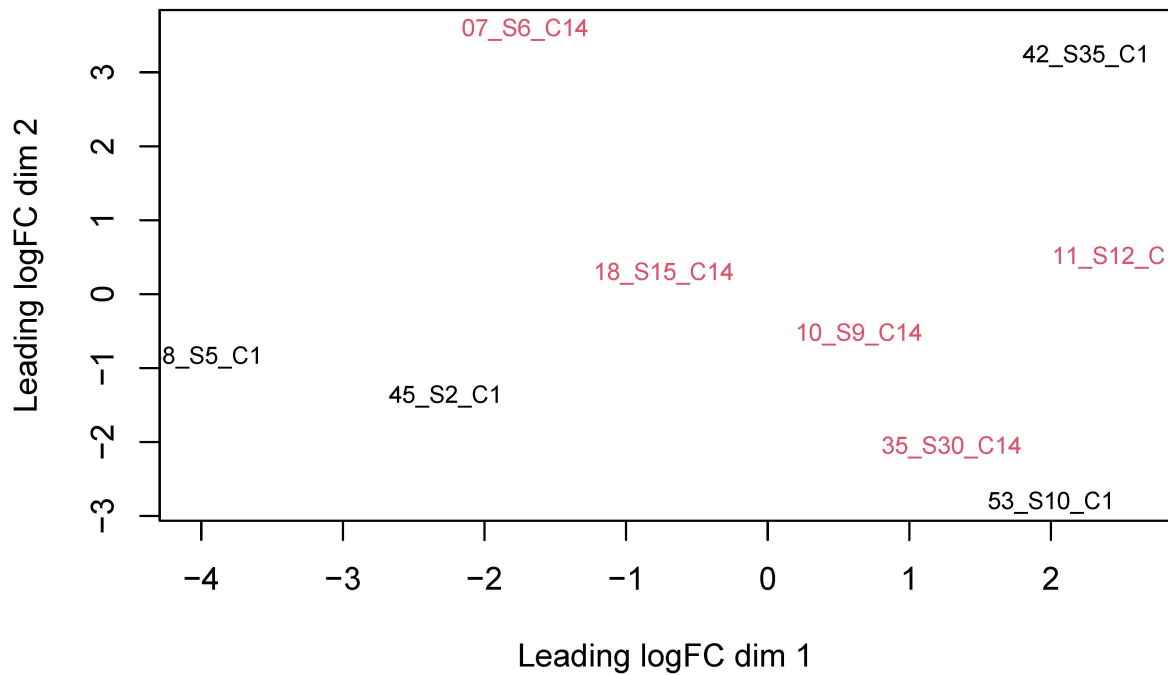
22 March, 2021

This analysis asks whether it is appropriate to combine the day 1 and day 14 control groups for the analysis between LPAIV-infected and uninfected control blue-winged teals. This is for the transcript-level data.

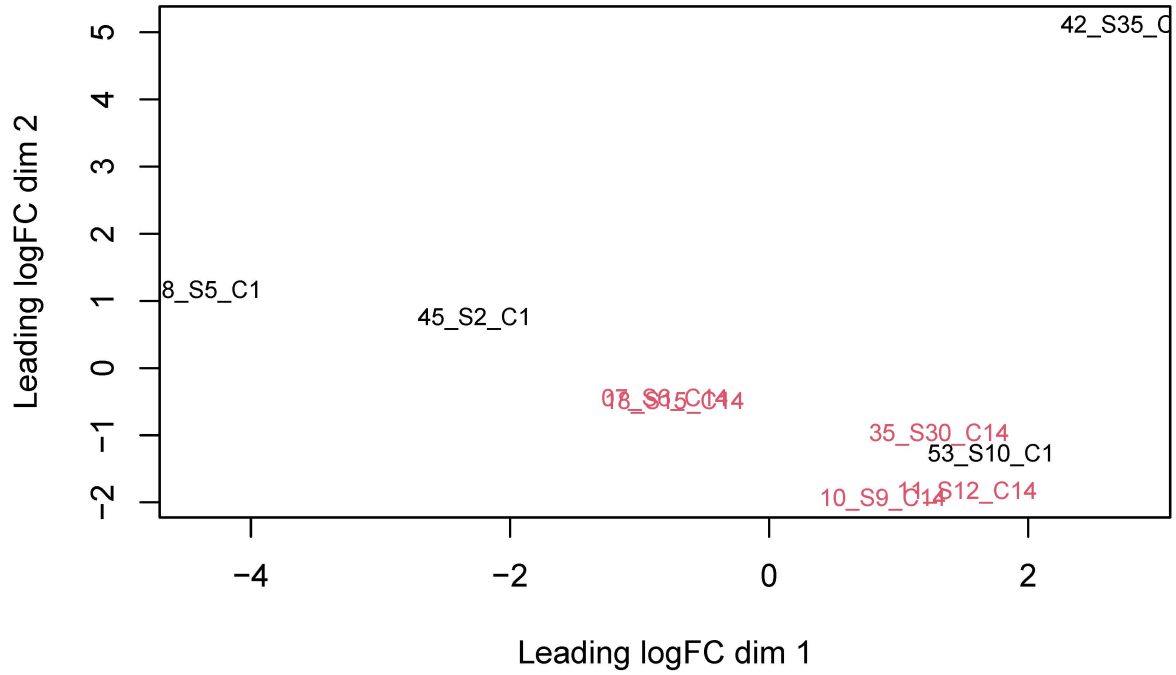
Plot MDS

Multidimensional scaling (MDS) plots are an ordination technique that lets us examine sample clustering based on overall transcript expression levels.

Control comparison – Bursa



Control comparison – Ileum



Differential expression analysis

Table 1: Count of DE bursa genes. For a gene to be considered differentially expressed, we require a p-value of 0.1 with a false discovery rate correction and a log fold change difference of 1.0.

	C1vC14
Down	0
NotSig	74436
Up	0

Table 2: Count of DE ileum genes. For a gene to be considered differentially expressed, we require a p-value of 0.1 with a false discovery rate correction and a log fold change difference of 1.0.

	C1vC14
Down	2
NotSig	66978
Up	0

Table 3: Annotations for differentially expressed transcripts. ns denotes non-significant transcripts for each comparison and numerical values are the log(fold change) difference

transcript	SwissProt_GeneName	C1vC14.ileum	C1vC14.bursa
DN5715_c0_g1_i5	MXRA5	down	0
DN1394_c1_g1_i3	JUN	down	0

Table 4: Transcript functions

transcript	SwissProt_GeneName	Kegg
DN5715_c0_g1_i5	MXRA5	KEGG:hsa:25878
DN1394_c1_g1_i3	JUN	KEGG:gga:424673'KO:K04448

LPAIV-Infected and Controls by DPI - Ileum - Gene

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23 March, 2021

This is an analysis of differential expression at the gene level between LPAIV-infected and uninfected control blue-winged teal ileum samples at each day post-infection (DPI). Differential expression was also analyzed between LPAIV-infected groups at different DPI.

Differential expression analysis

Table 1: Count of DE genes. For a gene to be considered differentially expressed, we require a p-value of 0.1 with a false discovery rate correction and a log fold change difference of 1.0.

	CtlvI1	CtlvI3	CtlvI5	CtlvI14	I1vI3	I3vI5	I5vI14
Down	42	12	0	0	0	0	0
NotSig	56914	56945	56959	56960	56961	56961	56961
Up	5	4	2	1	0	0	0

Volcano plot

Volcano plot reporting $-\log_{10}(\text{p-values})$ as a function of $\log_2(\text{fold change})$ between the samples (logFC, x axis). Genes that are identified as significantly differentially expressed following a false discovery rate correction ($q = 0.10$) are shown in red

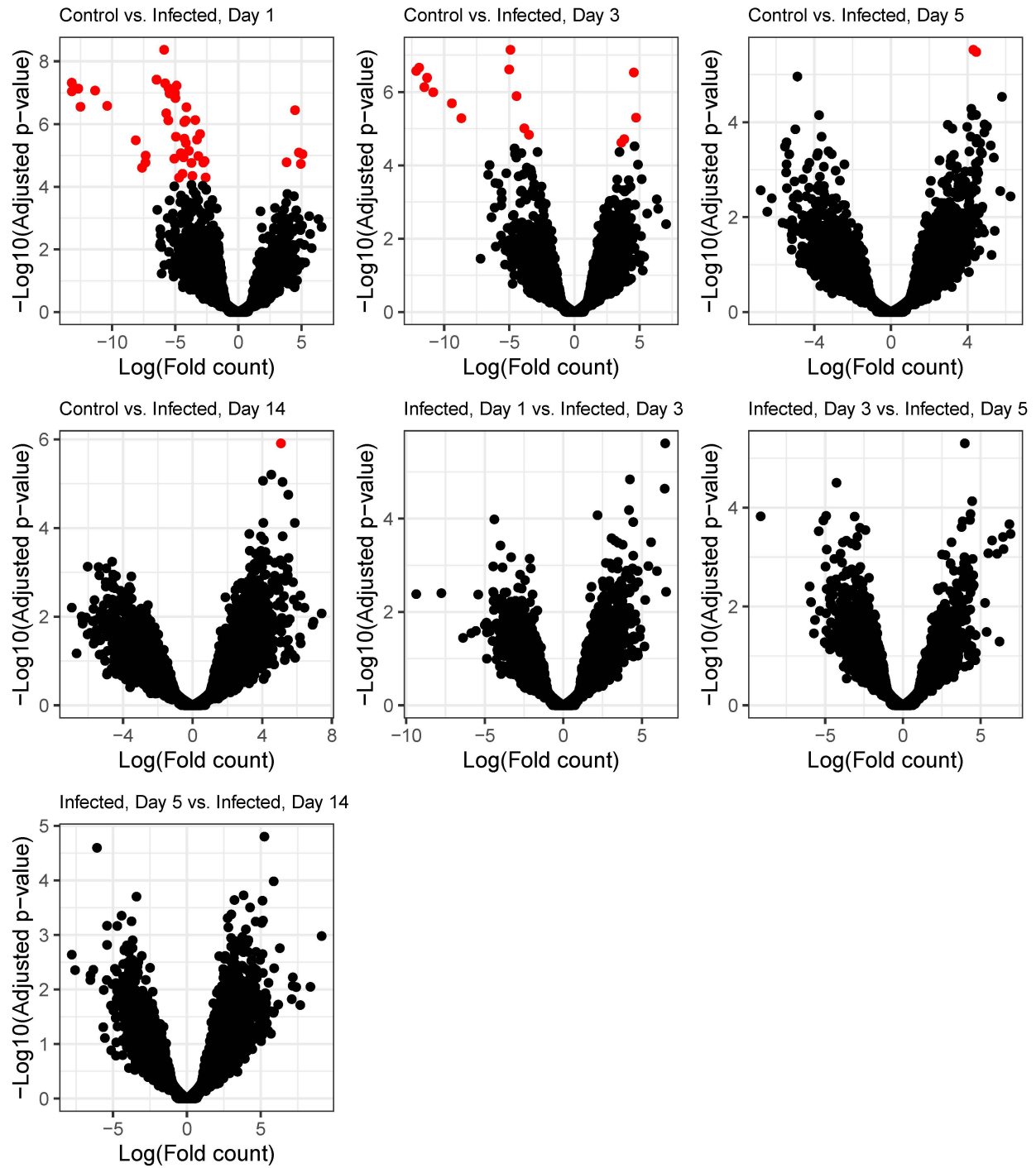


Table 2: Annotations for differentially expressed genes. ns denotes non-significant genes for each comparison and numerical values are the log(fold change) difference

gene_id	SwissProt_GeneName	CtlvI1	CtlvI3	CtlvI5	CtlvI14	I1vI3	I3vI5	I5vI14
DN17179_c0_g1	.	-5.88	-5.01	ns	ns	ns	ns	ns
DN151_c2_g1	.	-6.48	ns	ns	ns	ns	ns	ns
DN8513_c3_g1	M1_I80AD	-13.2	-11.93	ns	ns	ns	ns	ns
DN473_c1_g3	.	-5.8	ns	ns	ns	ns	ns	ns
DN69128_c0_g1	.	-4.9	ns	ns	ns	ns	ns	ns
DN6590_c0_g1	TMPS2_HUMAN	-5.53	ns	ns	ns	ns	ns	ns
DN15897_c0_g1	NCAP_I53A0	-12.68	-11.31	ns	ns	ns	ns	ns
DN7314_c1_g2	HEMA_I87A1	-12.69	-10.84	ns	ns	ns	ns	ns
DN7314_c1_g1	HEMA_I87A1	-11.35	-9.41	ns	ns	ns	ns	ns
DN8513_c3_g2	M2_I66A0	-13.19	-12.15	ns	ns	ns	ns	ns
DN428854_c0_g1	.	-5.03	ns	ns	ns	ns	ns	ns
DN10649_c1_g1	.	-5.45	ns	ns	ns	ns	ns	ns
DN614_c0_g2	CMPK2_HUMAN	-4.99	ns	ns	ns	ns	ns	ns
DN12097_c0_g2	NRAM_I85A8	-10.39	-8.68	ns	ns	ns	ns	ns
DN11336_c0_g1	NEP_I79A3	-12.51	-11.52	ns	ns	ns	ns	ns
DN43220_c0_g1	UBP18_HUMAN	-4.12	-3.49	ns	ns	ns	ns	ns
DN95654_c0_g1	DSG1_PIG	4.49	ns	ns	ns	ns	ns	ns
DN1765_c0_g1	.	-5.71	ns	ns	ns	ns	ns	ns
DN2085_c0_g2	MX_ANAPL	-3.41	ns	ns	ns	ns	ns	ns
DN8686_c0_g2	.	-5.55	ns	ns	ns	ns	ns	ns
DN2293_c0_g1	PIGY_HUMAN	-4.17	ns	ns	ns	ns	ns	ns
DN2198_c0_g1	DDX60_HUMAN	-4.28	-3.85	ns	ns	ns	ns	ns
DN3062_c0_g1	RN213_HUMAN	-3.03	ns	ns	ns	ns	ns	ns
DN17249_c1_g1	TMPS2_HUMAN	-4.94	ns	ns	ns	ns	ns	ns
DN2708_c1_g1	.	-4.28	ns	ns	ns	ns	ns	ns
DN164_c3_g1	DHX58_HUMAN	-3.28	ns	ns	ns	ns	ns	ns
DN10817_c0_g1	RDRP_I78AC	-8.13	ns	ns	ns	ns	ns	ns
DN2932_c0_g1	.	-4.16	-4.91	ns	ns	ns	ns	ns
DN9487_c0_g1	.	-3.92	ns	ns	ns	ns	ns	ns
DN184159_c0_g1	CRBN_CHICK	4.8	ns	ns	ns	ns	ns	ns
DN1920_c0_g1	RSAD2_BOVIN	-4.56	ns	ns	ns	ns	ns	ns
DN273679_c0_g1	DSG4_HUMAN	5.08	ns	ns	ns	ns	ns	ns
DN17714_c0_g1	.	-7.35	ns	ns	ns	ns	ns	ns
DN9247_c0_g1	GBP6_PONAB	-3.17	ns	ns	ns	ns	ns	ns
DN13412_c0_g1	.	-4.34	ns	ns	ns	ns	ns	ns
DN2145_c1_g1	.	-5.07	ns	ns	ns	ns	ns	ns
DN1934_c0_g1	IRF3_CHICK	-2.67	ns	ns	ns	ns	ns	ns
DN35422_c1_g1	.	3.82	3.82	ns	5.07	ns	ns	ns
DN135990_c0_g1	PB2_I80A6	-7.36	ns	ns	ns	ns	ns	ns
DN4591_c0_g1	SAM9L_HUMAN	-2.78	ns	ns	ns	ns	ns	ns
DN6178_c0_g1	UBP34_HUMAN	-3.71	ns	ns	ns	ns	ns	ns
DN444408_c0_g1	DSG4_MOUSE	4.95	ns	ns	ns	ns	ns	ns
DN135990_c0_g2	PB2_I02A7	-7.63	ns	ns	ns	ns	ns	ns
DN7131_c1_g1	.	-4.42	ns	ns	ns	ns	ns	ns
DN6190_c0_g1	OASL1_RAT	-3.64	ns	ns	ns	ns	ns	ns

Table 2: Annotations for differentially expressed genes. ns denotes non-significant genes for each comparison and numerical values are the log(fold change) difference (*continued*)

gene_id	SwissProt_GeneName	CtlvI1	CtlvI3	CtlvI5	CtlvI14	I1vI3	I3vI5	I5vI14
DN2559_c0_g1	MOV10_CHICK	-2.59	ns	ns	ns	ns	ns	ns
DN7658_c1_g1	CL17A_HUMAN	-4.7	ns	ns	ns	ns	ns	ns
DN30305_c0_g1	IC1_HUMAN	ns	-4.45	ns	ns	ns	ns	ns
DN252755_c0_g1	.	ns	4.73	ns	ns	ns	ns	ns
DN149999_c0_g1	.	ns	ns	4.46	ns	ns	ns	ns
DN229556_c0_g1	.	ns	4.56	ns	ns	ns	ns	ns
DN1946_c0_g3	.	ns	3.6	ns	ns	ns	ns	ns
DN8275_c0_g2	.	ns	ns	4.31	ns	ns	ns	ns

Table 3: Gene functions

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN8513_c3_g1	M1_I80AD	Matrix protein 1 {ECO:0000255 HAMAP- Rule:MF_04068};	.	NA
DN6590_c0_g1	TMPS2_HUMAN	Transmembrane protease serine 2;	KEGG:hsa:7113	KO:K09633
DN15897_c0_g1	NCAP_I53A0	Nucleoprotein {ECO:0000255 HAMAP- Rule:MF_04070};	.	NA
DN7314_c1_g2	HEMA_I87A1	Hemagglutinin {ECO:0000255 HAMAP- Rule:MF_04072};	.	NA
DN7314_c1_g1	HEMA_I87A1	Hemagglutinin {ECO:0000255 HAMAP- Rule:MF_04072};	.	NA
DN8513_c3_g2	M2_I66A0	Matrix protein 2 {ECO:0000255 HAMAP- Rule:MF_04069};	.	NA
DN614_c0_g2	CMPK2_HUMAN	UMP-CMP kinase 2, mitochondrial;	KEGG:hsa:129607	KO:K13809
DN12097_c0_g2	NRAM_I85A8	Neuraminidase {ECO:0000255 HAMAP- Rule:MF_04071};	.	NA
DN11336_c0_g1	NEP_I79A3	Nuclear export protein {ECO:0000255 HAMAP- Rule:MF_04067};	.	NA
DN43220_c0_g1	UBP18_HUMAN	Ubl carboxyl-terminal hydrolase 18;	KEGG:hsa:11274	KO:K11846
DN95654_c0_g1	DSG1_PIG	Desmoglein-1;	KEGG:ssc:641355	KO:K07596
DN2085_c0_g2	MX_ANAPL	Interferon-induced GTP-binding protein Mx;	KEGG:apla:101793492	KO:K14754
DN2293_c0_g1	PIGY_HUMAN	Phosphatidylinositol N-acetylglucosaminyltransferase subunit Y;	KEGG:hsa:84992	KO:K11001
DN2198_c0_g1	DDX60_HUMAN	Probable ATP-dependent RNA helicase DDX60;	KEGG:hsa:55601	KO:K20103

Table 3: Gene functions (*continued*)

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN3062_c0_g1	RN213_HUMAN	E3 ubiquitin-protein ligase RNF213 {ECO:0000305};	KEGG:hsa:57674	KO:K22754
DN17249_c1_g1	TMPS2_HUMAN	Transmembrane protease serine 2;	KEGG:hsa:7113	KO:K09633
DN164_c3_g1	DHX58_HUMAN	Probable ATP-dependent RNA helicase DHX58;	KEGG:hsa:79132	KO:K12649
DN10817_c0_g1	RDRP_I78AC	RNA-directed RNA polymerase catalytic subunit {ECO:0000255 HAMAP- Rule:MF_04065};	.	NA
DN184159_c0_g1	CRBN_CHICK	Protein cereblon;	.	NA
DN1920_c0_g1	RSAD2_BOVIN	Radical S-adenosyl methionine domain-containing protein 2;	KEGG:bta:506415	KO:K15045
DN273679_c0_g1	DSG4_HUMAN	Desmoglein-4;	KEGG:hsa:147409	KO:K07599
DN9247_c0_g1	GBP6_PONAB	Guanylate-binding protein 6;	KEGG:pon:100172797	KO:K20908
DN1934_c0_g1	IRF3_CHICK	Interferon regulatory factor 3;	KEGG:gga:396330	KO:K09447
DN135990_c0_g1	PB2_I80A6	Polymerase basic protein 2 {ECO:0000255 HAMAP- Rule:MF_04062};	.	NA
DN4591_c0_g1	SAM9L_HUMAN	Sterile alpha motif domain-containing protein 9-like;	KEGG:hsa:219285	NA
DN6178_c0_g1	UBP34_HUMAN	Ubiquitin carboxyl-terminal hydrolase 34;	KEGG:hsa:9736	KO:K11853
DN444408_c0_g1	DSG4_MOUSE	Desmoglein-4;	KEGG:mmu:16769	KO:K07599
DN135990_c0_g2	PB2_I02A7	Polymerase basic protein 2 {ECO:0000255 HAMAP- Rule:MF_04062};	.	NA
DN6190_c0_g1	OASL1_RAT	2'-5'-oligoadenylate synthase-like protein 1;	KEGG:mmu:246727	KO:K14216
DN2559_c0_g1	MOV10_CHICK	Putative helicase MOV-10;	KEGG:gga:419872	KO:K18422
DN7658_c1_g1	CL17A_HUMAN	C-type lectin domain family 17, member A;	KEGG:hsa:388512	KO:K17513
DN30305_c0_g1	IC1_HUMAN	Plasma protease C1 inhibitor;	KEGG:hsa:710	KO:K04001

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0001868	regulation of complement activation, lec...	5	1	0.00	0.00295	2.95e-03	BP	CtlvI3
GO:0001942	hair follicle development	76	2	0.14	0.00845	8.45e-03	BP	CtlvI1
GO:0002726	positive regulation of T cell cytokine p...	20	2	0.04	0.00060	6.00e-04	BP	CtlvI1
GO:0002830	positive regulation of type 2 immune res...	11	2	0.02	0.00018	1.80e-04	BP	CtlvI1
GO:0003724	RNA helicase activity	127	3	0.23	0.00158	1.58e-03	MF	CtlvI1
GO:0003725	double-stranded RNA binding	106	3	0.19	0.00094	9.40e-04	MF	CtlvI1
GO:0003727	single-stranded RNA binding	135	3	0.25	0.00188	1.88e-03	MF	CtlvI1
GO:0003968	RNA-directed 5'-3' RNA polymerase activi...	8	3	0.01	3.1e-07	3.00e-07	MF	CtlvI1
GO:0005044	scavenger receptor activity	62	2	0.11	0.00570	5.70e-03	MF	CtlvI1
GO:0006370	7-methylguanosine mRNA capping	35	2	0.06	0.00185	1.85e-03	BP	CtlvI1
GO:0007156	homophilic cell adhesion via plasma memb...	156	3	0.28	0.00284	2.84e-03	BP	CtlvI1
GO:0007597	blood coagulation, intrinsic pathway	8	1	0.00	0.00471	4.71e-03	BP	CtlvI3
GO:0009189	deoxyribonucleoside diphosphate biosynth...	5	1	0.01	0.00908	9.08e-03	BP	CtlvI1
GO:0010951	negative regulation of endopeptidase act...	113	2	0.07	0.00193	1.93e-03	BP	CtlvI3
GO:0016540	protein autoprocessing	19	2	0.03	0.00054	5.40e-04	BP	CtlvI1
GO:0019012	virion	169	9	0.30	5.5e-05	5.50e-05	CC	CtlvI1
GO:0019012	virion	169	7	0.09	0.00072	7.20e-04	CC	CtlvI3
GO:0019031	viral envelope	26	2	0.05	0.00095	9.50e-04	CC	CtlvI1
GO:0019031	viral envelope	26	2	0.01	9.0e-05	9.00e-05	CC	CtlvI3
GO:0019062	virion attachment to host cell	32	2	0.06	0.00155	1.55e-03	BP	CtlvI1
GO:0019062	virion attachment to host cell	32	2	0.02	0.00016	1.60e-04	BP	CtlvI3
GO:0019064	fusion of virus membrane with host plasm...	27	2	0.05	0.00110	1.10e-03	BP	CtlvI1
GO:0019064	fusion of virus membrane with host plasm...	27	2	0.02	0.00011	1.10e-04	BP	CtlvI3
GO:0019076	viral release from host cell	59	4	0.11	3.9e-06	3.90e-06	BP	CtlvI1
GO:0019076	viral release from host cell	59	4	0.03	2.9e-08	0.00e+00	BP	CtlvI3
GO:0019083	viral transcription	142	4	0.26	0.00013	1.30e-04	BP	CtlvI1
GO:0020002	host cell plasma membrane	113	4	0.20	4.5e-05	4.50e-05	CC	CtlvI1
GO:0020002	host cell plasma membrane	113	4	0.06	3.2e-07	3.00e-07	CC	CtlvI3
GO:0030057	desmosome	48	3	0.08	8.2e-05	8.20e-05	CC	CtlvI1
GO:0030430	host cell cytoplasm	117	4	0.21	5.2e-05	5.20e-05	CC	CtlvI1
GO:0030683	mitigation of host immune response by vi...	6	1	0.00	0.00353	3.53e-03	BP	CtlvI3
GO:0032481	positive regulation of type I interferon...	74	2	0.13	0.00803	8.03e-03	BP	CtlvI1

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched) (*continued*)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0035745	T-helper 2 cell cytokine production	5	1	0.01	0.00908	9.08e-03	BP	CtlvI1
GO:0039507	suppression by virus of host molecular f...	9	5	0.02	0.00642	6.42e-03	BP	CtlvI1
GO:0039507	suppression by virus of host molecular f...	9	1	0.01	0.00530	5.30e-03	BP	CtlvI3
GO:0039519	modulation by virus of host autophagy	5	1	0.01	0.00908	9.08e-03	BP	CtlvI1
GO:0039519	modulation by virus of host autophagy	5	1	0.00	0.00295	2.95e-03	BP	CtlvI3
GO:0039523	suppression by virus of host RNA polymer...	5	4	0.01	4.6e-11	0.00e+00	BP	CtlvI1
GO:0039694	viral RNA genome replication	39	4	0.07	7.2e-07	7.00e-07	BP	CtlvI1
GO:0042025	host cell nucleus	36	7	0.06	2.2e-13	0.00e+00	CC	CtlvI1
GO:0042025	host cell nucleus	36	3	0.02	8.9e-07	9.00e-07	CC	CtlvI3
GO:0042730	fibrinolysis	15	1	0.01	0.00882	8.82e-03	BP	CtlvI3
GO:0045071	negative regulation of viral genome repl...	52	3	0.09	0.00012	1.20e-04	BP	CtlvI1
GO:0045087	innate immune response	722	10	1.32	7.2e-05	7.20e-05	BP	CtlvI1
GO:0045824	negative regulation of innate immune res...	64	2	0.12	0.00606	6.06e-03	BP	CtlvI1
GO:0045824	negative regulation of innate immune res...	64	2	0.04	0.00063	6.30e-04	BP	CtlvI3
GO:0045916	negative regulation of complement activa...	12	1	0.01	0.00706	7.06e-03	BP	CtlvI3
GO:0046598	positive regulation of viral entry into ...	16	2	0.03	0.00038	3.80e-04	BP	CtlvI1
GO:0046755	viral budding	30	4	0.05	2.4e-07	2.00e-07	BP	CtlvI1
GO:0046755	viral budding	30	4	0.02	1.8e-09	0.00e+00	BP	CtlvI3
GO:0046794	transport of virus	76	4	0.14	1.7e-05	1.70e-05	BP	CtlvI1
GO:0046794	transport of virus	76	4	0.04	1.3e-06	1.30e-06	BP	CtlvI3
GO:0051607	defense response to virus	235	7	0.43	3.3e-05	3.30e-05	BP	CtlvI1
GO:0052203	modulation of catalytic activity in othe...	5	1	0.01	0.00908	9.08e-03	BP	CtlvI1
GO:0052203	modulation of catalytic activity in othe...	5	1	0.00	0.00295	2.95e-03	BP	CtlvI3
GO:0052553	modulation by symbiont of host immune re...	5	1	0.01	0.00908	9.08e-03	BP	CtlvI1
GO:0052553	modulation by symbiont of host immune re...	5	1	0.00	0.00295	2.95e-03	BP	CtlvI3
GO:0052794	exo-alpha-(2->3)-sialidase activity	9	1	0.00	0.005	5.00e-03	MF	CtlvI3
GO:0052795	exo-alpha-(2->6)-sialidase activity	9	1	0.00	0.005	5.00e-03	MF	CtlvI3
GO:0052796	exo-alpha-(2->8)-sialidase activity	9	1	0.00	0.005	5.00e-03	MF	CtlvI3
GO:0055036	virion membrane	29	5	0.05	1.5e-09	0.00e+00	CC	CtlvI1
GO:0055036	virion membrane	29	5	0.02	2.1e-12	0.00e+00	CC	CtlvI3
GO:0060338	regulation of type I interferon-mediated...	36	2	0.07	0.00196	1.96e-03	BP	CtlvI1

Table 4: Gene Ontology enrichment analysis: GO terms with p-values < 0.05 were determined as over-represented (enriched) (*continued*)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0060338	regulation of type I interferon-mediated...	36	2	0.02	0.00020	2.00e-04	BP	CtlvI3
GO:0072583	clathrin-dependent endocytosis	63	2	0.11	0.00588	5.88e-03	BP	CtlvI1
GO:0072583	clathrin-dependent endocytosis	63	2	0.04	0.00061	6.10e-04	BP	CtlvI3
GO:0075733	intracellular transport of virus	72	2	0.13	0.00762	7.62e-03	BP	CtlvI1
GO:0075733	intracellular transport of virus	72	2	0.04	0.00079	7.90e-04	BP	CtlvI3
GO:1900245	positive regulation of MDA-5 signaling p...	5	2	0.01	3.2e-05	3.20e-05	BP	CtlvI1
GO:1900245	positive regulation of MDA-5 signaling p...	5	1	0.00	0.00295	2.95e-03	BP	CtlvI3
GO:1900246	positive regulation of RIG-I signaling p...	17	2	0.03	0.00043	4.30e-04	BP	CtlvI1
GO:1900246	positive regulation of RIG-I signaling p...	17	1	0.01	0.00999	9.99e-03	BP	CtlvI3

LPAIV-Infected and Controls by DPI - Ileum - Transcript

Amanda Dolinski & Jared J. Homola

23 March, 2021

This is an analysis of differential expression at the transcript level between LPAIV-infected and uninfected control blue-winged teal ileum samples at each day post-infection (DPI). Differential expression was also analyzed between LPAIV-infected groups at different DPI.

Differential expression analysis

Table 1: Count of DE transcripts. For a transcript to be considered differentially expressed, we require a p-value of 0.1 with a false discovery rate correction and a log fold change difference of 1.0.

	CtlvI1	CtlvI3	CtlvI5	CtlvI14	I1vI3	I3vI5	I5vI14
Down	58	27	0	0	0	1	0
NotSig	66915	66947	66980	66979	66979	66979	66979
Up	7	6	0	1	1	0	1

Volcano plot

Volcano plot reporting $-\log_{10}(\text{p-values})$ as a function of $\log_2(\text{fold change})$ between the samples ($\log_{2}\text{FC}$, x axis). Transcripts that are identified as significantly differentially expressed following a false discovery rate correction ($q = 0.10$) are shown in red

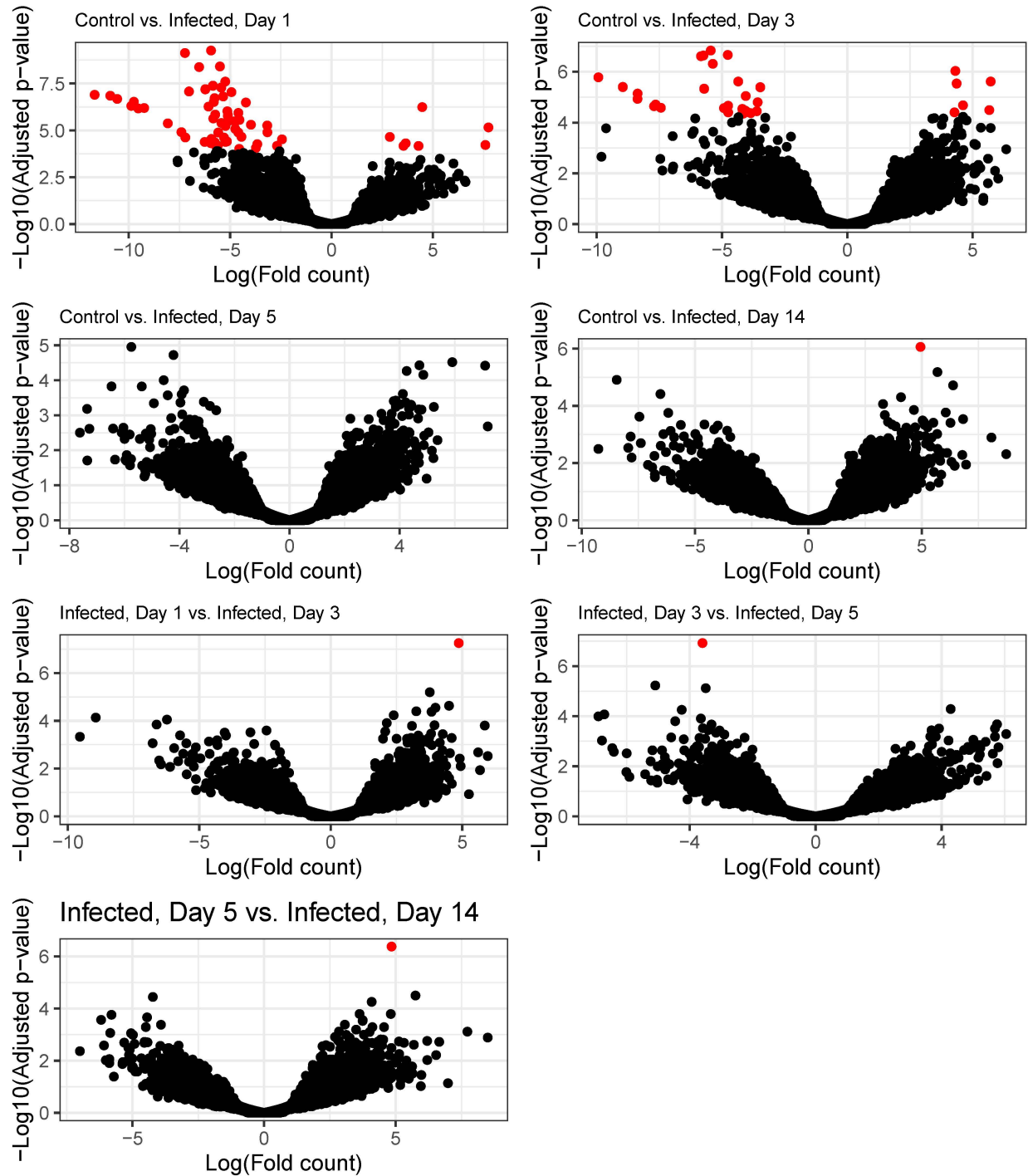


Table 2: Annotations for differentially expressed transcripts. ns denotes non-significant transcripts for each comparison and numerical values are the log(fold change) difference

transcript_id	SwissProt_GeneName	CtlvI1	CtlvI3	CtlvI5	CtlvI14	I1vI3	I3vI5	I5vI14
DN2085_c0_g2_i5	MX_ANAPL	-5.94	-4.77	ns	ns	ns	ns	ns
DN2085_c0_g2_i14	MX_ANAPL	-7.23	-5.74	ns	ns	ns	ns	ns
DN2085_c0_g2_i11	MX_ANAPL	-5.5	-4.05	ns	ns	ns	ns	ns
DN17179_c0_g1_i5	ESIP1_HUMAN	-6.53	-5.37	ns	ns	ns	ns	ns
DN2085_c0_g2_i16	MX_ANAPL	-5.24	-4.35	ns	ns	ns	ns	ns
DN614_c0_g2_i4	CMPK2_HUMAN	-5.85	-4.19	ns	ns	ns	ns	ns
DN6590_c0_g1_i1	TMPS2_HUMAN	-5.44	-4.07	ns	ns	ns	ns	ns
DN17179_c0_g1_i4	ESIP1_HUMAN	-6.22	-5.84	ns	ns	ns	ns	ns
DN2085_c0_g2_i15	MX_ANAPL	-7.03	-5.71	ns	ns	ns	ns	ns
DN428854_c0_g1_i1	.	-4.93	ns	ns	ns	ns	ns	ns
DN15897_c0_g1_i1	NCAP_I53A0	-11.68	-9.93	ns	ns	ns	ns	ns
DN8513_c3_g1_i1	M1_I80AD	-10.91	-8.96	ns	ns	ns	ns	ns
DN2085_c0_g2_i10	MX_ANAPL	-5.34	-4.19	ns	ns	ns	ns	ns
DN614_c0_g2_i1	CMPK2_HUMAN	-5.77	ns	ns	ns	ns	ns	ns
DN7314_c1_g2_i2	HEMA_I87A1	-10.57	-8.37	ns	ns	ns	ns	ns
DN7314_c1_g1_i2	HEMA_I87A1	-9.75	-7.65	ns	ns	ns	ns	ns
DN1765_c0_g1_i1	.	-5.81	ns	ns	ns	ns	ns	ns
DN43220_c0_g1_i9	UBP18_HUMAN	-4.22	-3.58	ns	ns	ns	ns	ns
DN11336_c0_g1_i2	NS1_I78A1	-9.87	-8.37	ns	ns	ns	ns	ns
DN17179_c0_g1_i2	ESIP1_HUMAN	-6.06	-4.92	ns	ns	ns	ns	ns
DN95654_c0_g1_i1	DSG1_PIG	4.47	ns	ns	ns	ns	ns	ns
DN12097_c0_g2_i4	NRAM_I85A8	-9.24	-7.44	ns	ns	ns	ns	ns
DN8513_c3_g2_i1	M2_I66A0	-9.53	-7.71	ns	ns	ns	ns	ns
DN17249_c1_g1_i1	TMPS2_HUMAN	-5.14	ns	ns	ns	ns	ns	ns
DN3062_c0_g1_i18	RN213_HUMAN	-4.59	ns	ns	ns	ns	ns	ns
DN2198_c0_g1_i1	DDX60_HUMAN	-5.73	-4.75	ns	ns	ns	ns	ns
DN2085_c0_g2_i13	MX_ANAPL	-5.11	ns	ns	ns	ns	ns	ns
DN591_c9_g2_i1	.	-5.12	ns	ns	ns	ns	ns	ns
DN14251_c0_g1_i13	.	-5.83	ns	ns	ns	ns	ns	ns
DN2198_c0_g1_i6	DDX60_HUMAN	-4.54	-3.98	ns	ns	ns	ns	ns
DN6178_c0_g1_i1	IFIT5_HUMAN	-5.06	ns	ns	ns	ns	ns	ns
DN2932_c0_g1_i6	IFI6_BOVIN	-4.77	-5.45	ns	ns	ns	ns	ns
DN1920_c0_g1_i9	RSAD2_BOVIN	-4.72	ns	ns	ns	ns	ns	ns
DN2085_c0_g2_i12	MX_ANAPL	-5.43	ns	ns	ns	ns	ns	ns
DN10817_c0_g1_i1	RDRP_I78AC	-8.07	ns	ns	ns	ns	ns	ns
DN2198_c0_g1_i10	DDX60_HUMAN	-3.97	-3.61	ns	ns	ns	ns	ns
DN3062_c0_g1_i12	RN213_HUMAN	-3.17	ns	ns	ns	ns	ns	ns
DN2559_c0_g1_i7	MOV10_CHICK	-5.23	ns	ns	ns	ns	ns	ns
DN7633_c1_g1_i16	BIRC6_HUMAN	7.74	ns	ns	ns	ns	ns	ns
DN1920_c0_g1_i11	RSAD2_PIG	-4.74	ns	ns	ns	ns	ns	ns
DN17714_c0_g1_i3	PA_I78AC	-7.4	ns	ns	ns	ns	ns	ns
DN4591_c0_g1_i4	SAM9L_HUMAN	-3.16	ns	ns	ns	ns	ns	ns
DN614_c0_g2_i8	CMPK2_HUMAN	-4.6	ns	ns	ns	ns	ns	ns
DN2145_c1_g1_i1	.	-5.59	ns	ns	ns	ns	ns	ns
DN9487_c0_g1_i2	.	-4.44	ns	ns	ns	ns	ns	ns

Table 2: Annotations for differentially expressed transcripts. ns denotes non-significant transcripts for each comparison and numerical values are the log(fold change) difference (*continued*)

transcript_id	SwissProt_GeneName	CtlvI1	CtlvI3	CtlvI5	CtlvI14	I1vI3	I3vI5	I5vI14
DN427_c0_g2_i4	NOX4_PONAB	2.88	ns	ns	ns	ns	ns	ns
DN135990_c0_g1_i1	PB2_I80A6	-7.21	ns	ns	ns	ns	ns	ns
DN2085_c0_g2_i6	MX_ANAPL	-5.3	ns	ns	ns	ns	ns	ns
DN9051_c0_g1_i3	GA2L1_MOUSE	-5.92	ns	ns	ns	ns	ns	ns
DN20874_c0_g1_i11	PAR12_HUMAN	-2.44	ns	ns	ns	ns	ns	ns
DN22_c0_g1_i2	MIRO1_CHICK	-5.16	ns	ns	ns	ns	ns	ns
DN1920_c0_g1_i1	RSAD2_BOVIN	-6.25	ns	ns	ns	ns	ns	ns
DN6190_c0_g1_i4	OASL2_MOUSE	-5.23	ns	ns	ns	ns	ns	ns
DN2767_c0_g1_i1	ISLR_HUMAN	-5.75	ns	ns	ns	ns	ns	ns
DN3062_c0_g1_i10	RN213_HUMAN	-5.96	ns	ns	ns	ns	ns	ns
DN24620_c0_g1_i11	.	3.66	ns	ns	ns	ns	ns	ns
DN6309_c0_g1_i12	.	-3.66	ns	ns	ns	ns	ns	ns
DN166_c0_g1_i5	RN141_CHICK	7.59	ns	ns	ns	ns	ns	ns
DN43220_c0_g1_i4	UBP18_HUMAN	-5.61	ns	ns	ns	ns	ns	ns
DN34132_c0_g1_i4	K2C74_MOUSE	3.55	ns	ns	ns	ns	ns	ns
DN1934_c0_g1_i11	IRF3_CHICK	-2.69	ns	ns	ns	ns	ns	ns
DN17171_c0_g1_i3	MTAP2_RAT	4.29	ns	ns	ns	ns	ns	ns
DN2293_c0_g1_i3	PIGY_HUMAN	-5.69	ns	ns	ns	ns	ns	ns
DN6190_c0_g1_i2	OASL1_RAT	-3.73	ns	ns	ns	ns	ns	ns
DN1934_c0_g1_i16	IRF3_CHICK	-4.55	ns	ns	ns	ns	ns	ns
DN5214_c0_g1_i6	CF062_MOUSE	ns	-4.76	ns	ns	ns	ns	ns
DN9772_c0_g1_i10	UQCC2_DANRE	ns	-4.15	ns	ns	ns	ns	ns
DN2228_c2_g1_i8	BMPR2_MOUSE	ns	5.66	ns	ns	ns	ns	ns
DN4998_c0_g1_i2	CNPY3_BOVIN	ns	-3.85	ns	ns	ns	ns	ns
DN14729_c0_g1_i4	FREM1_HUMAN	ns	4.62	ns	ns	ns	ns	ns
DN4239_c0_g1_i17	MYCB2_MOUSE	ns	5.72	ns	ns	ns	ns	ns
DN220085_c0_g1_i2	LAG3_MOUSE	ns	-3.47	ns	ns	ns	ns	ns
DN12331_c1_g1_i3	LRIG3_HUMAN	ns	4.28	ns	ns	ns	ns	ns
DN611_c1_g1_i6	LRRK2_HUMAN	ns	4.31	ns	ns	ns	ns	ns
DN2458_c0_g1_i1	DDX17_MOUSE	ns	4.36	ns	ns	4.87	ns	ns
DN1712_c0_g2_i10	DCAF4_HUMAN	ns	ns	ns	4.94	ns	ns	4.84
DN3176_c0_g1_i11	.	ns	ns	ns	ns	ns	-3.59	ns

Table 3: Transcript functions

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN2085_c0_g2_i5	MX_ANAPL	Interferon-induced GTP-binding protein Mx;	KEGG:apla:101793492	KO:K14754
DN2085_c0_g2_i14	MX_ANAPL	Interferon-induced GTP-binding protein Mx;	KEGG:apla:101793492	KO:K14754
DN2085_c0_g2_i11	MX_ANAPL	Interferon-induced GTP-binding protein Mx;	KEGG:apla:101793492	KO:K14754
DN17179_c0_g1_i5	ESIP1_HUMAN	Epithelial-stromal interaction protein 1;	KEGG:hsa:94240	NA
DN2085_c0_g2_i16	MX_ANAPL	Interferon-induced GTP-binding protein Mx;	KEGG:apla:101793492	KO:K14754
DN614_c0_g2_i4	CMPK2_HUMAN	UMP-CMP kinase 2, mitochondrial;	KEGG:hsa:129607	KO:K13809
DN6590_c0_g1_i1	TMPS2_HUMAN	Transmembrane protease serine 2;	KEGG:hsa:7113	KO:K09633
DN17179_c0_g1_i4	ESIP1_HUMAN	Epithelial-stromal interaction protein 1;	KEGG:hsa:94240	NA
DN2085_c0_g2_i15	MX_ANAPL	Interferon-induced GTP-binding protein Mx;	KEGG:apla:101793492	KO:K14754
DN15897_c0_g1_i1	NCAP_I53A0	Nucleoprotein {ECO:0000255 HAMAP- Rule:MF_04070}};	.	NA
DN8513_c3_g1_i1	M1_I80AD	Matrix protein 1 {ECO:0000255 HAMAP- Rule:MF_04068}};	.	NA
DN2085_c0_g2_i10	MX_ANAPL	Interferon-induced GTP-binding protein Mx;	KEGG:apla:101793492	KO:K14754
DN614_c0_g2_i1	CMPK2_HUMAN	UMP-CMP kinase 2, mitochondrial;	KEGG:hsa:129607	KO:K13809
DN7314_c1_g2_i2	HEMA_I87A1	Hemagglutinin {ECO:0000255 HAMAP- Rule:MF_04072}};	.	NA
DN7314_c1_g1_i2	HEMA_I87A1	Hemagglutinin {ECO:0000255 HAMAP- Rule:MF_04072}};	.	NA

Table 3: Transcript functions (*continued*)

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN43220_c0_g1_i9	UBP18_HUMAN	Ubl carboxyl-terminal hydrolase 18;	KEGG:hsa:11274	KO:K11846
DN11336_c0_g1_i2	NS1_I78A1	Non-structural protein 1 {ECO:0000255 HAMAP-Rule:MF_04066};	.	NA
DN17179_c0_g1_i2	ESIP1_HUMAN	Epithelial-stromal interaction protein 1;	KEGG:hsa:94240	NA
DN95654_c0_g1_i1	DSG1_PIG	Desmoglein-1;	KEGG:ssc:641355	KO:K07596
DN12097_c0_g2_i4	NRAM_I85A8	Neuraminidase {ECO:0000255 HAMAP-Rule:MF_04071};	.	NA
DN8513_c3_g2_i1	M2_I66A0	Matrix protein 2 {ECO:0000255 HAMAP-Rule:MF_04069};	.	NA
DN17249_c1_g1_i1	TMPS2_HUMAN	Transmembrane protease serine 2;	KEGG:hsa:7113	KO:K09633
DN3062_c0_g1_i18	RN213_HUMAN	E3 ubiquitin-protein ligase RNF213 {ECO:0000305};	KEGG:hsa:57674	KO:K22754
DN2198_c0_g1_i1	DDX60_HUMAN	Probable ATP-dependent RNA helicase DDX60;	KEGG:hsa:55601	KO:K20103
DN2085_c0_g2_i13	MX_ANAPL	Interferon-induced GTP-binding protein Mx;	KEGG:apla:101793492	KO:K14754
DN2198_c0_g1_i6	DDX60_HUMAN	Probable ATP-dependent RNA helicase DDX60;	KEGG:hsa:55601	KO:K20103
DN6178_c0_g1_i1	IFIT5_HUMAN	Interferon-induced protein with tetratricopeptide repeats 5;	KEGG:hsa:24138	NA
DN2932_c0_g1_i6	IFI6_BOVIN	Interferon alpha-inducible protein 6 {ECO:0000305};	KEGG:bta:512913	NA
DN1920_c0_g1_i9	RSAD2_BOVIN	Radical S-adenosyl methionine domain-containing protein 2;	KEGG:bta:506415	KO:K15045
DN2085_c0_g2_i12	MX_ANAPL	Interferon-induced GTP-binding protein Mx;	KEGG:apla:101793492	KO:K14754

Table 3: Transcript functions (*continued*)

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN10817_c0_g1_i1	RDRP_I78AC	RNA-directed RNA polymerase catalytic subunit {ECO:0000255 HAMAP-Rule:MF_04065};	.	NA
DN2198_c0_g1_i10	DDX60_HUMAN	Probable ATP-dependent RNA helicase DDX60;	KEGG:hsa:55601	KO:K20103
DN3062_c0_g1_i12	RN213_HUMAN	E3 ubiquitin-protein ligase RNF213 {ECO:0000305};	KEGG:hsa:57674	KO:K22754
DN2559_c0_g1_i7	MOV10_CHICK	Putative helicase MOV-10;	KEGG:gga:419872	KO:K18422
DN7633_c1_g1_i16	BIRC6_HUMAN	Baculoviral IAP repeat-containing protein 6;	KEGG:hsa:57448	KO:K10586
DN1920_c0_g1_i11	RSAD2_PIG	Radical S-adenosyl methionine domain-containing protein 2;	KEGG:ssc:396752	KO:K15045
DN17714_c0_g1_i3	PA_I78AC	Polymerase acidic protein {ECO:0000255 HAMAP-Rule:MF_04063};	.	NA
DN4591_c0_g1_i4	SAM9L_HUMAN	Sterile alpha motif domain-containing protein 9-like;	KEGG:hsa:219285	NA
DN614_c0_g2_i8	CMPK2_HUMAN	UMP-CMP kinase 2, mitochondrial;	KEGG:hsa:129607	KO:K13809
DN427_c0_g2_i4	NOX4_PONAB	NADPH oxidase 4;	KEGG:pon:100171782	KO:K21423
DN135990_c0_g1_i1	PB2_I80A6	Polymerase basic protein 2 {ECO:0000255 HAMAP-Rule:MF_04062};	.	NA
DN2085_c0_g2_i6	MX_ANAPL	Interferon-induced GTP-binding protein Mx;	KEGG:apla:101793492	KO:K14754
DN9051_c0_g1_i3	GA2L1_MOUSE	GAS2-like protein 1;	KEGG:mmu:78926	NA
DN20874_c0_g1_i11	PAR12_HUMAN	Protein mono-ADP-ribosyltransferase PARP12 {ECO:0000305};	KEGG:hsa:64761	KO:K15259
DN22_c0_g1_i2	MIRO1_CHICK	Mitochondrial Rho GTPase 1;	KEGG:gga:417410	KO:K07870
DN1920_c0_g1_i1	RSAD2_BOVIN	Radical S-adenosyl methionine domain-containing protein 2;	KEGG:bta:506415	KO:K15045

Table 3: Transcript functions (*continued*)

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN6190_c0_g1_i4	OASL2_MOUSE	2'-5'-oligoadenylate synthase-like protein 2;	KEGG:rno:304545	KO:K14608
DN2767_c0_g1_i1	ISLR_HUMAN	Immunoglobulin superfamily containing leucine-rich repeat protein;	KEGG:hsa:3671	NA
DN3062_c0_g1_i10	RN213_HUMAN	E3 ubiquitin-protein ligase RNF213 {ECO:0000305};	KEGG:hsa:57674	KO:K22754
DN166_c0_g1_i5	RN141_CHICK	RING finger protein 141;	KEGG:gga:423039	NA
DN43220_c0_g1_i4	UBP18_HUMAN	Ubl carboxyl-terminal hydrolase 18;	KEGG:hsa:11274	KO:K11846
DN34132_c0_g1_i4	K2C74_MOUSE	Keratin, type II cytoskeletal 74 {ECO:0000250 UniProtKB:Q7RT57};	KEGG:mmu:223917	KO:K07605
DN1934_c0_g1_i11	IRF3_CHICK	Interferon regulatory factor 3;	KEGG:gga:396330	KO:K09447
DN17171_c0_g1_i3	MTAP2_RAT	Microtubule-associated protein 2;	.	NA
DN2293_c0_g1_i3	PIGY_HUMAN	Phosphatidylinositol N-acetylglucosaminyltransferase subunit Y;	KEGG:hsa:84992	KO:K11001
DN6190_c0_g1_i2	OASL1_RAT	2'-5'-oligoadenylate synthase-like protein 1;	KEGG:rno:304545	KO:K14608
DN1934_c0_g1_i16	IRF3_CHICK	Interferon regulatory factor 3;	KEGG:gga:396330	KO:K09447
DN5214_c0_g1_i6	CF062_MOUSE	Uncharacterized protein C6orf62 homolog;	KEGG:mmu:79555	NA
DN9772_c0_g1_i10	UQCC2_DANRE	Ubiquinol-cytochrome-c reductase complex assembly factor 2;	KEGG:dre:393731	KO:K17682
DN2228_c2_g1_i8	BMPR2_MOUSE	Bone morphogenetic protein receptor type-2;	KEGG:mmu:12168	KO:K04671
DN4998_c0_g1_i2	CNPY3_BOVIN	Protein canopy homolog 3;	KEGG:bta:510220	KO:K22816
DN14729_c0_g1_i4	FREM1_HUMAN	FRAS1-related extracellular matrix protein 1 {ECO:0000305};	KEGG:hsa:158326	KO:K23380
DN4239_c0_g1_i17	MYCB2_MOUSE	E3 ubiquitin-protein ligase MYCBP2 {ECO:0000305};	KEGG:mmu:105689	KO:K10693
DN220085_c0_g1_i2	LAG3_MOUSE	Lymphocyte activation gene 3 protein {ECO:0000303 PubMed:8921170};	KEGG:hsa:3902	KO:K06565

Table 3: Transcript functions (*continued*)

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN12331_c1_g1_i3	LRIG3_HUMAN	Leucine-rich repeats and immunoglobulin-like domains protein 3;	KEGG:hsa:121227	NA
DN611_c1_g1_i6	LRRK2_HUMAN	Leucine-rich repeat serine/threonine-protein kinase 2;	KEGG:hsa:120892	KO:K08844
DN2458_c0_g1_i1	DDX17_MOUSE	Probable ATP-dependent RNA helicase DDX17;	KEGG:mmu:67040	KO:K13178
DN1712_c0_g2_i10	DCAF4_HUMAN	DDB1- and CUL4-associated factor 4;	KEGG:bta:511629	KO:K11799

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0000381	regulation of alternative mRNA splicing,...	267	1	0.01	0.0062	6.20e-03	BP	I1vI3
GO:0001837	epithelial to mesenchymal transition	352	1	0.01	0.0082	8.20e-03	BP	I1vI3
GO:0002040	sprouting angiogenesis	319	3	0.34	0.00462	4.62e-03	BP	CtlvI1
GO:0003186	tricuspid valve morphogenesis	10	1	0.01	0.00536	5.36e-03	BP	CtlvI3
GO:0003252	negative regulation of cell proliferatio...	10	1	0.01	0.00536	5.36e-03	BP	CtlvI3
GO:0003724	RNA helicase activity	317	4	0.40	0.00069	6.90e-04	MF	CtlvI1
GO:0003724	RNA helicase activity	317	4	0.21	5.2e-05	5.20e-05	MF	CtlvI3
GO:0003724	RNA helicase activity	317	1	0.01	0.0077	7.70e-03	MF	I1vI3
GO:0003725	double-stranded RNA binding	250	5	0.32	1.6e-05	1.60e-05	MF	CtlvI1
GO:0003725	double-stranded RNA binding	250	3	0.16	0.00058	5.80e-04	MF	CtlvI3
GO:0003727	single-stranded RNA binding	335	4	0.42	0.00085	8.50e-04	MF	CtlvI1
GO:0003727	single-stranded RNA binding	335	3	0.22	0.00134	1.34e-03	MF	CtlvI3
GO:0003924	GTPase activity	866	10	1.09	1.1e-07	1.00e-07	MF	CtlvI1
GO:0003924	GTPase activity	866	7	0.57	1.1e-06	1.10e-06	MF	CtlvI3
GO:0003968	RNA-directed 5'-3' RNA polymerase activi...	11	2	0.01	8.5e-05	8.50e-05	MF	CtlvI1
GO:0004127	cytidylate kinase activity	12	3	0.02	4.1e-07	4.00e-07	MF	CtlvI1
GO:0004127	cytidylate kinase activity	12	1	0.01	0.00783	7.83e-03	MF	CtlvI3
GO:0004550	nucleoside diphosphate kinase activity	41	3	0.05	1.9e-05	1.90e-05	MF	CtlvI1
GO:0004798	thymidylate kinase activity	9	3	0.01	1.6e-07	2.00e-07	MF	CtlvI1
GO:0004798	thymidylate kinase activity	9	1	0.01	0.00588	5.88e-03	MF	CtlvI3
GO:0005026	transforming growth factor beta receptor...	10	1	0.01	0.00653	6.53e-03	MF	CtlvI3
GO:0005525	GTP binding	1111	10	1.40	1.1e-06	1.10e-06	MF	CtlvI1
GO:0005525	GTP binding	1111	7	0.73	5.6e-06	5.60e-06	MF	CtlvI3
GO:0005811	lipid droplet	227	3	0.27	0.00251	2.51e-03	CC	CtlvI1
GO:0006165	nucleoside diphosphate phosphorylation	359	3	0.38	0.00640	6.40e-03	BP	CtlvI1
GO:0006227	dUDP biosynthetic process	9	3	0.01	9.1e-08	1.00e-07	BP	CtlvI1
GO:0006227	dUDP biosynthetic process	9	1	0.00	0.00483	4.83e-03	BP	CtlvI3
GO:0006233	dTDP biosynthetic process	9	3	0.01	9.1e-08	1.00e-07	BP	CtlvI1
GO:0006233	dTDP biosynthetic process	9	1	0.00	0.00483	4.83e-03	BP	CtlvI3
GO:0006235	dTTP biosynthetic process	11	3	0.01	1.8e-07	2.00e-07	BP	CtlvI1
GO:0006235	dTTP biosynthetic process	11	1	0.01	0.00590	5.90e-03	BP	CtlvI3
GO:0007026	negative regulation of microtubule depol...	114	2	0.12	0.00646	6.46e-03	BP	CtlvI1

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched) (*continued*)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0009041	uridylate kinase activity	14	3	0.02	6.8e-07	7.00e-07	MF	CtlvI1
GO:0009041	uridylate kinase activity	14	1	0.01	0.00913	9.13e-03	MF	CtlvI3
GO:0010507	negative regulation of autophagy	214	2	0.11	0.00587	5.87e-03	BP	CtlvI3
GO:0010586	miRNA metabolic process	111	1	0.00	0.0026	2.60e-03	BP	I1vI3
GO:0014916	regulation of lung blood pressure	7	1	0.00	0.00376	3.76e-03	BP	CtlvI3
GO:0016540	protein autoprocessing	39	2	0.04	0.00078	7.80e-04	BP	CtlvI1
GO:0019012	virion	131	7	0.16	0.00466	4.66e-03	CC	CtlvI1
GO:0019031	viral envelope	33	2	0.04	0.00071	7.10e-04	CC	CtlvI1
GO:0019031	viral envelope	33	2	0.02	0.0002	2.00e-04	CC	CtlvI3
GO:0019056	modulation by virus of host transcriptio...	5	3	0.01	1.1e-08	0.00e+00	BP	CtlvI1
GO:0019062	virion attachment to host cell	43	2	0.05	0.00095	9.50e-04	BP	CtlvI1
GO:0019062	virion attachment to host cell	43	2	0.02	0.00025	2.50e-04	BP	CtlvI3
GO:0019064	fusion of virus membrane with host plasm...	33	2	0.03	0.00056	5.60e-04	BP	CtlvI1
GO:0019064	fusion of virus membrane with host plasm...	33	2	0.02	0.00014	1.40e-04	BP	CtlvI3
GO:0019065	receptor-mediated endocytosis of virus b...	10	2	0.01	4.8e-05	4.80e-05	BP	CtlvI1
GO:0019065	receptor-mediated endocytosis of virus b...	10	2	0.01	1.2e-05	1.20e-05	BP	CtlvI3
GO:0019076	viral release from host cell	98	4	0.10	3.6e-06	3.60e-06	BP	CtlvI1
GO:0019076	viral release from host cell	98	4	0.05	2.2e-07	2.00e-07	BP	CtlvI3
GO:0019083	viral transcription	296	3	0.31	0.00375	3.75e-03	BP	CtlvI1
GO:0020002	host cell plasma membrane	94	4	0.11	5.0e-06	5.00e-06	CC	CtlvI1
GO:0020002	host cell plasma membrane	94	4	0.06	3.9e-07	4.00e-07	CC	CtlvI3
GO:0021785	branchiomotor neuron axon guidance	15	1	0.01	0.00803	8.03e-03	BP	CtlvI3
GO:0022028	tangential migration from the subventric...	17	1	0.01	0.00910	9.10e-03	BP	CtlvI3
GO:0030430	host cell cytoplasm	102	3	0.12	0.00025	2.50e-04	CC	CtlvI1
GO:0030520	intracellular estrogen receptor signalin...	135	1	0.00	0.0032	3.20e-03	BP	I1vI3
GO:0030521	androgen receptor signaling pathway	169	1	0.00	0.0039	3.90e-03	BP	I1vI3
GO:0030683	mitigation of host immune response by vi...	6	1	0.01	0.00629	6.29e-03	BP	CtlvI1
GO:0030683	mitigation of host immune response by vi...	6	1	0.00	0.00322	3.22e-03	BP	CtlvI3
GO:0032473	cytoplasmic side of mitochondrial outer ...	7	1	0.00	0.0044	4.40e-03	CC	CtlvI3
GO:0032474	otolith morphogenesis	18	1	0.01	0.00963	9.63e-03	BP	CtlvI3
GO:0034154	toll-like receptor 7 signaling pathway	19	3	0.02	1.0e-06	1.00e-06	BP	CtlvI1

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched) (*continued*)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0034165	positive regulation of toll-like recepto...	11	3	0.01	1.8e-07	2.00e-07	BP	CtlvI1
GO:0034211	GTP-dependent protein kinase activity	8	1	0.01	0.00522	5.22e-03	MF	CtlvI3
GO:0035279	mRNA cleavage involved in gene silencing...	8	1	0.01	0.00838	8.38e-03	BP	CtlvI1
GO:0035564	regulation of kidney size	11	1	0.01	0.00590	5.90e-03	BP	CtlvI3
GO:0035666	TRIF-dependent toll-like receptor signal...	59	2	0.06	0.00178	1.78e-03	BP	CtlvI1
GO:0035712	T-helper 2 cell activation	7	1	0.01	0.00734	7.34e-03	BP	CtlvI1
GO:0035713	response to nitrogen dioxide	6	1	0.01	0.00629	6.29e-03	BP	CtlvI1
GO:0036122	BMP binding	13	1	0.01	0.00848	8.48e-03	MF	CtlvI3
GO:0036479	peroxidase inhibitor activity	5	1	0.00	0.00327	3.27e-03	MF	CtlvI3
GO:0039507	suppression by virus of host molecular f...	14	4	0.01	1.1e-09	0.00e+00	BP	CtlvI1
GO:0039513	suppression by virus of host catalytic a...	10	1	0.01	0.00536	5.36e-03	BP	CtlvI3
GO:0039519	modulation by virus of host autophagy	9	1	0.01	0.00942	9.42e-03	BP	CtlvI1
GO:0039519	modulation by virus of host autophagy	9	1	0.00	0.00483	4.83e-03	BP	CtlvI3
GO:0039657	suppression by virus of host gene expres...	25	4	0.03	1.3e-08	0.00e+00	BP	CtlvI1
GO:0039694	viral RNA genome replication	103	3	0.11	0.00018	1.80e-04	BP	CtlvI1
GO:0039706	co-receptor binding	9	1	0.01	0.00588	5.88e-03	MF	CtlvI3
GO:0042025	host cell nucleus	34	6	0.04	2.7e-12	0.00e+00	CC	CtlvI1
GO:0042025	host cell nucleus	34	3	0.02	1.4e-06	1.40e-06	CC	CtlvI3
GO:0042289	MHC class II protein binding	11	1	0.01	0.00718	7.18e-03	MF	CtlvI3
GO:0043367	CD4-positive, alpha-beta T cell differen...	239	4	0.25	0.00012	1.20e-04	BP	CtlvI1
GO:0043382	positive regulation of memory T cell dif...	5	1	0.01	0.00525	5.25e-03	BP	CtlvI1
GO:0043621	protein self-association	175	3	0.22	0.00142	1.42e-03	MF	CtlvI1
GO:0044753	amphisome	9	1	0.01	0.0057	5.70e-03	CC	CtlvI3
GO:0045071	negative regulation of viral genome repl...	136	5	0.14	3.3e-07	3.00e-07	BP	CtlvI1
GO:0045085	negative regulation of interleukin-2 bio...	13	1	0.01	0.00696	6.96e-03	BP	CtlvI3
GO:0045087	innate immune response	1505	13	1.58	8.1e-07	8.00e-07	BP	CtlvI1
GO:0045087	innate immune response	1505	8	0.81	4.5e-05	4.50e-05	BP	CtlvI3
GO:0045111	intermediate filament cytoskeleton	311	4	0.37	0.00052	5.20e-04	CC	CtlvI1
GO:0045111	intermediate filament cytoskeleton	311	3	0.20	0.0010	1.00e-03	CC	CtlvI3
GO:0045445	myoblast differentiation	227	1	0.01	0.0053	5.30e-03	BP	I1vI3
GO:0045590	negative regulation of regulatory T cell...	8	1	0.01	0.00838	8.38e-03	BP	CtlvI1

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched) (*continued*)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0045590	negative regulation of regulatory T cell...	8	1	0.00	0.00429	4.29e-03	BP	CtlvI3
GO:0045906	negative regulation of vasoconstriction	12	1	0.01	0.00643	6.43e-03	BP	CtlvI3
GO:0046598	positive regulation of viral entry into ...	28	2	0.03	0.00040	4.00e-04	BP	CtlvI1
GO:0046718	viral entry into host cell	262	4	0.14	0.00523	5.23e-03	BP	CtlvI3
GO:0046755	viral budding	74	4	0.08	1.2e-06	1.20e-06	BP	CtlvI1
GO:0046755	viral budding	74	4	0.04	7.1e-08	1.00e-07	BP	CtlvI3
GO:0048295	positive regulation of isotype switching...	8	1	0.01	0.00838	8.38e-03	BP	CtlvI1
GO:0048842	positive regulation of axon extension in...	15	1	0.01	0.00803	8.03e-03	BP	CtlvI3
GO:0050709	negative regulation of protein secretion	312	3	0.33	0.00434	4.34e-03	BP	CtlvI1
GO:0051024	positive regulation of immunoglobulin se...	7	1	0.01	0.00734	7.34e-03	BP	CtlvI1
GO:0051539	4 iron, 4 sulfur cluster binding	170	3	0.21	0.00131	1.31e-03	MF	CtlvI1
GO:0051607	defense response to virus	526	12	0.55	1.1e-09	0.00e+00	BP	CtlvI1
GO:0051865	protein autoubiquitination	241	4	0.25	0.00012	1.20e-04	BP	CtlvI1
GO:0051900	regulation of mitochondrial depolarizati...	42	2	0.02	0.00023	2.30e-04	BP	CtlvI3
GO:0052027	modulation by symbiont of host signal tr...	6	1	0.01	0.00629	6.29e-03	BP	CtlvI1
GO:0052027	modulation by symbiont of host signal tr...	6	1	0.00	0.00322	3.22e-03	BP	CtlvI3
GO:0055036	virion membrane	32	5	0.04	3.8e-10	0.00e+00	CC	CtlvI1
GO:0055036	virion membrane	32	5	0.02	1.4e-11	0.00e+00	CC	CtlvI3
GO:0060161	positive regulation of dopamine receptor...	13	1	0.01	0.00696	6.96e-03	BP	CtlvI3
GO:0060338	regulation of type I interferon-mediated...	100	3	0.11	0.00016	1.60e-04	BP	CtlvI1
GO:0060338	regulation of type I interferon-mediated...	100	2	0.05	0.00132	1.32e-03	BP	CtlvI3
GO:0060349	bone morphogenesis	227	2	0.12	0.00658	6.58e-03	BP	CtlvI3
GO:0060700	regulation of ribonuclease activity	13	2	0.01	8.4e-05	8.40e-05	BP	CtlvI1
GO:0060836	lymphatic endothelial cell differentiati...	12	1	0.01	0.00643	6.43e-03	BP	CtlvI3
GO:0061614	pri-miRNA transcription by RNA polymeras...	116	1	0.00	0.0027	2.70e-03	BP	I1vI3
GO:0061626	pharyngeal arch artery morphogenesis	18	1	0.01	0.00963	9.63e-03	BP	CtlvI3
GO:0071222	cellular response to lipopolysaccharide	438	4	0.46	0.00116	1.16e-03	BP	CtlvI1
GO:0072583	clathrin-dependent endocytosis	166	2	0.09	0.00359	3.59e-03	BP	CtlvI3
GO:0080008	Cul4-RING E3 ubiquitin ligase complex	128	1	0.00	0.0028	2.80e-03	CC	CtlvI14
GO:0080008	Cul4-RING E3 ubiquitin ligase complex	128	1	0.00	0.0028	2.80e-03	CC	I5vI14
GO:0097487	multivesicular body, internal vesicle	11	1	0.01	0.0070	7.00e-03	CC	CtlvI3

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched) (*continued*)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0099400	caveola neck	5	1	0.00	0.0032	3.20e-03	CC	CtlvI3
GO:1900245	positive regulation of MDA-5 signaling p...	20	3	0.02	1.2e-06	1.20e-06	BP	CtlvI1
GO:1900245	positive regulation of MDA-5 signaling p...	20	3	0.01	1.5e-07	2.00e-07	BP	CtlvI3
GO:1900246	positive regulation of RIG-I signaling p...	31	3	0.03	4.8e-06	4.80e-06	BP	CtlvI1
GO:1900246	positive regulation of RIG-I signaling p...	31	3	0.02	6.0e-07	6.00e-07	BP	CtlvI3
GO:1901727	positive regulation of histone deacetyla...	17	1	0.01	0.00910	9.10e-03	BP	CtlvI3
GO:1901953	positive regulation of anterograde dense...	9	1	0.01	0.00942	9.42e-03	BP	CtlvI1
GO:1902499	positive regulation of protein autoubiqu...	9	1	0.00	0.00483	4.83e-03	BP	CtlvI3
GO:1902731	negative regulation of chondrocyte proli...	5	1	0.00	0.00268	2.68e-03	BP	CtlvI3
GO:1902823	negative regulation of late endosome to ...	7	1	0.00	0.00376	3.76e-03	BP	CtlvI3
GO:1903125	negative regulation of thioredoxin perox...	5	1	0.00	0.00268	2.68e-03	BP	CtlvI3
GO:1903217	negative regulation of protein processin...	8	1	0.00	0.00429	4.29e-03	BP	CtlvI3
GO:1903744	positive regulation of anterograde synap...	9	1	0.01	0.00942	9.42e-03	BP	CtlvI1
GO:1903980	positive regulation of microglial cell a...	12	1	0.01	0.00643	6.43e-03	BP	CtlvI3
GO:1904713	beta-catenin destruction complex binding	7	1	0.00	0.00457	4.57e-03	MF	CtlvI3
GO:1904887	Wnt signalosome assembly	5	1	0.00	0.00268	2.68e-03	BP	CtlvI3
GO:1905279	regulation of retrograde transport, endo...	8	1	0.00	0.00429	4.29e-03	BP	CtlvI3
GO:1905289	regulation of CAMKK-AMPK signaling casca...	10	1	0.01	0.00536	5.36e-03	BP	CtlvI3
GO:2000051	negative regulation of non-canonical Wnt...	17	3	0.02	7.3e-07	7.00e-07	BP	CtlvI1
GO:2000172	regulation of branching morphogenesis of...	18	1	0.01	0.00963	9.63e-03	BP	CtlvI3
GO:2000553	positive regulation of T-helper 2 cell c...	18	3	0.02	8.8e-07	9.00e-07	BP	CtlvI1
GO:2001014	regulation of skeletal muscle cell diffe...	62	2	0.03	0.00051	5.10e-04	BP	CtlvI3
GO:2001014	regulation of skeletal muscle cell diffe...	62	1	0.00	0.0014	1.40e-03	BP	I1vI3

LPAIV-Infected and Controls by DPI - Bursa - Gene

Amanda Dolinski & Jared J. Homola

23 March, 2021

This is an analysis of differential expression at the gene level between LPAIV-infected and uninfected control blue-winged teal bursa samples at each day post-infection (DPI). Differential expression was also analyzed between LPAIV-infected groups at different DPI.

Differential expression analysis

Table 1: Count of DE genes. For a gene to be considered differentially expressed, we require a p-value of 0.1 with a false discovery rate correction and a log fold change difference of 1.0.

	CtlvI1	CtlvI3	CtlvI5	CtlvI14	I1vI3	I3vI5	I5vI14
Down	1	0	0	0	0	0	0
NotSig	75289	75290	75290	75290	75290	75290	75290
Up	0	0	0	0	0	0	0

Volcano plot

Volcano plot reporting $-\log_{10}(\text{p-values})$ as a function of $\log_2(\text{fold change})$ between the samples (logFC, x axis). Genes that are identified as significantly differentially expressed following a false discovery rate correction ($q = 0.10$) are shown in red

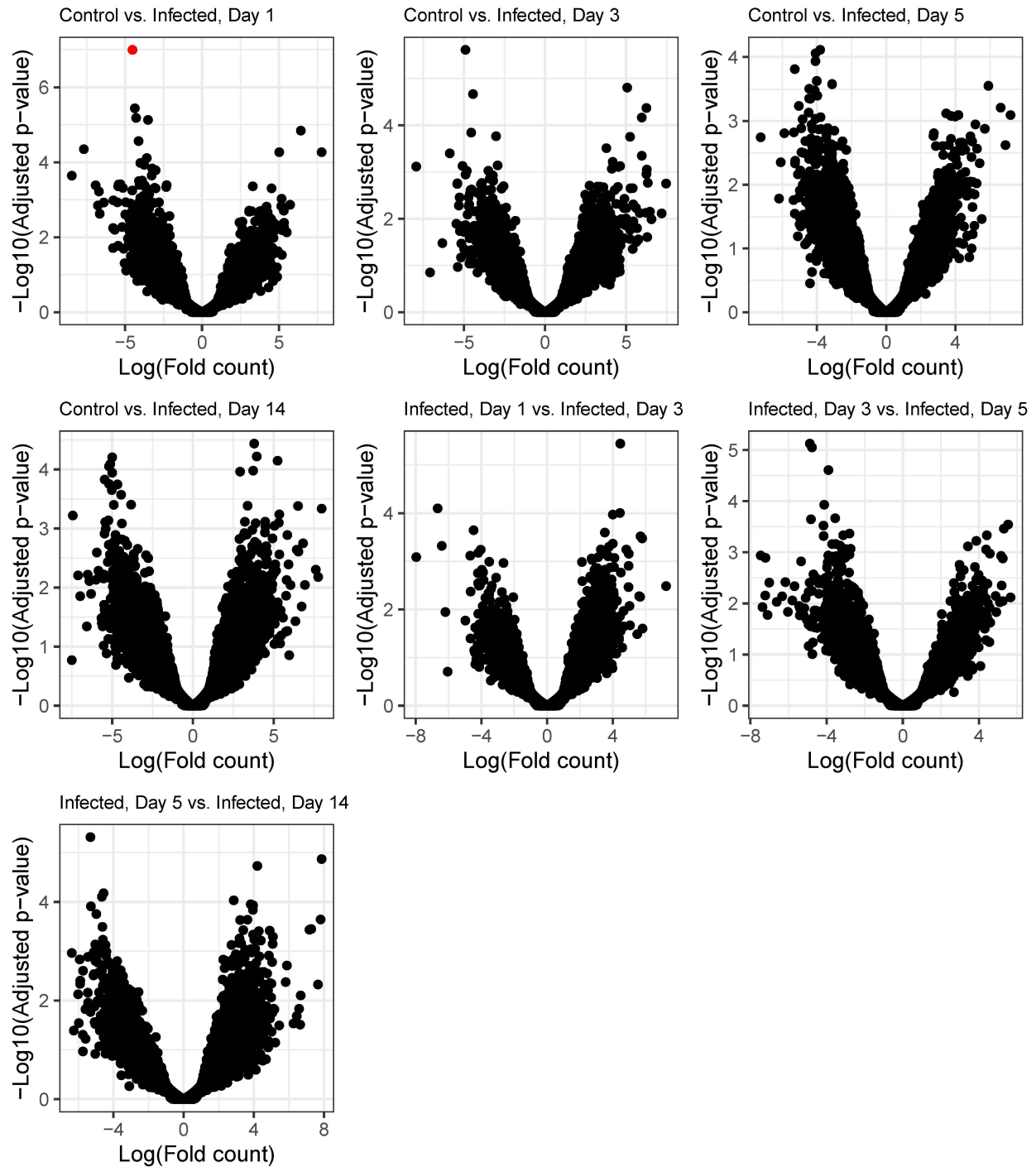


Table 2: Annotations for differentially expressed genes. ns denotes non-significant genes for each comparison and numerical values are the log(fold change) difference

gene_id	SwissProt_GeneName	CtlvI1	CtlvI3	CtlvI5	CtlvI14	I1vI3	I3vI5	I5vI14
DN19503_c0_g1	.	-4.52	ns	ns	ns	ns	ns	ns

LPAIV-Infected and Controls by DPI - Bursa - Transcript

Amanda Dolinski & Jared J. Homola

23 March, 2021

This is an analysis of differential expression at the transcript level between LPAIV-infected and uninfected control blue-winged teal bursa samples at each day post-infection (DPI). Differential expression was also analyzed between LPAIV-infected groups at different DPI.

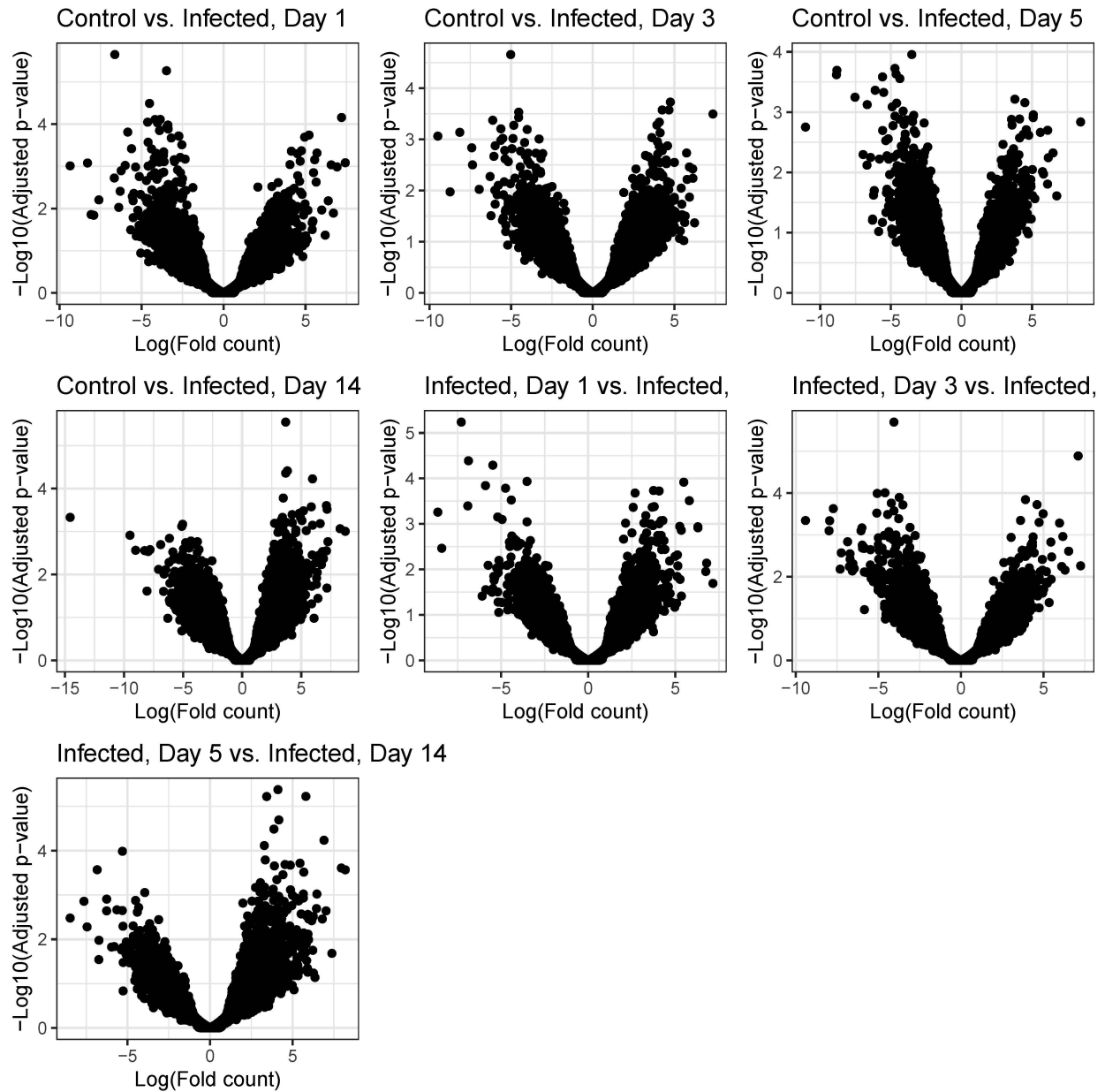
Differential expression analysis

Table 1: Count of DE transcripts. For a transcript to be considered differentially expressed, we require a p-value of 0.1 with a false discovery rate correction and a log fold change difference of 1.0.

	CtlvI1	CtlvI3	CtlvI5	CtlvI14	I1vI3	I3vI5	I5vI14
Down	0	0	0	0	0	0	0
NotSig	74436	74436	74436	74436	74436	74436	74436
Up	0	0	0	0	0	0	0

Volcano plot

Volcano plot reporting $-\log_{10}(\text{p-values})$ as a function of $\log_2(\text{fold change})$ between the samples (logFC, x axis). Transcripts that are identified as significantly differentially expressed following a false discovery rate correction ($q = 0.10$) are shown in red



Shed Level Early Infection - Ileum - Gene

Amanda Dolinski & Jared J. Homola

23 March, 2021

This is an analysis of differential expression at the gene level between low, moderate, and high LPAIV shedding blue-winged teals based on cloacal swab virus titers measured on the day of sacrifice for ileum samples on 1 and 3 days post infection (DPI).

Differential expression analysis

For this analysis, we conduct two sets of differential expression analyses - one for each LPAIV-infected group in early infection: I1 and I3.

Table 1: Count of DE genes. For a gene to be considered differentially expressed, we require a p-value of 0.1 with a false discovery rate correction and a log fold change difference of 1.0.

Direction	Comparison	N
I1		
Down	LvM	1
Up	LvM	1
Down	MvH	1
Up	MvH	0
Down	LvH	0
Up	LvH	0
I3		
Down	LvM	5
Up	LvM	1
Down	MvH	0
Up	MvH	1
Down	LvH	2
Up	LvH	1

Volcano plot

Volcano plot reporting $-\log_{10}(\text{p-values})$ as a function of $\log_2(\text{fold change})$ between the samples (logFC, x axis). Genes that are identified as significantly differentially expressed following a false discovery rate correction ($q = 0.10$) are shown in red

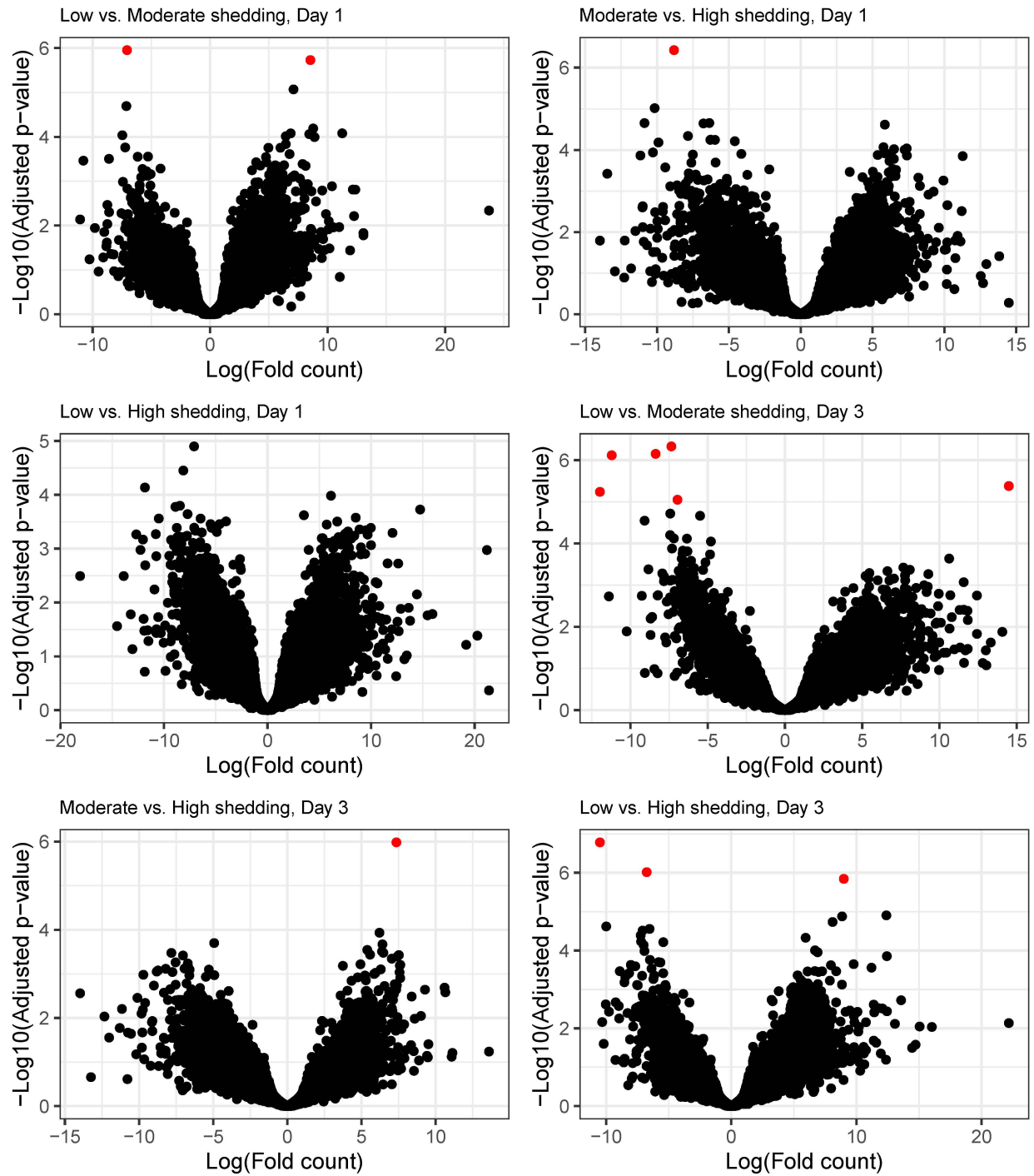


Table 2: Annotations for differentially expressed genes. ns denotes non-significant genes for each comparison and numerical values are the log(fold change) difference

gene_id	SwissProt_GeneName	LvM.I1	MvH.I1	LvH.I1	LvM.I3	MvH.I3	LvH.I3
DN5548_c1_g1	EFGM_XENLA	-7.07	ns	ns	ns	ns	ns
DN5485_c0_g1	.	8.54	-8.82	ns	ns	ns	ns
DN25337_c1_g1	.	ns	ns	ns	-11.21	ns	ns
DN4856_c1_g1	.	ns	ns	ns	-8.37	ns	-10.5
DN21959_c2_g1	.	ns	ns	ns	-7.35	ns	-6.76
DN10212_c0_g1	.	ns	ns	ns	-11.97	ns	ns
DN25071_c0_g1	.	ns	ns	ns	-6.95	7.35	ns
DN12358_c0_g1	BT3A1_HUMAN	ns	ns	ns	14.49	ns	ns
DN24808_c0_g1	.	ns	ns	ns	ns	ns	8.99

Table 3: Gene functions

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN5548_c1_g1	EFGM_XENLA	Elongation factor G, mitochondrial {ECO:0000255 HAMAP- Rule:MF_03061};	KEGG:xla:100101315	KO:K02355
DN12358_c0_g1	BT3A1_HUMAN	Butyrophilin subfamily 3 member A1;	KEGG:hsa:11119	KO:K06712

Table 4: Gene Ontology enrichment analysis: GO terms with p-values < 0.05 were determined as over-represented (enriched)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0003746	translation elongation factor activity	30	1	0	0.0017	0.0017	MF	LvM.I1
GO:0050798	activated T cell proliferation	69	1	0	0.0037	0.0037	BP	LvM.I3
GO:0070125	mitochondrial translational elongation	43	1	0	0.0023	0.0023	BP	LvM.I1
GO:0072643	interferon-gamma secretion	55	1	0	0.0029	0.0029	BP	LvM.I3

Shed Level Early Infection - Ileum - Transcript

Amanda Dolinski & Jared J. Homola

23 March, 2021

This is an analysis of differential expression at the transcript level between low, moderate, and high LPAIV shedding blue-winged teals based on cloacal swab virus titers measured on the day of sacrifice for ileum samples on 1 and 3 days post infection (DPI).

Differential expression analysis

For this analysis, we conduct two sets of differential expression analyses- one for each LPAIV-infected group in early infection: I1 and I3.

Table 1: Count of DE transcripts. For a transcript to be considered differentially expressed, we require a p-value of 0.1 with a false discovery rate correction and a log fold change difference of 1.0.

Direction	Comparison	N
I1		
Down	LvM	2
Up	LvM	1
Down	MvH	9
Up	MvH	6
Down	LvH	1
Up	LvH	0
I3		
Down	LvM	2
Up	LvM	1
Down	MvH	0
Up	MvH	0
Down	LvH	8
Up	LvH	11

Volcano plot

Volcano plot reporting $-\log_{10}(\text{p-values})$ as a function of $\log_2(\text{fold change})$ between the samples ($\log_{2}\text{FC}$, x axis). Transcripts that are identified as significantly differentially expressed following a false discovery rate correction ($q = 0.10$) are shown in red

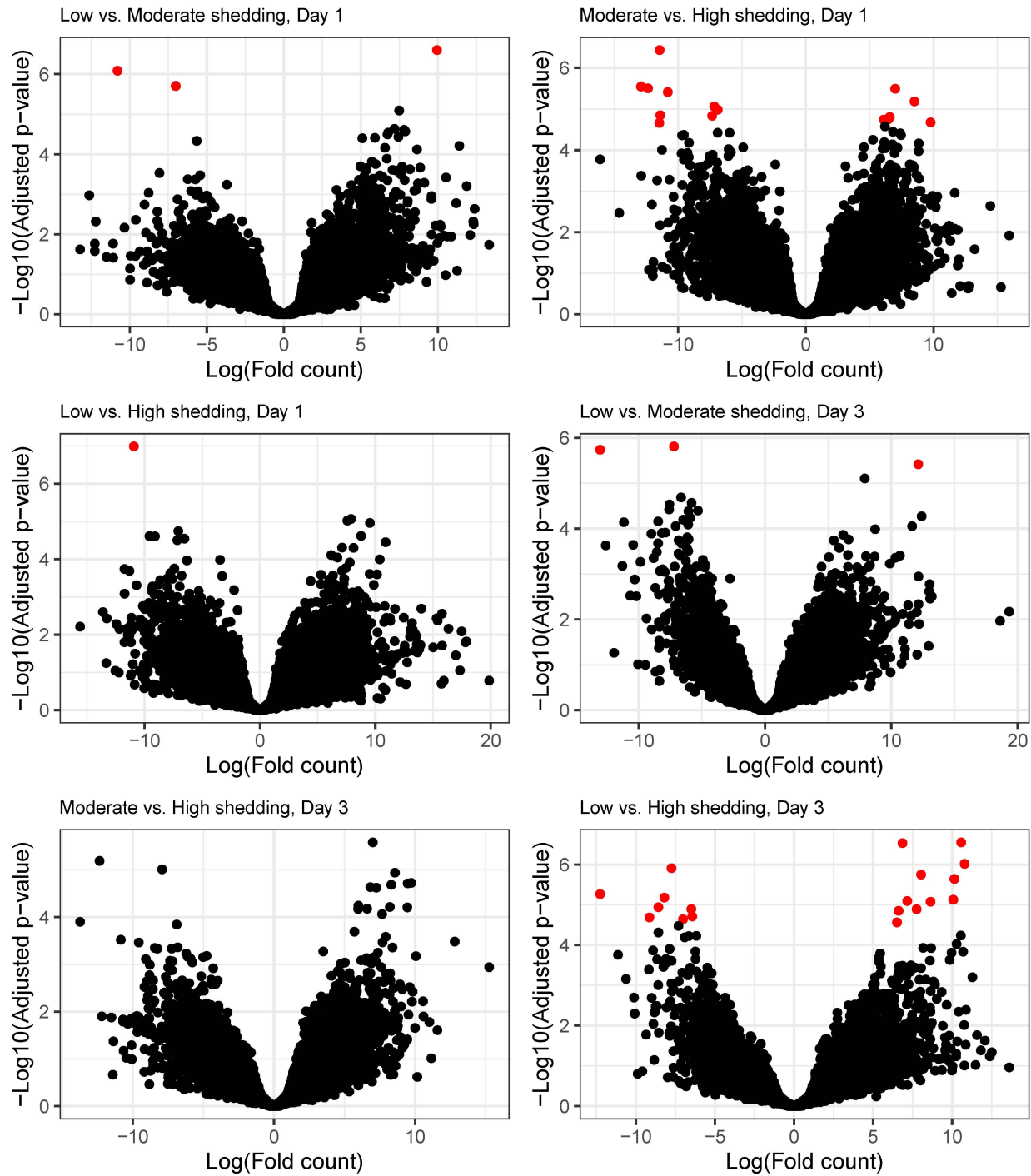


Table 2: Annotations for differentially expressed transcripts. ns denotes non-significant transcripts for each comparison and numerical values are the log(fold change) difference

transcript_id	SwissProt_GeneName	LvM.I1	MvH.I1	LvH.I1	LvM.I3	MvH.I3	LvH.I3
DN4857_c0_g1_i1	EVL_PONAB	9.94	ns	ns	ns	ns	ns
DN1210_c0_g1_i12	SC5D_MOUSE	-10.8	ns	ns	ns	ns	ns
DN5548_c1_g1_i1	EFGM_XENLA	-7.02	ns	ns	ns	ns	ns
DN8245_c0_g1_i4	TMCO4_HUMAN	ns	-7.18	ns	ns	ns	ns
DN806_c0_g1_i6	ZN384_HUMAN	ns	-12.37	ns	ns	ns	ns
DN1184_c0_g1_i4	GLSK_RAT	ns	-6.9	ns	ns	ns	ns
DN197_c0_g2_i1	F210A_CHICK	ns	-7.34	ns	ns	ns	ns
DN3196_c1_g1_i8	YETS2_MOUSE	ns	-12.91	ns	ns	ns	ns
DN1523_c1_g2_i8	TLR1_HUMAN	ns	-11.4	ns	ns	ns	ns
DN9149_c0_g2_i13	SH3G1_CHICK	ns	-11.48	ns	ns	ns	ns
DN5059_c0_g1_i6	ZN335_RAT	ns	ns	ns	ns	ns	10.14
DN2727_c0_g1_i2	MRP5_HUMAN	ns	-10.81	ns	ns	ns	ns
DN3655_c0_g1_i8	.	ns	ns	ns	-7.21	ns	-7.75
DN153_c0_g1_i9	MUC3B_HUMAN	ns	ns	ns	ns	ns	-9.14
DN4856_c1_g1_i1	.	ns	ns	ns	ns	ns	-8.2
DN175_c1_g1_i9	FASTK_HUMAN	ns	ns	ns	ns	ns	10.79
DN6808_c0_g1_i3	WWP2_MOUSE	ns	ns	ns	ns	ns	6.86
DN993_c0_g1_i8	POL_BAEVM	ns	9.77	ns	ns	ns	ns
DN5326_c0_g1_i2	F104A_HUMAN	ns	ns	ns	ns	ns	10.07
DN1200_c1_g1_i7	KMT5B_HUMAN	ns	ns	ns	ns	ns	-6.5
DN636_c1_g1_i9	ULK3_CHICK	ns	ns	ns	ns	ns	7.17
DN9734_c0_g1_i3	TRAF6_PIG	ns	ns	ns	ns	ns	7.76
DN2351_c0_g1_i1	MYH11_CHICK	ns	ns	ns	-13.05	ns	-12.26
DN4153_c0_g3_i3	SYIM_CHICK	ns	ns	ns	ns	ns	-6.44
DN7548_c1_g1_i8	DEGS1_CHICK	ns	ns	ns	12.13	ns	ns
DN8112_c0_g1_i6	ARRD4_HUMAN	ns	ns	ns	ns	ns	6.62
DN2169_c0_g1_i13	RELCH_HUMAN	ns	6.48	ns	ns	ns	ns
DN4081_c2_g1_i1	AXIN1_CHICK	ns	ns	ns	ns	ns	10.57
DN10680_c0_g1_i4	SIN3A_MOUSE	ns	-11.45	-10.93	ns	ns	ns
DN2134_c0_g1_i3	PTPRE_HUMAN	ns	7	ns	ns	ns	ns
DN7267_c0_g1_i8	FXL15_XENLA	ns	ns	ns	ns	ns	-7.02
DN59_c0_g1_i6	TALDO_RAT	ns	ns	ns	ns	ns	6.51
DN3985_c0_g1_i5	NR2C2_HUMAN	ns	ns	ns	ns	ns	8.04
DN7918_c0_g1_i7	JUPI1_BOVIN	ns	8.51	ns	ns	ns	ns
DN4058_c0_g1_i15	ST38L_MOUSE	ns	6.58	ns	ns	ns	ns
DN904_c0_g1_i19	DDX3X_HUMAN	ns	ns	ns	ns	ns	-8.58
DN596_c0_g1_i2	DMTF1_HUMAN	ns	6.1	ns	ns	ns	ns
DN7512_c0_g1_i4	RNF34_BOVIN	ns	ns	ns	ns	ns	8.63

Table 3: Transcript functions

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID
DN4857_c0_g1_i1	EVL_PONAB	Ena/VASP-like protein;	KEGG:pon:100173130
DN1210_c0_g1_i12	SC5D_MOUSE	Lathosterol oxidase;	KEGG:mmu:235293
DN5548_c1_g1_i1	EFGM_XENLA	Elongation factor G, mitochondrial {ECO:0000255 HAMAP-Rule:MF_03061};	KEGG:sla:100101315
DN8245_c0_g1_i4	TMCO4_HUMAN	Transmembrane and coiled-coil domain-containing protein 4;	KEGG:mmu:15565
DN806_c0_g1_i6	ZN384_HUMAN	Zinc finger protein 384;	KEGG:hsa:171017
DN1184_c0_g1_i4	GLSK_RAT	Glutaminase kidney isoform, mitochondrial;	KEGG:mmu:14660
DN197_c0_g2_i1	F210A_CHICK	Protein FAM210A;	KEGG:gga:421045
DN3196_c1_g1_i8	YETS2_MOUSE	YEATS domain-containing protein 2 {ECO:0000305};	KEGG:mmu:208146
DN1523_c1_g2_i8	TLR1_HUMAN	Toll-like receptor 1;	KEGG:hsa:7096
DN9149_c0_g2_i13	SH3G1_CHICK	Endophilin-A2;	KEGG:gga:395202
DN5059_c0_g1_i6	ZN335_RAT	Zinc finger protein 335;	KEGG:hsa:63925
DN2727_c0_g1_i2	MRP5_HUMAN	Multidrug resistance-associated protein 5;	KEGG:hsa:10057
DN153_c0_g1_i9	MUC3B_HUMAN	Mucin-3B {ECO:0000305};	.
DN175_c1_g1_i9	FASTK_HUMAN	Fas-activated serine/threonine kinase;	KEGG:hsa:10922
DN6808_c0_g1_i3	WWP2_MOUSE	NEDD4-like E3 ubiquitin-protein ligase WWP2;	KEGG:mmu:66894
DN993_c0_g1_i8	POL_BAEVM	Gag-Pol polyprotein;	KEGG:vg:22318531
DN5326_c0_g1_i2	F104A_HUMAN	Protein FAM104A;	KEGG:hsa:84923
DN1200_c1_g1_i7	KMT5B_HUMAN	Histone-lysine N-methyltransferase KMT5B {ECO:0000305};	KEGG:hsa:51111
DN636_c1_g1_i9	ULK3_CHICK	Serine/threonine-protein kinase ULK3;	.
DN9734_c0_g1_i3	TRAF6_PIG	TNF receptor-associated factor 6;	KEGG:ssc:396629
DN2351_c0_g1_i1	MYH11_CHICK	Myosin-11;	.
DN4153_c0_g3_i3	SYIM_CHICK	Isoleucine-tRNA ligase, mitochondrial;	KEGG:gga:421346
DN7548_c1_g1_i8	DEGS1_CHICK	Sphingolipid delta(4)-desaturase DES1;	KEGG:gga:421327
DN8112_c0_g1_i6	ARRD4_HUMAN	Arrestin domain-containing protein 4;	KEGG:hsa:91947
DN2169_c0_g1_i13	RELCH_HUMAN	RAB11-binding protein RELCH {ECO:0000305};	KEGG:mmu:227446
DN4081_c2_g1_i1	AXIN1_CHICK	Axin-1;	KEGG:gga:395786
DN10680_c0_g1_i4	SIN3A_MOUSE	Paired amphipathic helix protein Sin3a;	KEGG:mmu:20466
DN2134_c0_g1_i3	PTPRE_HUMAN	Receptor-type tyrosine-protein phosphatase epsilon;	KEGG:hsa:5791
DN7267_c0_g1_i8	FXL15_XENLA	F-box/LRR-repeat protein 15;	KEGG:sla:379436
DN59_c0_g1_i6	TALDO_RAT	Transaldolase;	KEGG:rno:83688
DN3985_c0_g1_i5	NR2C2_HUMAN	Nuclear receptor subfamily 2 group C member 2;	KEGG:hsa:7182
DN7918_c0_g1_i7	JUPI1_BOVIN	Jupiter microtubule associated homolog 1 {ECO:0000250 UniProtKB:Q9UK76};	KEGG:bta:613381
DN4058_c0_g1_i15	ST38L_MOUSE	Serine/threonine-protein kinase 38-like;	KEGG:mmu:232533

Table 3: Transcript functions (*continued*)

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID
DN904_c0_g1_i19	DDX3X_HUMAN	ATP-dependent RNA helicase DDX3X;	KEGG:mmu:13205
DN596_c0_g1_i2	DMTF1_HUMAN	Cyclin-D-binding Myb-like transcription factor 1;	KEGG:hsa:9988
DN7512_c0_g1_i4	RNF34_BOVIN	E3 ubiquitin-protein ligase RNF34 {ECO:0000305};	KEGG:bta:506764

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0000012	single strand break repair	27	1	0.01	0.0088	0.00880	BP	MvH.I1
GO:0000146	microfilament motor activity	70	1	0.00	0.00339	0.00339	MF	LvM.I3
GO:0000248	C-5 sterol desaturase activity	6	1	0.00	0.00044	0.00044	MF	LvM.I1
GO:0001102	RNA polymerase II activating transcripti...	134	1	0.00	0.0032	0.00320	MF	LvH.I1
GO:0001103	RNA polymerase II repressing transcripti...	130	1	0.00	0.0032	0.00320	MF	LvH.I1
GO:0002087	regulation of respiratory gaseous exchan...	22	1	0.01	0.0072	0.00720	BP	MvH.I1
GO:0002218	activation of innate immune response	199	1	0.00	0.00465	0.00465	BP	LvH.I1
GO:0002230	positive regulation of defense response ...	64	1	0.00	0.00150	0.00150	BP	LvH.I1
GO:0002244	hematopoietic progenitor cell differenti...	355	1	0.01	0.00829	0.00829	BP	LvH.I1
GO:0003700	DNA-binding transcription factor activit...	2525	4	0.86	0.0085	0.00850	MF	MvH.I1
GO:0003746	translation elongation factor activity	64	1	0.00	0.00465	0.00465	MF	LvM.I1
GO:0004359	glutaminase activity	10	1	0.00	0.0034	0.00340	MF	MvH.I1
GO:0004801	sedoheptulose-7-phosphate:D-glyceraldehy...	8	1	0.00	0.0029	0.00290	MF	LvH.I3
GO:0004822	isoleucine-tRNA ligase activity	14	1	0.01	0.0051	0.00510	MF	LvH.I3
GO:0005522	profilin binding	49	1	0.00	0.00356	0.00356	MF	LvM.I1
GO:0005859	muscle myosin complex	11	1	0.00	0.0039	0.00390	CC	LvH.I3
GO:0005859	muscle myosin complex	11	1	0.00	0.00048	0.00048	CC	LvM.I3
GO:0006428	isoleucyl-tRNA aminoacylation	14	1	0.01	0.0052	0.00520	BP	LvH.I3
GO:0006464	cellular protein modification process	11205	12	4.19	0.0027	0.00270	BP	LvH.I3
GO:0006537	glutamate biosynthetic process	18	1	0.01	0.0059	0.00590	BP	MvH.I1
GO:0006543	glutamine catabolic process	5	1	0.00	0.0016	0.00160	BP	MvH.I1
GO:0008307	structural constituent of muscle	108	1	0.01	0.00523	0.00523	MF	LvM.I3
GO:0008625	extrinsic apoptotic signaling pathway vi...	195	2	0.07	0.0024	0.00240	BP	LvH.I3
GO:0010501	RNA secondary structure unwinding	25	1	0.01	0.0093	0.00930	BP	LvH.I3
GO:0010971	positive regulation of G2/M transition o...	92	1	0.00	0.00215	0.00215	BP	LvH.I1
GO:0014050	negative regulation of glutamate secreti...	13	1	0.00	0.0042	0.00420	BP	MvH.I1
GO:0014053	negative regulation of gamma-aminobutyri...	12	1	0.00	0.0039	0.00390	BP	MvH.I1
GO:0014054	positive regulation of gamma-aminobutyri...	11	1	0.00	0.0036	0.00360	BP	MvH.I1
GO:0014056	regulation of acetylcholine secretion, n...	7	1	0.00	0.0023	0.00230	BP	MvH.I1
GO:0016191	synaptic vesicle uncoating	16	1	0.01	0.0052	0.00520	BP	MvH.I1
GO:0016575	histone deacetylation	276	1	0.01	0.00645	0.00645	BP	LvH.I1
GO:0016580	Sin3 complex	35	1	0.00	0.00077	0.00077	CC	LvH.I1

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched) (*continued*)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0017053	transcription repressor complex	204	1	0.00	0.00448	0.00448	CC	LvH.I1
GO:0021895	cerebral cortex neuron differentiation	43	1	0.00	0.00100	0.00100	BP	LvH.I1
GO:0030213	hyaluronan biosynthetic process	29	1	0.01	0.0094	0.00940	BP	MvH.I1
GO:0030241	skeletal muscle myosin thick filament as...	31	1	0.00	0.0014	0.00140	BP	LvM.I3
GO:0030516	regulation of axon extension	270	1	0.01	0.00631	0.00631	BP	LvH.I1
GO:0030877	beta-catenin destruction complex	28	1	0.01	0.0098	0.00980	CC	LvH.I3
GO:0030898	actin-dependent ATPase activity	44	1	0.00	0.00213	0.00213	MF	LvM.I3
GO:0031666	positive regulation of lipopolysaccharid...	16	1	0.01	0.0060	0.00600	BP	LvH.I3
GO:0031937	positive regulation of chromatin silenci...	15	1	0.00	0.00035	0.00035	BP	LvH.I1
GO:0031937	positive regulation of chromatin silenci...	15	1	0.00	0.0049	0.00490	BP	MvH.I1
GO:0032027	myosin light chain binding	12	1	0.00	0.0044	0.00440	MF	LvH.I3
GO:0032027	myosin light chain binding	12	1	0.00	0.00058	0.00058	MF	LvM.I3
GO:0032982	myosin filament	30	1	0.00	0.00132	0.00132	CC	LvM.I3
GO:0033490	cholesterol biosynthetic process via lat...	12	1	0.00	0.00084	0.00084	BP	LvM.I1
GO:0033558	protein deacetylase activity	111	1	0.00	0.0027	0.00270	MF	LvH.I1
GO:0033592	RNA strand annealing activity	24	1	0.01	0.0087	0.00870	MF	LvH.I3
GO:0033603	positive regulation of dopamine secretio...	12	1	0.00	0.0039	0.00390	BP	MvH.I1
GO:0033699	DNA 5'-adenosine monophosphate hydrolase...	7	1	0.00	0.0024	0.00240	MF	MvH.I1
GO:0033867	Fas-activated serine/threonine kinase ac...	6	1	0.00	0.0022	0.00220	MF	LvH.I3
GO:0034137	positive regulation of toll-like recepto...	14	1	0.00	0.0046	0.00460	BP	MvH.I1
GO:0034773	histone H4-K20 trimethylation	20	1	0.01	0.0075	0.00750	BP	LvH.I3
GO:0035663	Toll-like receptor 2 binding	8	1	0.00	0.0027	0.00270	MF	MvH.I1
GO:0042256	mature ribosome assembly	25	1	0.01	0.0093	0.00930	BP	LvH.I3
GO:0042494	detection of bacterial lipoprotein	12	1	0.00	0.0039	0.00390	BP	MvH.I1
GO:0042535	positive regulation of tumor necrosis fa...	23	1	0.01	0.0075	0.00750	BP	MvH.I1
GO:0042754	negative regulation of circadian rhythm	22	1	0.00	0.00051	0.00051	BP	LvH.I1
GO:0042754	negative regulation of circadian rhythm	22	1	0.01	0.0072	0.00720	BP	MvH.I1
GO:0042799	histone methyltransferase activity (H4-K...	23	1	0.01	0.0083	0.00830	MF	LvH.I3
GO:0043011	myeloid dendritic cell differentiation	21	1	0.01	0.0078	0.00780	BP	LvH.I3
GO:0043273	CTPase activity	8	1	0.00	0.0029	0.00290	MF	LvH.I3
GO:0043531	ADP binding	124	1	0.01	0.00600	0.00600	MF	LvM.I3

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched) (*continued*)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0043619	regulation of transcription from RNA pol...	34	1	0.00	0.00079	0.00079	BP	LvH.I1
GO:0045075	regulation of interleukin-12 biosynthesi...	14	1	0.01	0.0052	0.00520	BP	LvH.I3
GO:0045159	myosin II binding	58	1	0.00	0.00281	0.00281	MF	LvM.I3
GO:0045410	positive regulation of interleukin-6 bio...	23	1	0.01	0.0086	0.00860	BP	LvH.I3
GO:0045410	positive regulation of interleukin-6 bio...	23	1	0.01	0.0075	0.00750	BP	MvH.I1
GO:0046330	positive regulation of JNK cascade	374	2	0.14	0.0084	0.00840	BP	LvH.I3
GO:0046513	ceramide biosynthetic process	176	1	0.01	0.0082	0.00820	BP	LvM.I3
GO:0048251	elastic fiber assembly	23	1	0.01	0.0086	0.00860	BP	LvH.I3
GO:0048251	elastic fiber assembly	23	1	0.00	0.0011	0.00110	BP	LvM.I3
GO:0048739	cardiac muscle fiber development	37	1	0.00	0.0017	0.00170	BP	LvM.I3
GO:0050671	positive regulation of lymphocyte prolif...	278	2	0.10	0.0047	0.00470	BP	LvH.I3
GO:0051023	regulation of immunoglobulin secretion	26	1	0.01	0.0097	0.00970	BP	LvH.I3
GO:0051595	response to methylglyoxal	18	1	0.00	0.00042	0.00042	BP	LvH.I1
GO:0051595	response to methylglyoxal	18	1	0.01	0.0059	0.00590	BP	MvH.I1
GO:0051865	protein autoubiquitination	241	2	0.09	0.0036	0.00360	BP	LvH.I3
GO:0061630	ubiquitin protein ligase activity	671	3	0.24	0.0017	0.00170	MF	LvH.I3
GO:0070125	mitochondrial translational elongation	71	1	0.00	0.00497	0.00497	BP	LvM.I1
GO:0070417	cellular response to cold	23	1	0.01	0.0086	0.00860	BP	LvH.I3
GO:0070534	protein K63-linked ubiquitination	175	2	0.07	0.0019	0.00190	BP	LvH.I3
GO:0071333	cellular response to glucose stimulus	378	1	0.01	0.00883	0.00883	BP	LvH.I1
GO:0071651	positive regulation of chemokine (C-C mo...	18	1	0.01	0.0067	0.00670	BP	LvH.I3
GO:0071723	lipopeptide binding	11	1	0.00	0.0037	0.00370	MF	MvH.I1
GO:0071727	cellular response to triacyl bacterial l...	5	1	0.00	0.0016	0.00160	BP	MvH.I1
GO:0090461	glutamate homeostasis	9	1	0.00	0.0029	0.00290	BP	MvH.I1
GO:0120108	DNA-3'-diphospho-5'-guanosine diphosphat...	9	1	0.00	0.0031	0.00310	MF	MvH.I1
GO:1900028	negative regulation of ruffle assembly	17	1	0.00	0.00119	0.00119	BP	LvM.I1
GO:1900181	negative regulation of protein localizat...	75	1	0.00	0.00175	0.00175	BP	LvH.I1
GO:1901675	negative regulation of histone H3-K27 ac...	6	1	0.00	0.00014	0.00014	BP	LvH.I1
GO:1901675	negative regulation of histone H3-K27 ac...	6	1	0.00	0.0020	0.00200	BP	MvH.I1
GO:1903351	cellular response to dopamine	85	1	0.00	0.00199	0.00199	BP	LvH.I1
GO:1903608	protein localization to cytoplasmic stre...	26	1	0.01	0.0097	0.00970	BP	LvH.I3

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched) (*continued*)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:1990165	single-strand break-containing DNA bindi...	7	1	0.00	0.0024	0.00240	MF	MvH.I1
GO:1990756	ubiquitin ligase-substrate adaptor activ...	24	1	0.01	0.0087	0.00870	MF	LvH.I3
GO:2000327	positive regulation of nuclear receptor ...	20	1	0.01	0.0075	0.00750	BP	LvH.I3
GO:2000374	regulation of oxygen metabolic process	8	1	0.00	0.0030	0.00300	BP	LvH.I3
GO:2000484	positive regulation of interleukin-8 sec...	30	1	0.01	0.0098	0.00980	BP	MvH.I1
GO:2000678	negative regulation of transcription reg...	36	1	0.00	0.00084	0.00084	BP	LvH.I1
GO:2001271	negative regulation of cysteine-type end...	16	1	0.01	0.0060	0.00600	BP	LvH.I3

Shed Level Early Infection - Bursa - Gene

Amanda Dolinski & Jared J. Homola

23 March, 2021

This is an analysis of differential expression at the gene level between low, moderate, and high LPAIV shedding blue-winged teals based on cloacal swab virus titers measured on the day of sacrifice for bursa samples on 1 and 3 days post infection (DPI).

Differential expression analysis

For this analysis, we conduct two sets of differential expression analyses- one for each LPAIV-infected group in early infection: I1 and I3.

Numbers of DE genes

Table 1: Count of DE genes. For a gene to be considered differentially expressed, we require a p-value of 0.1 with a false discovery rate correction and a log fold change difference of 1.0.

Direction	Comparison	N
I1		
Down	LvM	13
Up	LvM	3
Down	MvH	1
Up	MvH	5
Down	LvH	5
Up	LvH	3
I3		
Down	LvM	3
Up	LvM	1
Down	MvH	0
Up	MvH	0
Down	LvH	2
Up	LvH	0

Volcano plot

Volcano plot reporting $-\log_{10}(\text{p-values})$ as a function of $\log_2(\text{fold change})$ between the samples (logFC, x axis). Genes that are identified as significantly differentially expressed following a false discovery rate correction ($q = 0.10$) are shown in red

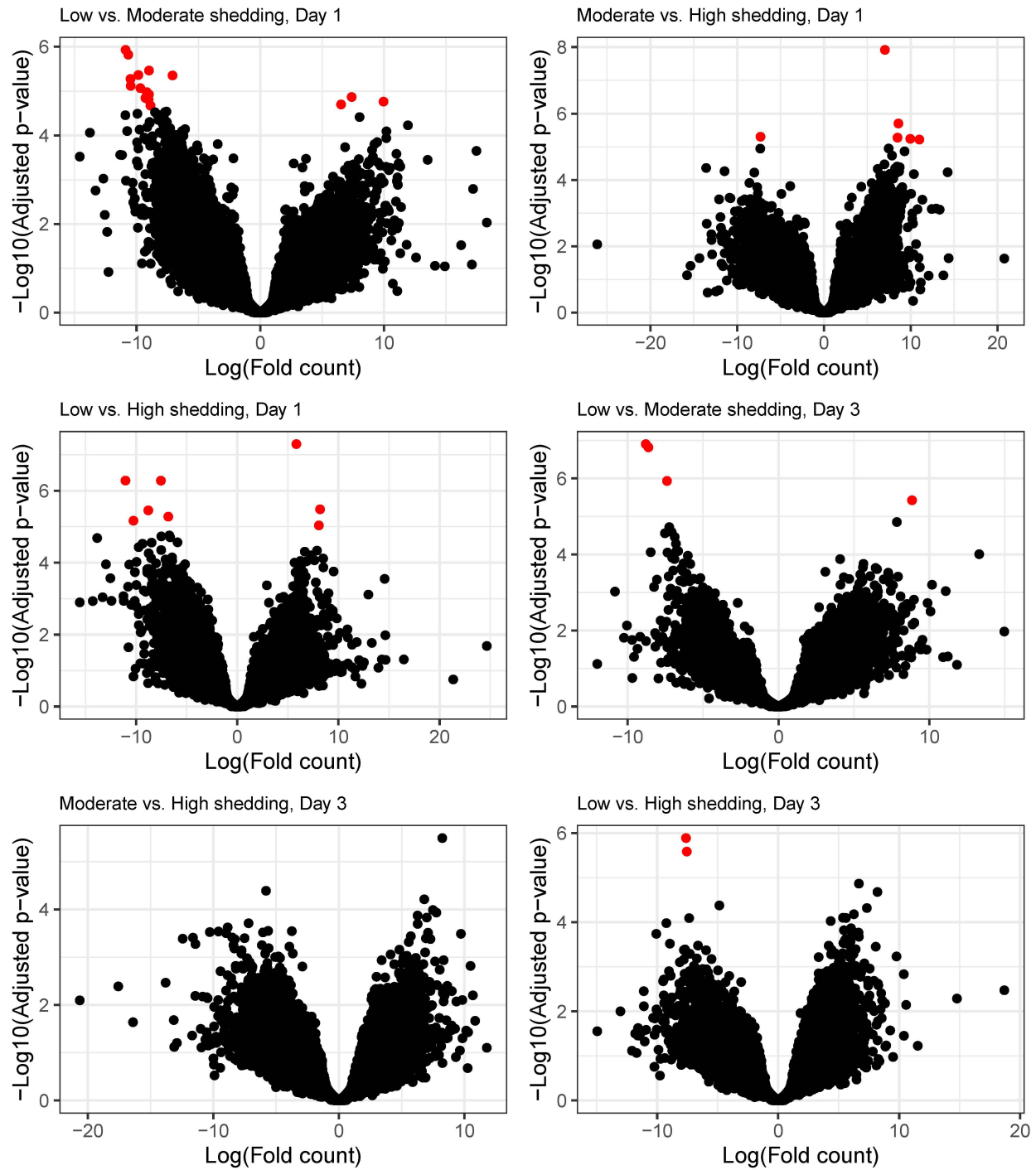


Table 2: Annotations for differentially expressed genes. ns denotes non-significant genes for each comparison and numerical values are the log(fold change) difference

gene_id	SwissProt_GeneName	LvM.I1	MvH.I1	LvH.I1	LvM.I3	MvH.I3	LvH.I3
DN16207_c0_g1	TBB3_RAT	-10.88	ns	ns	ns	ns	ns
DN12223_c0_g1	.	-10.67	ns	-11.05	ns	ns	ns
DN11038_c0_g1	.	-8.99	ns	ns	ns	ns	ns
DN58849_c0_g1	.	-9.85	9.95	ns	ns	ns	ns
DN93375_c0_g1	.	-7.09	ns	-7.55	ns	ns	ns
DN25207_c2_g1	.	-10.49	11	ns	ns	ns	ns
DN55400_c0_g1	.	-10.47	ns	ns	ns	ns	ns
DN8962_c1_g1	.	-9.69	ns	ns	ns	ns	ns
DN105154_c0_g2	PITM1_HUMAN	-9.17	ns	ns	ns	ns	ns
DN36346_c0_g1	.	-9	ns	ns	ns	ns	ns
DN5125_c4_g1	.	7.38	ns	ns	ns	ns	ns
DN7422_c1_g1	.	-9.28	ns	ns	ns	ns	ns
DN195899_c0_g1	.	-9.02	ns	ns	ns	ns	ns
DN122391_c0_g1	.	9.96	ns	ns	ns	ns	ns
DN425292_c0_g1	.	6.53	-7.31	ns	ns	ns	ns
DN42839_c0_g3	.	-8.87	ns	ns	ns	ns	ns
DN343712_c0_g1	ANPRB_BOVIN	ns	ns	-6.81	ns	ns	ns
DN14696_c1_g1	.	ns	ns	-10.26	ns	ns	ns
DN6106_c0_g1	.	ns	ns	ns	-7.39	ns	-7.55
DN21606_c0_g1	.	ns	ns	ns	-8.63	ns	-7.62
DN20979_c0_g1	.	ns	ns	ns	-8.8	ns	ns
DN38607_c0_g1	.	ns	ns	ns	8.85	ns	ns
DN943_c0_g1	.	ns	7.03	5.84	ns	ns	ns
DN12412_c0_g2	.	ns	ns	-8.79	ns	ns	ns
DN14098_c3_g1	.	ns	8.48	8.07	ns	ns	ns
DN21402_c2_g1	.	ns	8.58	8.19	ns	ns	ns

Table 3: Gene functions

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN16207_c0_g1	TBB3_RAT	Tubulin beta-3 chain;	KEGG:rno:246118	KO:K07375
DN105154_c0_g2	PITM1_HUMAN	Membrane-associated phosphatidylinositol transfer protein 1;	KEGG:hsa:9600	NA
DN343712_c0_g1	ANPRB_BOVIN	Atrial natriuretic peptide receptor 2;	KEGG:bta:281357	KO:K12324

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0004383	guanylate cyclase activity	12	1	0.00	0.00074	0.00074	MF	LvH.I1
GO:0005200	structural constituent of cytoskeleton	111	1	0.01	0.0069	0.00690	MF	LvM.I1
GO:0006182	cGMP biosynthetic process	12	1	0.00	0.00072	0.00072	BP	LvH.I1
GO:0007168	receptor guanylyl cyclase signaling path...	9	1	0.00	0.00054	0.00054	BP	LvH.I1
GO:0016941	natriuretic peptide receptor activity	5	1	0.00	0.00031	0.00031	MF	LvH.I1
GO:0017046	peptide hormone binding	29	1	0.00	0.00180	0.00180	MF	LvH.I1
GO:0030175	filopodium	138	1	0.01	0.0078	0.00780	CC	LvM.I1
GO:0038007	netrin-activated signaling pathway	7	1	0.00	0.00042	0.00042	BP	LvM.I1
GO:0051447	negative regulation of meiotic cell cycl...	16	1	0.00	0.00096	0.00096	BP	LvH.I1
GO:0097011	cellular response to granulocyte macroph...	14	1	0.00	0.00084	0.00084	BP	LvH.I1
GO:1900194	negative regulation of oocyte maturation	5	1	0.00	0.00030	0.00030	BP	LvH.I1
GO:1990791	dorsal root ganglion development	9	1	0.00	0.00054	0.00054	BP	LvM.I1

Shed Level Early Infection - Bursa - Transcript

Amanda Dolinski & Jared J. Homola

23 March, 2021

This is an analysis of differential expression at the transcript level between low, moderate, and high LPAIV shedding blue-winged teals based on cloacal swab virus titers measured on the day of sacrifice for bursa samples on 1 and 3 days post infection (DPI).

Differential expression analysis

For this analysis, we conduct two sets of differential expression analyses- one for each LPAIV-infected group in early infection: I1 and I3.

Table 1: Count of DE transcripts. For a transcript to be considered differentially expressed, we require a p-value of 0.1 with a false discovery rate correction and a log fold change difference of 1.0.

Direction	Comparison	N
I1		
Down	LvM	2
Up	LvM	0
Down	MvH	0
Up	MvH	1
Down	LvH	0
Up	LvH	0
I3		
Down	LvM	5
Up	LvM	2
Down	MvH	0
Up	MvH	0
Down	LvH	3
Up	LvH	4

Volcano plot

Volcano plot reporting $-\log_{10}(\text{p-values})$ as a function of $\log_2(\text{fold change})$ between the samples (logFC, x axis). Transcripts that are identified as significantly differentially expressed following a false discovery rate correction ($q = 0.10$) are shown in red

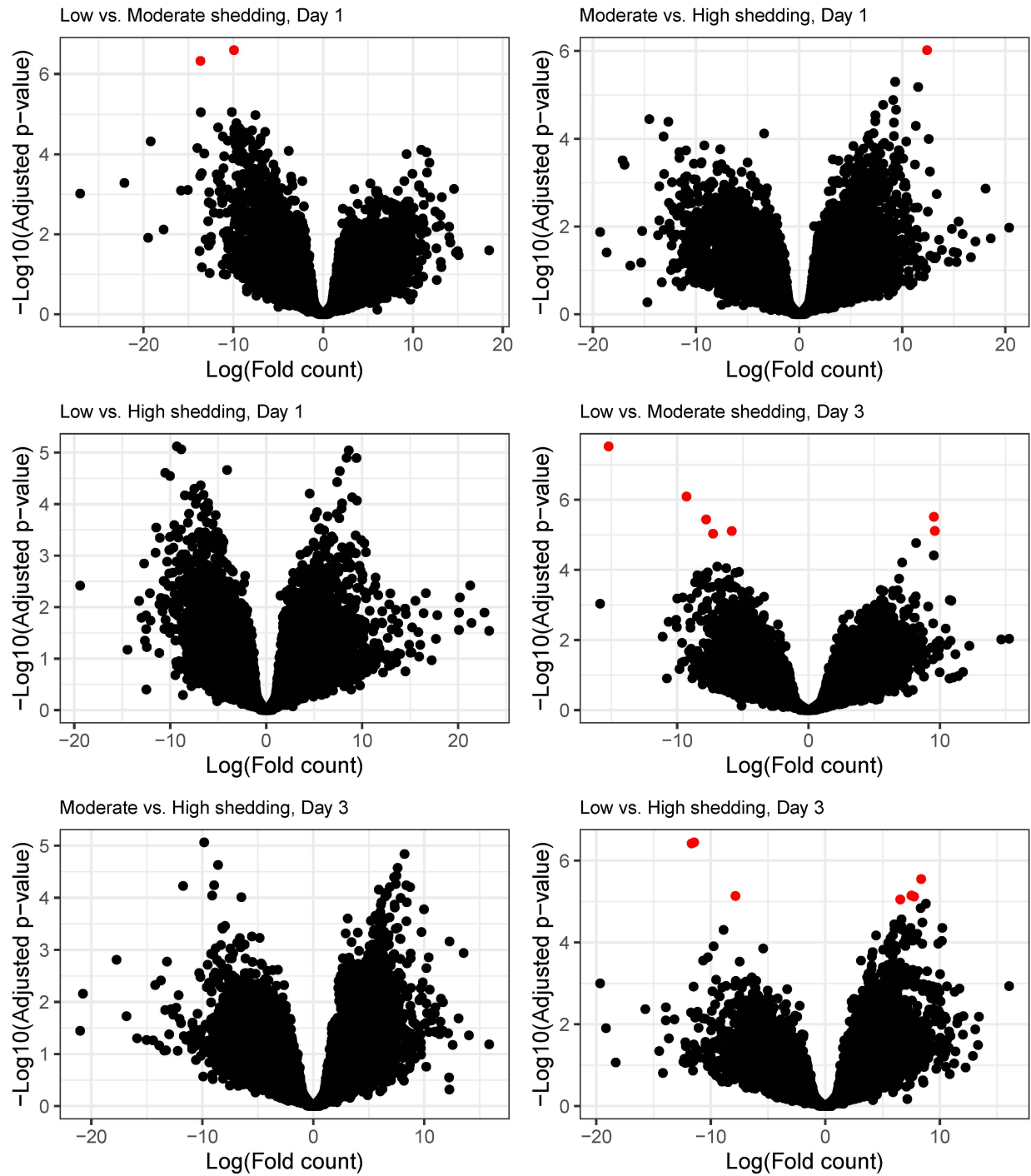


Table 2: Annotations for differentially expressed transcripts. ns denotes non-significant transcripts for each comparison and numerical values are the log(fold change) difference

transcript_id	SwissProt_GeneName	LvM.I1	MvH.I1	LvH.I1	LvM.I3	MvH.I3	LvH.I3
DN1664_c0_g1_i8	.	-9.93	ns	ns	ns	ns	ns
DN2044_c0_g1_i4	WDFY3_HUMAN	-13.66	12.41	ns	ns	ns	ns
DN4250_c2_g2_i5	.	ns	ns	ns	9.54	ns	ns
DN2781_c0_g1_i7	.	ns	ns	ns	-9.29	ns	-7.85
DN2227_c0_g1_i12	ROA3_RAT	ns	ns	ns	9.62	ns	ns
DN6839_c0_g1_i1	VP35L_HUMAN	ns	ns	ns	ns	ns	7.75
DN5730_c0_g2_i9	MRP1_CHICK	ns	ns	ns	-5.85	ns	ns
DN9734_c0_g1_i3	TRAF6_PIG	ns	ns	ns	ns	ns	7.53
DN3611_c0_g1_i2	CAVN2_HUMAN	ns	ns	ns	-7.8	ns	-11.46
DN2660_c0_g1_i1	TGON2_HUMAN	ns	ns	ns	-15.22	ns	-11.67
DN1906_c0_g1_i6	ACS2L_MOUSE	ns	ns	ns	ns	ns	6.55
DN1622_c0_g1_i8	CS047_MOUSE	ns	ns	ns	-7.27	ns	ns
DN15150_c0_g1_i17	PUR4_HUMAN	ns	ns	ns	ns	ns	8.37

Table 3: Transcript functions

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN2044_c0_g1_i4	WDFY3_HUMAN	WD repeat and FYVE domain-containing protein 3;	KEGG:hsa:23001	KO:K22262
DN2227_c0_g1_i12	ROA3_RAT	Heterogeneous nuclear ribonucleoprotein A3;	KEGG:rno:362152	KO:K12741
DN6839_c0_g1_i1	VP35L_HUMAN	VPS35 endosomal protein sorting factor-like {ECO:0000305};	KEGG:hsa:124152	NA
DN5730_c0_g2_i9	MRP1_CHICK	Multidrug resistance-associated protein 1;	KEGG:gga:395416	KO:K05665
DN9734_c0_g1_i3	TRAF6_PIG	TNF receptor-associated factor 6;	KEGG:ssc:396629	KO:K03175
DN3611_c0_g1_i2	CAVN2_HUMAN	Caveolae-associated protein 2 {ECO:0000312 HGNC:HGNC:10690};	KEGG:hsa:8436	NA
DN2660_c0_g1_i1	TGON2_HUMAN	Trans-Golgi network integral membrane protein 2 {ECO:0000305};	KEGG:hsa:10618	NA
DN1906_c0_g1_i6	ACS2L_MOUSE	Acetyl-coenzyme A synthetase 2-like, mitochondrial;	KEGG:mmu:68738	KO:K01895
DN1622_c0_g1_i8	CS047_MOUSE	Uncharacterized protein C19orf47 homolog;	KEGG:mmu:66367	NA
DN15150_c0_g1_i17	PUR4_HUMAN	Phosphoribosylformylglycinamide synthase;	KEGG:hsa:5198	KO:K01952

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0002726	positive regulation of T cell cytokine p...	60	1	0.01	0.00929	0.00929	BP	LvH.I3
GO:0003831	beta-N-acetylglucosaminylglycopeptide be...	18	1	0.00	0.00049	0.00049	MF	LvM.I1
GO:0003831	beta-N-acetylglucosaminylglycopeptide be...	18	1	0.00	0.00049	0.00049	MF	MvH.I1
GO:0003987	acetate-CoA ligase activity	8	1	0.00	0.0011	0.00110	MF	LvH.I3
GO:0005080	protein kinase C binding	100	1	0.01	0.0081	0.00810	MF	LvM.I3
GO:0005545	1-phosphatidylinositol binding	59	1	0.00	0.00159	0.00159	MF	LvM.I1
GO:0005545	1-phosphatidylinositol binding	59	1	0.00	0.00159	0.00159	MF	MvH.I1
GO:0006189	'de novo' IMP biosynthetic process	11	1	0.00	0.00171	0.00171	BP	LvH.I3
GO:0007250	activation of NF-kappaB-inducing kinase ...	58	1	0.01	0.00898	0.00898	BP	LvH.I3
GO:0016208	AMP binding	41	1	0.01	0.0055	0.00550	MF	LvH.I3
GO:0016234	inclusion body	228	1	0.01	0.00556	0.00556	CC	LvM.I1
GO:0016234	inclusion body	228	1	0.01	0.00556	0.00556	CC	MvH.I1
GO:0016605	PML body	348	1	0.01	0.00848	0.00848	CC	LvM.I1
GO:0016605	PML body	348	1	0.01	0.00848	0.00848	CC	MvH.I1
GO:0016884	carbon-nitrogen ligase activity, with gl...	29	1	0.00	0.0039	0.00390	MF	LvH.I3
GO:0019413	acetate biosynthetic process	6	1	0.00	0.00093	0.00093	BP	LvH.I3
GO:0019427	acetyl-CoA biosynthetic process from ace...	6	1	0.00	0.00093	0.00093	BP	LvH.I3
GO:0019542	propionate biosynthetic process	6	1	0.00	0.00093	0.00093	BP	LvH.I3
GO:0031435	mitogen-activated protein kinase kinase ...	63	1	0.01	0.0085	0.00850	MF	LvH.I3
GO:0031666	positive regulation of lipopolysaccharid...	15	1	0.00	0.00233	0.00233	BP	LvH.I3
GO:0031996	thioesterase binding	29	1	0.00	0.0039	0.00390	MF	LvH.I3
GO:0032735	positive regulation of interleukin-12 pr...	59	1	0.01	0.00914	0.00914	BP	LvH.I3
GO:0035631	CD40 receptor complex	49	1	0.01	0.0071	0.00710	CC	LvH.I3
GO:0035973	aggrephagy	30	1	0.00	0.00078	0.00078	BP	LvM.I1
GO:0035973	aggrephagy	30	1	0.00	0.00078	0.00078	BP	MvH.I1
GO:0043011	myeloid dendritic cell differentiation	18	1	0.00	0.00280	0.00280	BP	LvH.I3
GO:0043204	perikaryon	316	1	0.01	0.00770	0.00770	CC	LvM.I1
GO:0043204	perikaryon	316	1	0.01	0.00770	0.00770	CC	MvH.I1
GO:0043422	protein kinase B binding	39	1	0.01	0.0053	0.00530	MF	LvH.I3
GO:0045075	regulation of interleukin-12 biosynthesi...	13	1	0.00	0.00202	0.00202	BP	LvH.I3
GO:0045410	positive regulation of interleukin-6 bio...	18	1	0.00	0.00280	0.00280	BP	LvH.I3
GO:0045672	positive regulation of osteoclast differ...	34	1	0.01	0.00527	0.00527	BP	LvH.I3

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched) (*continued*)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0050218	propionate-CoA ligase activity	10	1	0.00	0.0013	0.00130	MF	LvH.I3
GO:0051023	regulation of immunoglobulin secretion	24	1	0.00	0.00373	0.00373	BP	LvH.I3
GO:0051033	RNA transmembrane transporter activity	15	1	0.00	0.0012	0.00120	MF	LvM.I3
GO:0097065	anterior head development	8	1	0.00	0.00124	0.00124	BP	LvH.I3
GO:0097320	plasma membrane tubulation	74	1	0.01	0.0076	0.00760	BP	LvM.I3
GO:0097635	extrinsic component of autophagosome mem...	13	1	0.00	0.00032	0.00032	CC	LvM.I1
GO:0097635	extrinsic component of autophagosome mem...	13	1	0.00	0.00032	0.00032	CC	MvH.I1
GO:0098805	whole membrane	3973	3	0.48	0.0078	0.00780	CC	LvM.I3
GO:0101003	ficolin-1-rich granule membrane	56	1	0.01	0.0082	0.00820	CC	LvH.I3
GO:1904996	positive regulation of leukocyte adhesio...	30	1	0.00	0.00466	0.00466	BP	LvH.I3
GO:1990124	messenger ribonucleoprotein complex	39	1	0.00	0.0047	0.00470	CC	LvM.I3
GO:2000679	positive regulation of transcription reg...	26	1	0.00	0.00404	0.00404	BP	LvH.I3

Shed Level Late Stage Infection - Ileum - Gene

Amanda Dolinski & Jared J. Homola

23 March, 2021

This is an analysis of differential expression at the gene level between between low, moderate, and high LPAIV shedding blue-winged teals based on cloacal swab virus titers averaged across 1-5 days post-infection (DPI) for ileum samples collected on 5 DPI.

Differential expression analysis

Table 1: Count of DE genes. For a gene to be considered differentially expressed, we require a p-value of 0.1 with a false discovery rate correction and a log fold change difference of 1.0.

Direction	Comparison	N
Down	LvM	0
Up	LvM	3
Down	MvH	3
Up	MvH	22
Down	LvH	3
Up	LvH	88

Volcano plot

Volcano plot reporting $-\log_{10}(\text{p-values})$ as a function of $\log_2(\text{fold change})$ between the samples ($\log\text{FC}$, x axis). Genes that are identified as significantly differentially expressed following a false discovery rate correction ($q = 0.10$) are shown in red

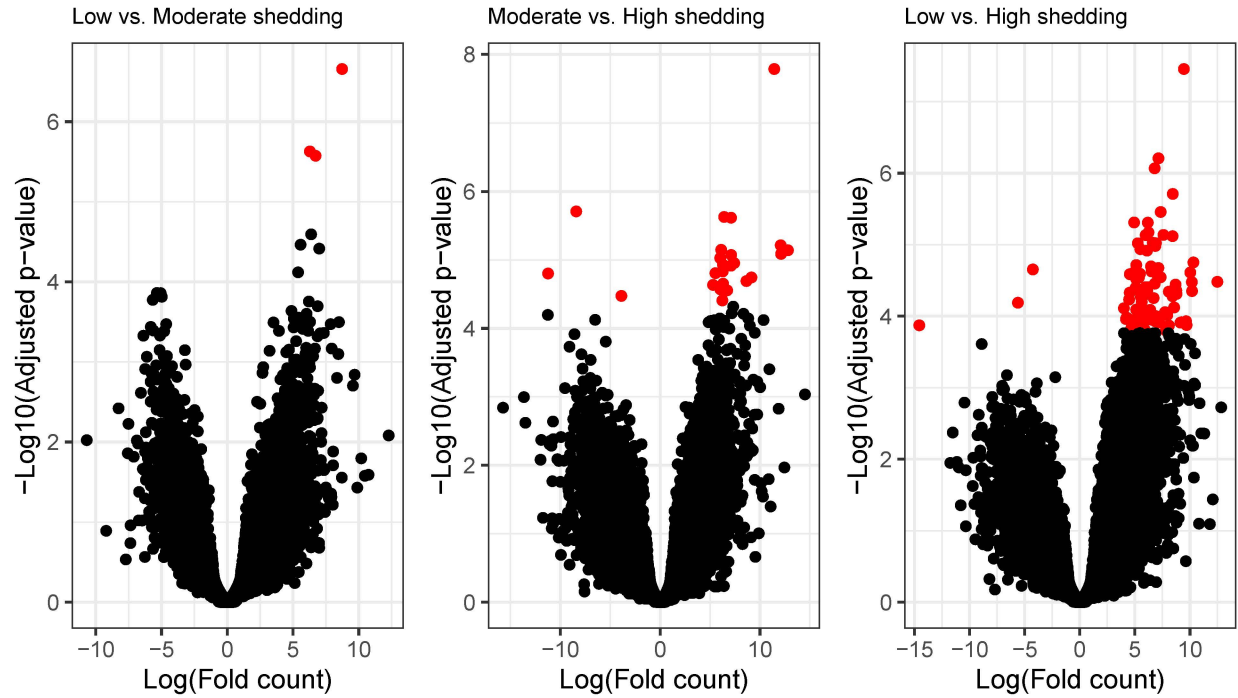


Table 2: Annotations for differentially expressed genes. ns denotes non-significant genes for each comparison and numerical values are the log(fold change) difference

gene_id	SwissProt_GeneName	LvM	MvH	LvH
DN50685_c0_g1	.	8.73	ns	8.44
DN11986_c0_g2	.	6.28	-8.41	ns
DN50685_c1_g1	.	6.72	ns	6.51
DN21964_c0_g1	.	ns	9.15	ns
DN34832_c1_g1	.	ns	7.09	ns
DN5471_c0_g1	.	ns	6.27	ns
DN18436_c0_g1	.	ns	ns	8.42
DN4596_c1_g4	.	ns	ns	12.49
DN66339_c0_g1	.	ns	ns	7.06
DN12551_c1_g1	.	ns	ns	8.76
DN3264_c0_g1	.	ns	12.8	ns
DN23183_c0_g1	.	ns	-11.23	ns
DN27940_c0_g1	.	ns	6.71	ns
DN16824_c0_g1	.	ns	ns	10.17
DN23887_c0_g1	.	ns	ns	5.13
DN375967_c0_g1	.	ns	ns	7.14
DN539_c1_g1	.	ns	ns	8.78
DN190935_c0_g1	.	ns	11.43	9.45
DN37622_c0_g1	AT1A2_CHICK	ns	ns	8.57
DN146506_c0_g1	.	ns	ns	8.41
DN11360_c0_g1	.	ns	ns	9.14
DN6169_c1_g1	.	ns	ns	6.41
DN11038_c0_g1	.	ns	ns	-14.56
DN42303_c0_g1	.	ns	ns	6.87
DN11765_c0_g3	SYNA_MOUSE	ns	ns	6.13
DN14276_c3_g3	.	ns	5.3	7.14
DN2205_c0_g5	FOXQ1_RAT	ns	7.11	5.37
DN16158_c0_g1	.	ns	ns	9.65
DN26298_c0_g1	.	ns	6.41	4.93
DN15948_c2_g1	.	ns	ns	4.48
DN40322_c0_g1	DJC14_RAT	ns	ns	8.09
DN17711_c1_g1	.	ns	ns	6.7
DN2350_c0_g1	.	ns	12.11	10.03
DN15525_c0_g1	TCPD_MOUSE	ns	ns	6.17
DN61995_c0_g1	.	ns	6.12	4.54
DN132891_c1_g1	K2C75_HUMAN	ns	ns	6.05
DN33799_c0_g1	SGSM2_MOUSE	ns	ns	5.97
DN44914_c3_g1	RTJK_DROFU	ns	ns	5.62
DN413234_c0_g1	.	ns	ns	5.5
DN32165_c0_g1	DMB_HUMAN	ns	12.08	10.31
DN27277_c2_g1	.	ns	ns	4.61
DN12250_c2_g1	.	ns	ns	6.12
DN76955_c1_g2	.	ns	ns	9.23
DN10182_c0_g1	.	ns	ns	5.12
DN1425_c4_g1	BT2A2_MOUSE	ns	ns	7.34

Table 2: Annotations for differentially expressed genes. ns denotes non-significant genes for each comparison and numerical values are the log(fold change) difference (*continued*)

gene_id	SwissProt_GeneName	LvM	MvH	LvH
DN106161_c0_g1	.	ns	ns	8.56
DN15935_c0_g1	.	ns	ns	7.21
DN6803_c0_g1	.	ns	ns	9.69
DN16856_c0_g1	GVIN1_MOUSE	ns	ns	10.19
DN26626_c0_g1	.	ns	ns	7.34
DN36121_c1_g2	.	ns	ns	5.84
DN58830_c0_g1	.	ns	ns	5.54
DN17030_c0_g1	.	ns	ns	4.19
DN11783_c0_g3	.	ns	ns	4
DN32715_c1_g1	.	ns	ns	6.07
DN592_c4_g1	.	ns	ns	8.08
DN5800_c0_g1	.	ns	ns	5.12
DN91540_c0_g2	VLDLR_CHICK	ns	8.64	7.59
DN15257_c0_g1	.	ns	ns	6.46
DN28286_c0_g2	.	ns	ns	5.9
DN17046_c0_g1	.	ns	ns	5.68
DN13466_c1_g1	.	ns	ns	5.86
DN367032_c0_g1	.	ns	ns	4.58
DN804_c0_g2	UBP24_HUMAN	ns	ns	4.25
DN13161_c2_g1	.	ns	ns	7.74
DN172162_c0_g1	.	ns	ns	7.38
DN23410_c4_g1	.	ns	6.2	5.46
DN390280_c0_g1	.	ns	6.02	5.27
DN15475_c0_g1	.	ns	ns	5.21
DN112257_c1_g1	.	ns	ns	6.39
DN3385_c0_g2	.	ns	5.53	4.8
DN265143_c0_g1	PGAP1_XENLA	ns	ns	5.75
DN209_c1_g4	POL_SFV1	ns	ns	6.83
DN2770_c0_g2	FBP1L_HUMAN	ns	ns	4.8
DN95640_c0_g2	.	ns	7.42	6.86
DN9190_c1_g1	.	ns	ns	6.91
DN11170_c1_g1	.	ns	ns	4.88
DN156217_c0_g1	.	ns	ns	5.4
DN44437_c0_g1	.	ns	ns	7.81
DN20766_c0_g1	S2611_MOUSE	ns	ns	5.55
DN46437_c0_g1	PFKAL_MOUSE	ns	ns	7.94
DN79800_c0_g1	GSHR_HUMAN	ns	ns	6.62
DN5026_c0_g3	.	ns	6.29	5.98
DN87539_c0_g1	.	ns	ns	5.18
DN13540_c0_g1	.	ns	7.1	6.79
DN21662_c0_g1	.	ns	ns	4.53
DN11066_c0_g1	.	ns	ns	-5.61
DN10908_c0_g1	.	ns	ns	8.69
DN16860_c0_g1	.	ns	ns	6.93
DN91803_c0_g1	.	ns	-3.88	-4.26

Table 2: Annotations for differentially expressed genes. ns denotes non-significant genes for each comparison and numerical values are the log(fold change) difference (*continued*)

gene_id	SwissProt_GeneName	LvM	MvH	LvH
DN59276_c0_g1	SCRT2_MOUSE	ns	6.3	6.1
DN155424_c0_g1	.	ns	6.03	6.17
DN191666_c0_g1	.	ns	ns	6.81
DN9110_c0_g1	.	ns	ns	6.62
DN422858_c0_g1	.	ns	ns	4.71
DN36643_c0_g1	.	ns	ns	5.54
DN369367_c0_g1	.	ns	ns	5.07
DN73246_c0_g1	BTNL2_HUMAN	ns	6.23	6.24

Table 3: Gene functions

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN37622_c0_g1	AT1A2_CHICK	Sodium/potassium-transporting ATPase subunit alpha-2;	.	NA
DN11765_c0_g3	SYNA_MOUSE	Syncytin-A {ECO:0000303 PubMed:15644441};	KEGG:mmu:214292	NA
DN2205_c0_g5	FOXQ1_RAT	Forkhead box protein Q1;	.	NA
DN40322_c0_g1	DJC14_RAT	DnaJ homolog subfamily C member 14;	KEGG:rno:114481	KO:K09534
DN15525_c0_g1	TCPD_MOUSE	T-complex protein 1 subunit delta;	KEGG:mmu:12464	KO:K09496
DN132891_c1_g1	K2C75_HUMAN	Keratin, type II cytoskeletal 75;	KEGG:hsa:9119	KO:K07605
DN33799_c0_g1	SGSM2_MOUSE	Small G protein signaling modulator 2;	KEGG:mmu:97761	KO:K21851
DN44914_c3_g1	RTJK_DROFU	RNA-directed DNA polymerase from mobile element jockey;	.	NA
DN32165_c0_g1	DMB_HUMAN	HLA class II histocompatibility antigen, DM beta chain;	KEGG:hsa:3109	KO:K06752
DN1425_c4_g1	BT2A2_MOUSE	Butyrophilin subfamily 2 member A2;	KEGG:mmu:238555	KO:K06712
DN16856_c0_g1	GVIN1_MOUSE	Interferon-induced very large GTPase 1;	KEGG:mmu:100042856	NA
DN91540_c0_g2	VLDLR_CHICK	Very low-density lipoprotein receptor;	KEGG:gga:396154	KO:K20053
DN804_c0_g2	UBP24_HUMAN	Ubiquitin carboxyl-terminal hydrolase 24;	KEGG:hsa:23358	KO:K11840
DN265143_c0_g1	PGAP1_XENLA	GPI inositol-deacylase;	KEGG:xla:447534	KO:K05294
DN209_c1_g4	POL_SFV1	Pro-Pol polyprotein;	.	NA
DN2770_c0_g2	FBP1L_HUMAN	Formin-binding protein 1-like;	KEGG:hsa:54874	KO:K20121
DN20766_c0_g1	S2611_MOUSE	Sodium-independent sulfate anion transporter;	KEGG:mmu:268512	KO:K14708
DN46437_c0_g1	PFKAL_MOUSE	ATP-dependent 6-phosphofructokinase, liver type {ECO:0000255 HAMAP-Rule:MF_03184};	KEGG:mmu:18641	KO:K00850

Table 3: Gene functions (*continued*)

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN79800_c0_g1	GSHR_HUMAN	Glutathione reductase, mitochondrial;	KEGG:hsa:2936	KO:K00383
DN59276_c0_g1	SCRT2_MOUSE	Transcriptional repressor scratch 2;	KEGG:mmu:545474	KO:K09219
DN73246_c0_g1	BTNL2_HUMAN	Butyrophilin-like protein 2;	KEGG:hsa:56244	NA

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0002503	peptide antigen assembly with MHC class ...	6	1	0.01	0.0077	0.00770	BP	LvH.I5
GO:0002503	peptide antigen assembly with MHC class ...	6	1	0.00	0.00289	0.00289	BP	MvH.I5
GO:0004362	glutathione-disulfide reductase activity	5	1	0.01	0.0069	0.00690	MF	LvH.I5
GO:0005945	6-phosphofructokinase complex	7	1	0.01	0.00878	0.00878	CC	LvH.I5
GO:0008321	Ral guanyl-nucleotide exchange factor ac...	9	1	0.00	0.0045	0.00450	MF	MvH.I5
GO:0009897	external side of plasma membrane	488	5	0.61	0.00031	0.00031	CC	LvH.I5
GO:0009897	external side of plasma membrane	488	3	0.22	0.0011	0.00110	CC	MvH.I5
GO:0015798	myo-inositol transport	5	1	0.01	0.0064	0.00640	BP	LvH.I5
GO:0023026	MHC class II protein complex binding	13	1	0.01	0.0064	0.00640	MF	MvH.I5
GO:0030229	very-low-density lipoprotein particle re...	14	1	0.01	0.0069	0.00690	MF	MvH.I5
GO:0032485	regulation of Ral protein signal transdu...	10	1	0.00	0.00482	0.00482	BP	MvH.I5
GO:0034499	late endosome to Golgi transport	7	1	0.01	0.0090	0.00900	BP	LvH.I5
GO:0042102	positive regulation of T cell proliferat...	83	2	0.11	0.0051	0.00510	BP	LvH.I5
GO:0042102	positive regulation of T cell proliferat...	83	2	0.04	0.00069	0.00069	BP	MvH.I5
GO:0042613	MHC class II protein complex	14	1	0.01	0.0063	0.00630	CC	MvH.I5
GO:0050852	T cell receptor signaling pathway	310	2	0.15	0.00918	0.00918	BP	MvH.I5
GO:0050860	negative regulation of T cell receptor s...	58	2	0.07	0.0025	0.00250	BP	LvH.I5
GO:1900042	positive regulation of interleukin-2 sec...	6	1	0.01	0.0077	0.00770	BP	LvH.I5
GO:1900042	positive regulation of interleukin-2 sec...	6	1	0.00	0.00289	0.00289	BP	MvH.I5
GO:2001190	positive regulation of T cell activation...	6	1	0.01	0.0077	0.00770	BP	LvH.I5
GO:2001190	positive regulation of T cell activation...	6	1	0.00	0.00289	0.00289	BP	MvH.I5

Shed Level Late Stage Infection - Ileum - Transcript

Amanda Dolinski & Jared J. Homola

23 March, 2021

This is an analysis of differential expression at the transcript level between between low, moderate, and high LPAIV shedding blue-winged teals based on cloacal swab virus titers averaged across 1-5 days post-infection (DPI) for ileum samples collected on 5 DPI.

Differential expression analysis

Table 1: Count of DE transcripts. For a transcript to be considered differentially expressed, we require a p-value of 0.1 with a false discovery rate correction and a log fold change difference of 1.0.

Direction	Comparison	N
Down	LvM	6
Up	LvM	20
Down	MvH	6
Up	MvH	61
Down	LvH	3
Up	LvH	138

Volcano plot

Volcano plot reporting $-\log_{10}(\text{p-values})$ as a function of $\log_2(\text{fold change})$ between the samples (logFC, x axis). Transcripts that are identified as significantly differentially expressed following a false discovery rate correction ($q = 0.10$) are shown in red

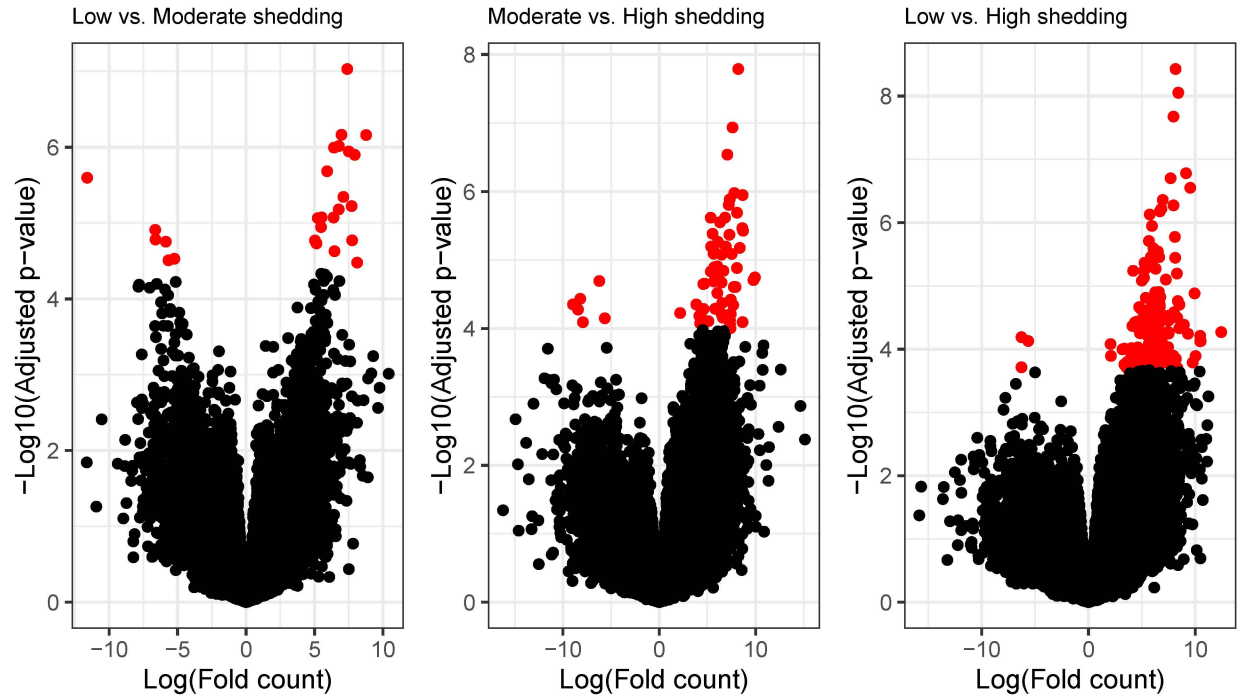


Table 2: Annotations for differentially expressed transcripts. ns denotes non-significant transcripts for each comparison and numerical values are the log(fold change) difference

transcript_id	SwissProt_GeneName	LvM	MvH	LvH
DN6177_c1_g1_i1	.	7.39	-6.23	ns
DN3720_c0_g1_i13	ZN236_HUMAN	6.97	ns	6.59
DN5256_c1_g1_i2	NHSL1_HUMAN	8.77	-7.93	ns
DN868_c0_g1_i10	MCUR1_HUMAN	6.77	ns	ns
DN220579_c0_g1_i4	RYSR3_HUMAN	6.42	-5.66	ns
DN3854_c0_g1_i4	RAB1A_PIG	7.5	-8.21	ns
DN7007_c0_g1_i3	.	7.93	-8.44	ns
DN15746_c0_g1_i1	.	5.92	ns	5.68
DN5256_c1_g1_i8	NHSL1_HUMAN	-11.6	ns	-6.27
DN4480_c0_g1_i1	DCAF6_HUMAN	7.11	ns	6.4
DN1674_c0_g2_i2	MTMR6_HUMAN	7.71	ns	ns
DN4480_c0_g1_i8	DCAF6_HUMAN	6.77	ns	ns
DN18060_c0_g1_i6	VP26A_BOVIN	5.52	ns	ns
DN861_c2_g1_i5	CASP9_MOUSE	6.39	ns	ns
DN47_c0_g1_i10	TP53B_MOUSE	5.24	ns	ns
DN33794_c0_g1_i2	.	5.47	ns	ns
DN7987_c0_g1_i1	LRIF1_HUMAN	-6.63	ns	-6.27
DN643_c0_g1_i7	SGO1_XENLA	-6.61	ns	ns
DN15286_c0_g1_i8	KDM3A_CHICK	7.74	ns	ns
DN1962_c0_g1_i12	SYNE3_HUMAN	5.03	ns	ns
DN2397_c1_g1_i4	IRAK4_HUMAN	-5.86	8.07	ns
DN33986_c0_g1_i1	.	5.14	ns	ns
DN2256_c0_g1_i7	PP6R3_CHICK	6.45	ns	ns
DN17611_c0_g1_i10	.	-5.23	ns	-5.64
DN2238_c0_g1_i7	.	-5.66	ns	ns
DN5456_c0_g1_i9	C560_HUMAN	8.11	ns	ns
DN7361_c0_g1_i4	PCFT_XENLA	ns	7.52	ns
DN4162_c0_g1_i1	HNRPC_RAT	ns	7.67	ns
DN3362_c0_g1_i6	.	ns	8.7	ns
DN1386_c0_g1_i3	F264_HUMAN	ns	-8.96	ns
DN467_c0_g1_i14	IKKE_HUMAN	ns	6.47	ns
DN374_c0_g1_i10	YO9_ADEG1	ns	7.34	ns
DN1956_c0_g1_i7	LPIN1_MOUSE	ns	ns	7.99
DN114_c0_g1_i11	MISP_MOUSE	ns	ns	6.76
DN17295_c0_g2_i6	CLN3_CANLF	ns	ns	7.45
DN9768_c0_g1_i7	CCNE2_HUMAN	ns	ns	4.18
DN4847_c0_g1_i1	IF2M_BOVIN	ns	7.42	ns
DN7841_c1_g1_i3	.	ns	7.92	ns
DN5831_c0_g1_i4	CDT1_XENLA	ns	ns	8.27
DN308_c0_g1_i5	ZCHC2_HUMAN	ns	ns	6.25
DN597_c0_g1_i6	ATG9A_PONAB	ns	ns	12.42
DN784_c0_g2_i2	.	ns	ns	6.07
DN613_c2_g1_i7	MRVI1_HUMAN	ns	ns	8.93
DN2224_c0_g1_i1	.	ns	9.78	6.45
DN12393_c0_g1_i2	MCRS1_MOUSE	ns	ns	6.95

Table 2: Annotations for differentially expressed transcripts. ns denotes non-significant transcripts for each comparison and numerical values are the log(fold change) difference (*continued*)

transcript_id	SwissProt_GeneName	LvM	MvH	LvH
DN154_c3_g1_i4	.	ns	ns	9.93
DN6658_c2_g1_i10	.	ns	ns	6.25
DN2832_c0_g1_i12	.	ns	ns	7.09
DN2043_c0_g1_i3	KBR220_CHICK	ns	ns	4.88
DN3001_c0_g1_i6	PR15B_HUMAN	ns	ns	10.45
DN6883_c1_g1_i6	.	ns	ns	8.12
DN4679_c0_g1_i10	SMCA4_HUMAN	ns	4.57	3.35
DN14971_c0_g1_i9	DCC1_MOUSE	ns	ns	6.14
DN6423_c0_g1_i4	IFT74_HUMAN	ns	ns	10.45
DN11629_c0_g1_i9	.	ns	ns	6.57
DN1357_c0_g1_i11	DIC_HUMAN	ns	ns	3.63
DN10599_c0_g1_i1	PEDF_MOUSE	ns	9.93	8.36
DN9865_c0_g1_i2	FLII_MOUSE	ns	ns	5.22
DN89_c3_g1_i2	MEIS1_MOUSE	ns	7.07	7.95
DN1022_c0_g1_i18	S45A1_MOUSE	ns	ns	8.49
DN13672_c0_g1_i5	CD86_HUMAN	ns	7.34	ns
DN10663_c0_g1_i2	SIR5_CHICK	ns	6.3	5.19
DN8480_c0_g2_i2	ARI5B_CHICK	ns	7.6	8.4
DN3676_c0_g1_i10	CNOT6_XENLA	ns	ns	7.1
DN5083_c0_g1_i5	CHIC1_HUMAN	ns	ns	2.1
DN1230_c0_g1_i13	CFLAR_HUMAN	ns	ns	8.3
DN8461_c0_g2_i12	.	ns	ns	6.22
DN10078_c1_g1_i12	PARN_HUMAN	ns	4.16	5.17
DN7842_c0_g1_i8	ALG13_RAT	ns	6.53	5.13
DN15518_c0_g1_i8	SCNNB_PELSI	ns	6.66	5.47
DN6099_c0_g1_i3	SC22A_HUMAN	ns	8.62	9.52
DN347_c0_g1_i15	ERP44_HUMAN	ns	ns	10.5
DN606_c0_g1_i18	ICK_HUMAN	ns	ns	6.16
DN25095_c0_g1_i9	INT3_MOUSE	ns	4.6	3.66
DN5091_c0_g2_i6	ATL2_HUMAN	ns	6.47	5.38
DN2333_c1_g1_i1	F135A_HUMAN	ns	ns	8.32
DN3018_c0_g1_i18	KHK_RAT	ns	5.66	4.74
DN1128_c0_g1_i5	RCC1_HUMAN	ns	ns	7.19
DN130272_c0_g3_i2	CPTP_XENLA	ns	ns	6.72
DN885_c0_g1_i1	BUD31_RAT	ns	ns	9.75
DN7377_c0_g1_i8	ATAD3_BOVIN	ns	ns	6.56
DN25185_c0_g1_i5	.	ns	ns	5.93
DN7496_c1_g2_i7	RPR1A_CHICK	ns	ns	7.38
DN7817_c0_g1_i11	PROD_MOUSE	ns	ns	4.91
DN21_c0_g1_i11	BRD2_CANLF	ns	ns	3.17
DN3620_c0_g1_i11	AT132_HUMAN	ns	4.31	3.55
DN3101_c0_g2_i11	SOS1_HUMAN	ns	ns	4.81
DN143_c2_g1_i2	.	ns	7.74	6.66
DN18178_c0_g1_i6	PMGE_HUMAN	ns	ns	4.61
DN4309_c0_g1_i7	PCSK6_HUMAN	ns	5.97	5.19

Table 2: Annotations for differentially expressed transcripts. ns denotes non-significant transcripts for each comparison and numerical values are the log(fold change) difference (*continued*)

transcript_id	SwissProt_GeneName	LvM	MvH	LvH
DN2376_c1_g1_i6	AT8B2_HUMAN	ns	7.28	7.95
DN22798_c0_g1_i8	SNX17_DANRE	ns	ns	5.96
DN4275_c1_g1_i1	FGD2_HUMAN	ns	ns	8.18
DN3638_c0_g1_i3	ANR40_HUMAN	ns	ns	4.02
DN5255_c0_g2_i6	TMCC1_MOUSE	ns	ns	7.44
DN12268_c0_g1_i8	KYNU_HUMAN	ns	7.31	6.67
DN12360_c0_g1_i1	AGR2_PONAB	ns	ns	6.45
DN3262_c1_g1_i6	SBP2L_HUMAN	ns	ns	6.14
DN9334_c0_g1_i4	CARM1_HUMAN	ns	6.03	5.36
DN2785_c0_g1_i2	UBA5_CHICK	ns	ns	7.5
DN8881_c0_g1_i6	CRIM1_CHICK	ns	ns	6.7
DN582_c0_g1_i1	RAD21_BOVIN	ns	8.66	9.12
DN6333_c0_g1_i3	TTPAL_PONAB	ns	ns	7.93
DN751_c2_g2_i2	.	ns	ns	7.17
DN6089_c0_g2_i9	.	ns	6.91	6.28
DN7924_c0_g1_i6	CAMP1_HUMAN	ns	5.9	6.49
DN603_c0_g1_i9	TERT_CANLF	ns	ns	3.86
DN4235_c0_g1_i1	SIM13_DANRE	ns	3.84	3.36
DN2447_c4_g1_i3	.	ns	7.42	6.67
DN5702_c0_g1_i6	LMBL3_HUMAN	ns	ns	4.35
DN88100_c1_g2_i8	DCLK1_HUMAN	ns	ns	6.36
DN5373_c0_g1_i5	RGS3_RAT	ns	ns	5.67
DN10956_c0_g1_i1	MRC1_HUMAN	ns	ns	5.62
DN591_c2_g1_i10	KPB1_RABIT	ns	ns	9.31
DN1463_c0_g1_i8	FKBP7_PONAB	ns	4.84	4.28
DN2129_c0_g1_i12	OGFD2_DANRE	ns	6.6	7.24
DN2823_c0_g1_i12	PO210_MOUSE	ns	ns	5.08
DN15503_c0_g1_i2	POL_MLVFF	ns	5.33	5.73
DN21599_c0_g1_i6	MNS1_HUMAN	ns	5.35	5.8
DN6850_c1_g1_i3	ELMO2_HUMAN	ns	5.64	6.08
DN9837_c0_g1_i9	HOP2_HUMAN	ns	ns	4.59
DN3033_c0_g2_i8	CEP63_CHICK	ns	ns	5.83
DN682_c0_g3_i4	RRAGA_RAT	ns	5.62	5.94
DN5905_c0_g1_i6	B2L14_MOUSE	ns	ns	3.97
DN745_c0_g1_i22	SEPT7_PONAB	ns	ns	7.09
DN9743_c0_g1_i21	CXXC1_BOVIN	ns	ns	5.65
DN6804_c0_g1_i7	.	ns	4.68	4.99
DN10879_c1_g1_i8	RLF_HUMAN	ns	ns	7.33
DN4397_c0_g1_i1	.	ns	ns	4.74
DN133_c1_g1_i1	LRWD1_XENLA	ns	7.21	6.95
DN2036_c0_g1_i4	MBD2_HUMAN	ns	8.36	8.08
DN8539_c0_g1_i1	CHAC1_HUMAN	ns	5.79	5.43
DN5108_c0_g1_i1	TBC13_HUMAN	ns	ns	10.02
DN4247_c0_g1_i13	DPOG2_HUMAN	ns	5.63	5.39
DN18178_c0_g1_i3	PMGE_HUMAN	ns	ns	6.61

Table 2: Annotations for differentially expressed transcripts. ns denotes non-significant transcripts for each comparison and numerical values are the log(fold change) difference (*continued*)

transcript_id	SwissProt_GeneName	LvM	MvH	LvH
DN5860_c0_g1_i2	PACR_BOVIN	ns	6.09	5.87
DN3646_c0_g1_i1	COMT_MOUSE	ns	ns	4.4
DN3442_c1_g1_i3	VATB2_BOVIN	ns	ns	6.1
DN4008_c0_g1_i8	PTPRK_HUMAN	ns	ns	4.77
DN343_c1_g2_i2	.	ns	ns	3.77
DN2387_c1_g1_i3	.	ns	6.02	5.81
DN10398_c0_g1_i3	RHG29_DANRE	ns	ns	6.85
DN3358_c1_g1_i14	TRPS1_HUMAN	ns	ns	5.55
DN6364_c0_g1_i4	PLGT2_HUMAN	ns	ns	6.55
DN5692_c0_g1_i8	FA72A_BOVIN	ns	ns	5.49
DN1264_c0_g1_i2	REEP2_HUMAN	ns	6.68	6.45
DN21574_c0_g1_i1	.	ns	5.39	5.24
DN3490_c0_g1_i10	HYOU1_CHICK	ns	ns	4.51
DN208_c2_g2_i4	RBM28_MOUSE	ns	4.24	4.11
DN2519_c0_g1_i4	.	ns	6.47	6.61
DN3137_c0_g1_i9	S2536_CHICK	ns	5.66	5.8
DN2173_c0_g1_i4	HECD1_HUMAN	ns	2.16	2.06
DN6130_c0_g1_i8	GCN1_HUMAN	ns	5.53	5.65
DN3084_c0_g1_i13	.	ns	5.1	4.95
DN3044_c1_g1_i4	ANR26_HUMAN	ns	7.79	7.68
DN16556_c0_g1_i2	BICRL_MOUSE	ns	5.72	5.83
DN3733_c0_g1_i14	COG4_MOUSE	ns	ns	5.24
DN10513_c0_g1_i2	FBLN7_HUMAN	ns	ns	6.62
DN5456_c0_g1_i2	C560_HUMAN	ns	8.64	8.51
DN304_c0_g2_i4	ZN574_PONAB	ns	ns	5.61
DN10839_c0_g1_i3	RPAB5_MOUSE	ns	ns	6.27
DN1044_c0_g1_i3	ZN318_HUMAN	ns	7.39	7.49
DN7628_c0_g1_i2	DIEXF_CHICK	ns	8.2	8.14
DN751_c2_g3_i2	.	ns	ns	4.82
DN538_c1_g1_i1	TM41A_BOVIN	ns	ns	3.84
DN3594_c0_g1_i2	.	ns	8.06	8.11
DN7437_c0_g1_i8	PIRT_MOUSE	ns	ns	7.11
DN1929_c1_g1_i9	COOA1_HUMAN	ns	ns	4.38
DN9924_c0_g2_i7	.	ns	6.83	6.82
DN32038_c0_g1_i1	.	ns	ns	4.6

Table 3: Transcript functions

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN3720_c0_g1_i13	ZN236_HUMAN	Zinc finger protein 236;	KEGG:hsa:7776	NA
DN5256_c1_g1_i2	NHSL1_HUMAN	NHS-like protein 1;	KEGG:hsa:57224	NA
DN868_c0_g1_i10	MCUR1_HUMAN	Mitochondrial calcium uniporter regulator 1 {ECO:0000303 PubMed:23178883};	KEGG:hsa:63933	KO:K22137
DN220579_c0_g1_i4	RYR3_HUMAN	Ryanodine receptor 3;	KEGG:hsa:6263	KO:K04963
DN3854_c0_g1_i4	RAB1A_PIG	Ras-related protein Rab-1A;	KEGG:ssc:595116	KO:K07874
DN5256_c1_g1_i8	NHSL1_HUMAN	NHS-like protein 1;	KEGG:hsa:57224	NA
DN4480_c0_g1_i1	DCAF6_HUMAN	DDB1- and CUL4-associated factor 6;	KEGG:hsa:55827	KO:K11795
DN1674_c0_g2_i2	MTMR6_HUMAN	Myotubularin-related protein 6;	KEGG:hsa:9107	KO:K18083
DN4480_c0_g1_i8	DCAF6_HUMAN	DDB1- and CUL4-associated factor 6;	KEGG:hsa:55827	KO:K11795
DN18060_c0_g1_i6	VP26A_BOVIN	Vacuolar protein sorting-associated protein 26A;	KEGG:bta:510574	KO:K18466
DN861_c2_g1_i5	CASP9_MOUSE	Caspase-9;	KEGG:mmu:12371	KO:K04399
DN47_c0_g1_i10	TP53B_MOUSE	TP53-binding protein 1 {ECO:0000305};	KEGG:mmu:27223	KO:K20915
DN7987_c0_g1_i1	LRIF1_HUMAN	Ligand-dependent nuclear receptor-interacting factor 1 {ECO:0000305};	KEGG:hsa:55791	KO:K23220
DN643_c0_g1_i7	SGO1_XENLA	Shugoshin 1 {ECO:0000250 UniProtKB:Q5FBB7};	KEGG:xla:735145	KO:K11580
DN15286_c0_g1_i8	KDM3A_CHICK	Lysine-specific demethylase 3A;	KEGG:gga:422917	KO:K15601
DN1962_c0_g1_i12	SYNE3_HUMAN	Nesprin-3;	KEGG:hsa:161176	KO:K21761
DN2397_c1_g1_i4	IRAK4_HUMAN	Interleukin-1 receptor-associated kinase 4;	KEGG:hsa:51135	KO:K04733
DN2256_c0_g1_i7	PP6R3_CHICK	Serine/threonine-protein phosphatase 6 regulatory subunit 3;	KEGG:gga:423116	KO:K15501
DN5456_c0_g1_i9	C560_HUMAN	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial;	KEGG:ssc:100524676	KO:K00236
DN7361_c0_g1_i4	PCFT_XENLA	Proton-coupled folate transporter;	KEGG:dre:393255	KO:K14613

Table 3: Transcript functions (*continued*)

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN4162_c0_g1_i1	HNRPC_RAT	Heterogeneous nuclear ribonucleoprotein C {ECO:0000305};	KEGG:hsa:343069	NA
DN1386_c0_g1_i3	F264_HUMAN	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4;	KEGG:hsa:5210	KO:K19030
DN467_c0_g1_i14	IKKE_HUMAN	Inhibitor of nuclear factor kappa-B kinase subunit epsilon;	KEGG:hsa:9641	KO:K07211
DN374_c0_g1_i10	YO9_ADEG1	Uncharacterized protein ORF9;	KEGG:vg:1733469	NA
DN1956_c0_g1_i7	LPIN1_MOUSE	Phosphatidate phosphatase LPIN1;	KEGG:mmu:14245	KO:K15728
DN114_c0_g1_i11	MISP_MOUSE	Mitotic interactor and substrate of PLK1 {ECO:0000250 UniProtKB:Q8IVT2};	KEGG:mmu:78906	NA
DN17295_c0_g2_i6	CLN3_CANLF	Battenin;	.	NA
DN9768_c0_g1_i7	CCNE2_HUMAN	G1/S-specific cyclin-E2;	KEGG:hsa:9134	KO:K06626
DN4847_c0_g1_i1	IF2M_BOVIN	Translation initiation factor IF-2, mitochondrial;	KEGG:bta:281923	KO:K02519
DN5831_c0_g1_i4	CDT1_XENLA	DNA replication factor Cdt1;	KEGG:xla:398024	KO:K10727
DN308_c0_g1_i5	ZCHC2_HUMAN	Zinc finger CCHC domain-containing protein 2;	KEGG:hsa:54877	KO:K22700
DN597_c0_g1_i6	ATG9A_PONAB	Autophagy-related protein 9A;	KEGG:pon:100174344	KO:K17907
DN613_c2_g1_i7	MRVI1_HUMAN	Protein MRVI1;	KEGG:hsa:10335	KO:K12337
DN12393_c0_g1_i2	MCRS1_MOUSE	Microspherule protein 1;	KEGG:mmu:51812	KO:K11674
DN2043_c0_g1_i3	KBRS2_CHICK	NF-kappa-B inhibitor-interacting Ras-like protein 2;	KEGG:gga:420032	KO:K17197
DN3001_c0_g1_i6	PR15B_HUMAN	Protein phosphatase 1 regulatory subunit 15B;	.	NA
DN4679_c0_g1_i10	SMCA4_HUMAN	Transcription activator BRG1;	KEGG:bta:414274	KO:K11647
DN14971_c0_g1_i9	DCC1_MOUSE	Sister chromatid cohesion protein DCC1;	KEGG:mmu:72107	KO:K11271
DN6423_c0_g1_i4	IFT74_HUMAN	Intraflagellar transport protein 74 homolog;	KEGG:mmu:67694	KO:K19679

Table 3: Transcript functions (*continued*)

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN1357_c0_g1_i11	DIC_HUMAN	Mitochondrial dicarboxylate carrier;	KEGG:hsa:1468	KO:K13577
DN10599_c0_g1_i1	PEDF_MOUSE	Pigment epithelium-derived factor;	KEGG:mmu:20317	KO:K19614
DN9865_c0_g1_i2	FLII_MOUSE	Protein flightless-1 homolog;	KEGG:mmu:14248	NA
DN89_c3_g1_i2	MEIS1_MOUSE	Homeobox protein Meis1;	KEGG:mmu:17268	KO:K15613
DN1022_c0_g1_i18	S45A1_MOUSE	Proton-associated sugar transporter A;	KEGG:hsa:50651	KO:K15378
DN13672_c0_g1_i5	CD86_HUMAN	T-lymphocyte activation antigen CD86;	KEGG:hsa:942	KO:K05413
DN10663_c0_g1_i2	SIR5_CHICK	NAD-dependent protein deacylase sirtuin-5, mitochondrial {ECO:0000255 HAMAP-Rule:MF_03160};	KEGG:gga:420834	KO:K11415
DN8480_c0_g2_i2	ARI5B_CHICK	AT-rich interactive domain-containing protein 5B;	KEGG:gga:423661	NA
DN3676_c0_g1_i10	CNOT6_XENLA	CCR4-NOT transcription complex subunit 6;	KEGG:rno:287249	KO:K12603
DN5083_c0_g1_i5	CHIC1_HUMAN	Cysteine-rich hydrophobic domain-containing protein 1;	KEGG:hsa:53344	NA
DN1230_c0_g1_i13	CFLAR_HUMAN	CASP8 and FADD-like apoptosis regulator;	KEGG:hsa:8837	KO:K04724
DN10078_c1_g1_i12	PARN_HUMAN	Poly(A)-specific ribonuclease PARN;	KEGG:hsa:5073	KO:K01148
DN7842_c0_g1_i8	ALG13_RAT	UDP-N-acetylglucosamine transferase subunit ALG13 homolog;	KEGG:rno:300284	KO:K07432
DN15518_c0_g1_i8	SCNNB_PELSI	Amiloride-sensitive sodium channel subunit beta;	.	NA
DN6099_c0_g1_i3	SC22A_HUMAN	Vesicle-trafficking protein SEC22a;	KEGG:hsa:26984	KO:K08520
DN347_c0_g1_i15	ERP44_HUMAN	Endoplasmic reticulum resident protein 44;	KEGG:hsa:23071	KO:K17264

Table 3: Transcript functions (*continued*)

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN606_c0_g1_i18	ICK_HUMAN	Serine/threonine-protein kinase ICK;	KEGG:hsa:22858	KO:K08828
DN25095_c0_g1_i9	INT3_MOUSE	Integrator complex subunit 3;	KEGG:mmu:229543	KO:K13140
DN5091_c0_g2_i6	ATL2_HUMAN	ADAMTS-like protein 2;	KEGG:hsa:9719	NA
DN2333_c1_g1_i1	F135A_HUMAN	Protein FAM135A;	KEGG:hsa:57579	NA
DN3018_c0_g1_i18	KHK_RAT	Ketohexokinase {ECO:0000312 RGD:2966};	KEGG:hsa:3795	KO:K00846
DN1128_c0_g1_i5	RCC1_HUMAN	Regulator of chromosome condensation;	KEGG:hsa:1104	KO:K11493
DN130272_c0_g3_i2	CPTP_XENLA	Ceramide-1-phosphate transfer protein;	KEGG:xla:735049	NA
DN885_c0_g1_i1	BUD31_RAT	Protein BUD31 homolog;	KEGG:rno:89819	KO:K12873
DN7377_c0_g1_i8	ATAD3_BOVIN	ATPase family AAA domain-containing protein 3;	KEGG:bta:784353	KO:K17681
DN7496_c1_g2_i7	RPR1A_CHICK	Regulation of nuclear pre-mRNA domain-containing protein 1A;	KEGG:gga:420953	NA
DN7817_c0_g1_i11	PROD_MOUSE	Proline dehydrogenase 1, mitochondrial;	KEGG:mmu:19125	KO:K00318
DN21_c0_g1_i11	BRD2_CANLF	Bromodomain-containing protein 2;	KEGG:cfa:474868	KO:K08871
DN3620_c0_g1_i11	AT132_HUMAN	Cation-transporting ATPase 13A2;	KEGG:hsa:23400	KO:K13526
DN3101_c0_g2_i11	SOS1_HUMAN	Son of sevenless homolog 1;	KEGG:hsa:6654	KO:K03099
DN18178_c0_g1_i6	PMGE_HUMAN	Bisphosphoglycerate mutase;	KEGG:hsa:669	KO:K01837
DN4309_c0_g1_i7	PCSK6_HUMAN	Proprotein convertase subtilisin/kexin type 6;	KEGG:hsa:5046	KO:K08672
DN2376_c1_g1_i6	AT8B2_HUMAN	Phospholipid-transporting ATPase ID;	KEGG:hsa:57198	KO:K01530
DN22798_c0_g1_i8	SNX17_DANRE	Sorting nexin-17;	KEGG:dre:568263	KO:K17929
DN4275_c1_g1_i1	FGD2_HUMAN	FYVE, RhoGEF and PH domain-containing protein 2;	KEGG:mmu:26382	KO:K05721
DN3638_c0_g1_i3	ANR40_HUMAN	Ankyrin repeat domain-containing protein 40;	KEGG:hsa:6452	KO:K07984

Table 3: Transcript functions (*continued*)

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN5255_c0_g2_i6	TMCC1_MOUSE	Transmembrane and coiled-coil domains protein 1	KEGG:mmu:330401	NA
DN12268_c0_g1_i8	KYNU_HUMAN	{ECO:0000250 UniProtKB:O94876}; Kynureninase	KEGG:hsa:8942	KO:K01556
DN12360_c0_g1_i1	AGR2_PONAB	{ECO:0000255 HAMAP-Rule:MF_03017}; Anterior gradient protein 2 homolog;	KEGG:pon:100174601	KO:K20356
DN3262_c1_g1_i6	SBP2L_HUMAN	Selenocysteine insertion sequence-binding protein 2-like;	KEGG:hsa:9728	NA
DN9334_c0_g1_i4	CARM1_HUMAN	Histone-arginine methyltransferase CARM1;	KEGG:hsa:10498	KO:K05931
DN2785_c0_g1_i2	UBA5_CHICK	Ubiquitin-like modifier-activating enzyme 5;	KEGG:gga:414879	KO:K12164
DN8881_c0_g1_i6	CRIM1_CHICK	Cysteine-rich motor neuron 1 protein;	KEGG:gga:395067	NA
DN582_c0_g1_i1	RAD21_BOVIN	Double-strand-break repair protein rad21 homolog;	KEGG:bta:540966	KO:K06670
DN6333_c0_g1_i3	TTPAL_PONAB	Alpha-tocopherol transfer protein-like;	KEGG:pon:100171424	NA
DN7924_c0_g1_i6	CAMP1_HUMAN	Calmodulin-regulated spectrin-associated protein 1;	KEGG:hsa:157922	KO:K17493
DN603_c0_g1_i9	TERT_CANLF	Telomerase reverse transcriptase;	KEGG:cfa:403412	KO:K11126
DN4235_c0_g1_i1	SIM13_DANRE	Small integral membrane protein 13;	KEGG:hsa:221710	NA
DN5702_c0_g1_i6	LMBL3_HUMAN	Lethal(3)malignant brain tumor-like protein 3;	KEGG:hsa:84456	NA
DN88100_c1_g2_i8	DCLK1_HUMAN	Serine/threonine-protein kinase DCLK1;	KEGG:hsa:9201	KO:K08805
DN5373_c0_g1_i5	RGS3_RAT	Regulator of G-protein signaling 3;	KEGG:rno:54293	KO:K07524
DN10956_c0_g1_i1	MRC1_HUMAN	Macrophage mannose receptor 1;	KEGG:hsa:4360	KO:K06560

Table 3: Transcript functions (*continued*)

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN591_c2_g1_i10	KPB1_RABIT	Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform;	KEGG:ocu:100303771	KO:K07190
DN1463_c0_g1_i8	FKBP7_PONAB	Peptidyl-prolyl cis-trans isomerase FKBP7;	KEGG:mmu:14231	KO:K09573
DN2129_c0_g1_i12	OGFD2_DANRE	2-oxoglutarate and iron-dependent oxygenase domain-containing protein 2;	KEGG:dre:790923	NA
DN2823_c0_g1_i12	PO210_MOUSE	Nuclear pore membrane glycoprotein 210;	KEGG:rno:58958	KO:K14314
DN15503_c0_g1_i2	POL_MLVFF	Gag-Pol polyprotein;	KEGG:vg:1491877	NA
DN21599_c0_g1_i6	MNS1_HUMAN	Meiosis-specific nuclear structural protein 1;	KEGG:mmu:17427	NA
DN6850_c1_g1_i3	ELMO2_HUMAN	Engulfment and cell motility protein 2;	KEGG:hsa:63916	KO:K18985
DN9837_c0_g1_i9	HOP2_HUMAN	Homologous-pairing protein 2 homolog;	KEGG:hsa:29893	KO:K06695
DN3033_c0_g2_i8	CEP63_CHICK	Centrosomal protein of 63 kDa;	.	NA
DN682_c0_g3_i4	RRAGA_RAT	Ras-related GTP-binding protein A {ECO:0000305};	KEGG:rno:117044	KO:K16185
DN5905_c0_g1_i6	B2L14_MOUSE	Apoptosis facilitator Bcl-2-like protein 14;	KEGG:mmu:66813	NA
DN745_c0_g1_i22	SEPT7_PONAB	Septin-7;	KEGG:pon:100173884	KO:K16944
DN9743_c0_g1_i21	CXXC1_BOVIN	CXXC-type zinc finger protein 1;	KEGG:bta:511446	KO:K14960
DN10879_c1_g1_i8	RLF_HUMAN	Zinc finger protein Rlf;	KEGG:hsa:6018	NA
DN133_c1_g1_i1	LRWD1_XENLA	Leucine-rich repeat and WD repeat-containing protein 1;	KEGG:xtr:100145159	NA
DN2036_c0_g1_i4	MBD2_HUMAN	Methyl-CpG-binding domain protein 2 {ECO:0000305};	KEGG:hsa:8932	KO:K11590
DN8539_c0_g1_i1	CHAC1_HUMAN	Glutathione-specific gamma-glutamylcyclotransferase 1 {ECO:0000303 PubMed:27913623};	KEGG:hsa:79094	KO:K07232
DN5108_c0_g1_i1	TBC13_HUMAN	TBC1 domain family member 13;	KEGG:hsa:54662	NA

Table 3: Transcript functions (*continued*)

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN4247_c0_g1_i13	DPOG2_HUMAN	DNA polymerase subunit gamma-2, mitochondrial;	KEGG:bta:505152	KO:K02333
DN18178_c0_g1_i3	PMGE_HUMAN	Bisphosphoglycerate mutase;	KEGG:hsa:669	KO:K01837
DN5860_c0_g1_i2	PACR_BOVIN	Pituitary adenylate cyclase-activating polypeptide type I receptor;	KEGG:bta:319095	KO:K04587
DN3646_c0_g1_i1	COMT_MOUSE	Catechol O-methyltransferase;	KEGG:mmu:12846	KO:K00545
DN3442_c1_g1_i3	VATB2_BOVIN	V-type proton ATPase subunit B, brain isoform;	KEGG:rno:117596	KO:K02147
DN4008_c0_g1_i8	PTPRK_HUMAN	Receptor-type tyrosine-protein phosphatase kappa;	KEGG:hsa:5796	KO:K06776
DN10398_c0_g1_i3	RHG29_DANRE	Rho GTPase-activating protein 29;	KEGG:hsa:9411	KO:K20644
DN3358_c1_g1_i14	TRPS1_HUMAN	Zinc finger transcription factor Trps1;	KEGG:hsa:7227	KO:K22040
DN6364_c0_g1_i4	PLGT2_HUMAN	Protein O-glucosyltransferase 2 {ECO:0000305 PubMed:30127001};	KEGG:hsa:79070	NA
DN5692_c0_g1_i8	FA72A_BOVIN	Protein FAM72A;	KEGG:bta:616965	NA
DN1264_c0_g1_i2	REEP2_HUMAN	Receptor expression-enhancing protein 2;	KEGG:hsa:51308	KO:K17338
DN3490_c0_g1_i10	HYOU1_CHICK	Hypoxia up-regulated protein 1;	KEGG:gga:428251	KO:K09486
DN208_c2_g2_i4	RBM28_MOUSE	RNA-binding protein 28;	KEGG:mmu:68272	KO:K14573
DN3137_c0_g1_i9	S2536_CHICK	Solute carrier family 25 member 36;	KEGG:gga:424817	KO:K15116
DN2173_c0_g1_i4	HECD1_HUMAN	E3 ubiquitin-protein ligase HECD1;	KEGG:hsa:25831	KO:K12231
DN6130_c0_g1_i8	GCN1_HUMAN	eIF-2-alpha kinase activator GCN1 {ECO:0000250 UniProtKB:E9PVA8};	KEGG:hsa:10985	NA
DN3044_c1_g1_i4	ANR26_HUMAN	Ankyrin repeat domain-containing protein 26 {ECO:0000305};	KEGG:hsa:22852	NA

Table 3: Transcript functions (*continued*)

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN16556_c0_g1_i2	BICRL_MOUSE	BRD4-interacting chromatin-remodeling complex-associated protein-like {ECO:0000250 UniProtKB:Q6AI39};	KEGG:mmu:210982	NA
DN3733_c0_g1_i14	COG4_MOUSE	Conserved oligomeric Golgi complex subunit 4;	KEGG:mmu:102339	KO:K20291
DN10513_c0_g1_i2	FBLN7_HUMAN	Fibulin-7;	KEGG:hsa:129804	KO:K17342
DN5456_c0_g1_i2	C560_HUMAN	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial;	KEGG:ssc:100524676	KO:K00236
DN304_c0_g2_i4	ZN574_PONAB	Zinc finger protein 574;	KEGG:pon:100173939	NA
DN10839_c0_g1_i3	RPAB5_MOUSE	DNA-directed RNA polymerases I, II, and III subunit RPABC5;	KEGG:mmu:66491	KO:K03007
DN1044_c0_g1_i3	ZN318_HUMAN	Zinc finger protein 318;	KEGG:hsa:24149	NA
DN7628_c0_g1_i2	DIEXF_CHICK	Digestive organ expansion factor homolog;	KEGG:gga:421384	KO:K14774
DN538_c1_g1_i1	TM41A_BOVIN	Transmembrane protein 41A;	KEGG:bta:505368	NA
DN7437_c0_g1_i8	PIRT_MOUSE	Phosphoinositide-interacting protein;	KEGG:mmu:193003	NA
DN1929_c1_g1_i9	COOA1_HUMAN	Collagen alpha-1(XXIV) chain;	KEGG:hsa:255631	KO:K19721

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0000002	mitochondrial genome maintenance	87	2	0.10	0.00434	0.004340	BP	MvH.I5
GO:0000262	mitochondrial chromosome	9	1	0.01	0.0096	0.009600	CC	MvH.I5
GO:0000777	condensed chromosome kinetochore	371	2	0.13	0.00736	0.007360	CC	LvM.I5
GO:0001740	Barr body	23	1	0.01	0.00805	0.008050	CC	LvM.I5
GO:0003839	gamma-glutamylcyclotransferase activity	8	1	0.01	0.0089	0.008900	MF	MvH.I5
GO:0004082	bisphosphoglycerate mutase activity	6	2	0.01	9.2e-05	0.000092	MF	LvH.I5
GO:0004535	poly(A)-specific ribonuclease activity	40	2	0.10	0.0045	0.004500	MF	LvH.I5
GO:0004619	phosphoglycerate mutase activity	6	2	0.01	9.2e-05	0.000092	MF	LvH.I5
GO:0004999	vasoactive intestinal polypeptide recept...	8	1	0.01	0.0089	0.008900	MF	MvH.I5
GO:0005149	interleukin-1 receptor binding	22	1	0.01	0.0080	0.008000	MF	LvM.I5
GO:0005219	ryanodine-sensitive calcium-release chan...	20	1	0.01	0.0072	0.007200	MF	LvM.I5
GO:0005749	mitochondrial respiratory chain complex ...	19	1	0.01	0.00666	0.006660	CC	LvM.I5
GO:0005788	endoplasmic reticulum lumen	525	5	1.27	0.0091	0.009100	CC	LvH.I5
GO:0006000	fructose metabolic process	49	2	0.05	0.00140	0.001400	BP	MvH.I5
GO:0006121	mitochondrial electron transport, succin...	15	1	0.01	0.0066	0.006600	BP	LvM.I5
GO:0007354	zygotic determination of anterior/poster...	5	1	0.01	0.00559	0.005590	BP	MvH.I5
GO:0007568	aging	740	4	0.83	0.00945	0.009450	BP	MvH.I5
GO:0007614	short-term memory	21	2	0.05	0.0012	0.001200	BP	LvH.I5
GO:0008177	succinate dehydrogenase (ubiquinone) act...	16	1	0.01	0.0058	0.005800	MF	LvM.I5
GO:0008327	methyl-CpG binding	50	2	0.12	0.0070	0.007000	MF	LvH.I5
GO:0008327	methyl-CpG binding	50	2	0.06	0.0014	0.001400	MF	MvH.I5
GO:0010043	response to zinc ion	79	2	0.09	0.00359	0.003590	BP	MvH.I5
GO:0015269	calcium-activated potassium channel acti...	19	1	0.01	0.0069	0.006900	MF	LvM.I5
GO:0016243	regulation of autophagosome size	8	1	0.01	0.00894	0.008940	BP	MvH.I5
GO:0016514	SWI/SNF complex	98	2	0.11	0.0050	0.005000	CC	MvH.I5
GO:0016823	hydrolase activity, acting on acid carbo...	6	1	0.01	0.0067	0.006700	MF	MvH.I5
GO:0019048	modulation by virus of host process	100	2	0.11	0.00568	0.005680	BP	MvH.I5
GO:0019442	tryptophan catabolic process to acetyl-C...	6	1	0.01	0.00671	0.006710	BP	MvH.I5
GO:0019805	quinolinate biosynthetic process	8	1	0.01	0.00894	0.008940	BP	MvH.I5
GO:0019842	vitamin binding	314	3	0.35	0.0052	0.005200	MF	MvH.I5
GO:0030374	nuclear receptor transcription coactivat...	238	4	0.59	0.0031	0.003100	MF	LvH.I5
GO:0030374	nuclear receptor transcription coactivat...	238	2	0.09	0.0033	0.003300	MF	LvM.I5

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched) (*continued*)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0030906	retromer, cargo-selective complex	9	1	0.00	0.00316	0.003160	CC	LvM.I5
GO:0031514	motile cilium	261	4	0.63	0.0038	0.003800	CC	LvH.I5
GO:0031667	response to nutrient levels	1155	5	1.30	0.00930	0.009300	BP	MvH.I5
GO:0032902	nerve growth factor production	6	1	0.01	0.00671	0.006710	BP	MvH.I5
GO:0043231	intracellular membrane-bounded organelle	29684	16	10.43	0.00248	0.002480	CC	LvM.I5
GO:0043293	apoptosome	9	1	0.00	0.00316	0.003160	CC	LvM.I5
GO:0043420	anthranilate metabolic process	6	1	0.01	0.00671	0.006710	BP	MvH.I5
GO:0044030	regulation of DNA methylation	48	2	0.12	0.0062	0.006200	BP	LvH.I5
GO:0045404	positive regulation of interleukin-4 bio...	7	1	0.01	0.00782	0.007820	BP	MvH.I5
GO:0048763	calcium-induced calcium release activity	24	1	0.01	0.0087	0.008700	MF	LvM.I5
GO:0048821	erythrocyte development	94	3	0.23	0.0016	0.001600	BP	LvH.I5
GO:0050916	sensory perception of sweet taste	7	1	0.01	0.00782	0.007820	BP	MvH.I5
GO:0051091	positive regulation of DNA-binding trans...	607	4	0.68	0.00476	0.004760	BP	MvH.I5
GO:0055067	monovalent inorganic cation homeostasis	331	4	0.81	0.0091	0.009100	BP	LvH.I5
GO:0061621	canonical glycolysis	39	2	0.10	0.0042	0.004200	BP	LvH.I5
GO:0061649	ubiquitin modification-dependent histone...	26	1	0.01	0.0094	0.009400	MF	LvM.I5
GO:0061928	glutathione specific gamma-glutamylcyclo...	7	1	0.01	0.0078	0.007800	MF	MvH.I5
GO:0070124	mitochondrial translational initiation	7	1	0.01	0.00782	0.007820	BP	MvH.I5
GO:0070577	lysine-acetylated histone binding	86	3	0.21	0.0013	0.001300	MF	LvH.I5
GO:0070577	lysine-acetylated histone binding	86	2	0.10	0.0042	0.004200	MF	MvH.I5
GO:0071168	protein localization to chromatin	99	3	0.24	0.0019	0.001900	BP	LvH.I5
GO:0071168	protein localization to chromatin	99	3	0.11	0.00019	0.000190	BP	MvH.I5
GO:0071248	cellular response to metal ion	389	3	0.44	0.00952	0.009520	BP	MvH.I5
GO:0071466	cellular response to xenobiotic stimulus	307	2	0.14	0.0081	0.008100	BP	LvM.I5
GO:0071962	mitotic sister chromatid cohesion, centr...	19	1	0.01	0.0084	0.008400	BP	LvM.I5
GO:0080008	Cul4-RING E3 ubiquitin ligase complex	128	2	0.04	0.00092	0.000920	CC	LvM.I5
GO:0090367	negative regulation of mRNA modification	7	1	0.01	0.00782	0.007820	BP	MvH.I5
GO:0106018	phosphatidylinositol-3,5-bisphosphate ph...	26	1	0.01	0.0094	0.009400	MF	LvM.I5
GO:0110008	ncRNA deadenylation	7	1	0.01	0.00782	0.007820	BP	MvH.I5
GO:1903135	cupric ion binding	6	1	0.01	0.0067	0.006700	MF	MvH.I5
GO:1990826	nucleoplasmic periphery of the nuclear p...	7	1	0.01	0.0075	0.007500	CC	MvH.I5

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched) (*continued*)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:1990827	deaminase binding	7	1	0.01	0.0078	0.007800	MF	MvH.I5
GO:1990938	peptidyl-aspartic acid autophosphorylati...	8	1	0.01	0.00894	0.008940	BP	MvH.I5

Shed Level Late Stage Infection - Bursa - Gene

Amanda Dolinski & Jared J. Homola

23 March, 2021

This is an analysis of differential expression at the gene level between between low, moderate, and high LPAIV shedding blue-winged teals based on cloacal swab virus titers averaged across 1-5 days post-infection (DPI) for bursa samples collected on 5 DPI.

Differential expression analysis

Table 1: Count of DE genes. For a gene to be considered differentially expressed, we require a p-value of 0.1 with a false discovery rate correction and a log fold change difference of 1.0.

Direction	Comparison	N
Down	LvM	0
Up	LvM	1
Down	MvH	0
Up	MvH	0
Down	LvH	0
Up	LvH	0

Volcano plot

Volcano plot reporting $-\log_{10}(\text{p-values})$ as a function of $\log_2(\text{fold change})$ between the samples ($\log_{2}\text{FC}$, x axis). Genes that are identified as significantly differentially expressed following a false discovery rate correction ($q = 0.10$) are shown in red

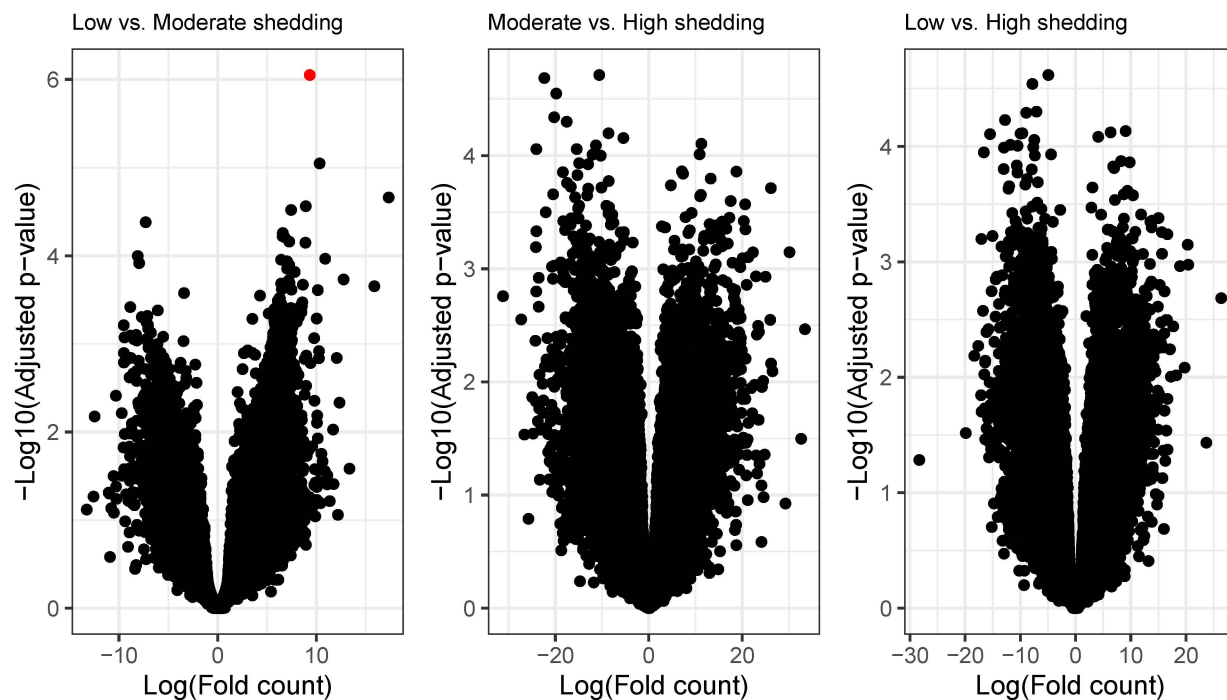


Table 2: Annotations for differentially expressed genes. ns denotes non-significant genes for each comparison and numerical values are the $\log_2(\text{fold change})$ difference

gene_id	SwissProt_GeneName	LvM	MvH	LvH
DN24349_c0_g3	.	9.33	ns	ns

Shed Level Late Stage Infection - Bursa - Transcript

Amanda Dolinski & Jared J. Homola

23 March, 2021

This is an analysis of differential expression at the transcript level between between low, moderate, and high LPAIV shedding blue-winged teals based on cloacal swab virus titers averaged across 1-5 days post-infection (DPI) for bursa samples collected on 5 DPI.

Differential expression analysis

Table 1: Count of DE transcripts. For a transcript to be considered differentially expressed, we require a p-value of 0.1 with a false discovery rate correction and a log fold change difference of 1.0.

Direction	Comparison	N
Down	LvM	0
Up	LvM	2
Down	MvH	0
Up	MvH	0
Down	LvH	0
Up	LvH	0

Volcano plot

Volcano plot reporting $-\log_{10}(\text{p-values})$ as a function of $\log_2(\text{fold change})$ between the samples ($\log\text{FC}$, x axis). Transcripts that are identified as significantly differentially expressed following a false discovery rate correction ($q = 0.10$) are shown in red

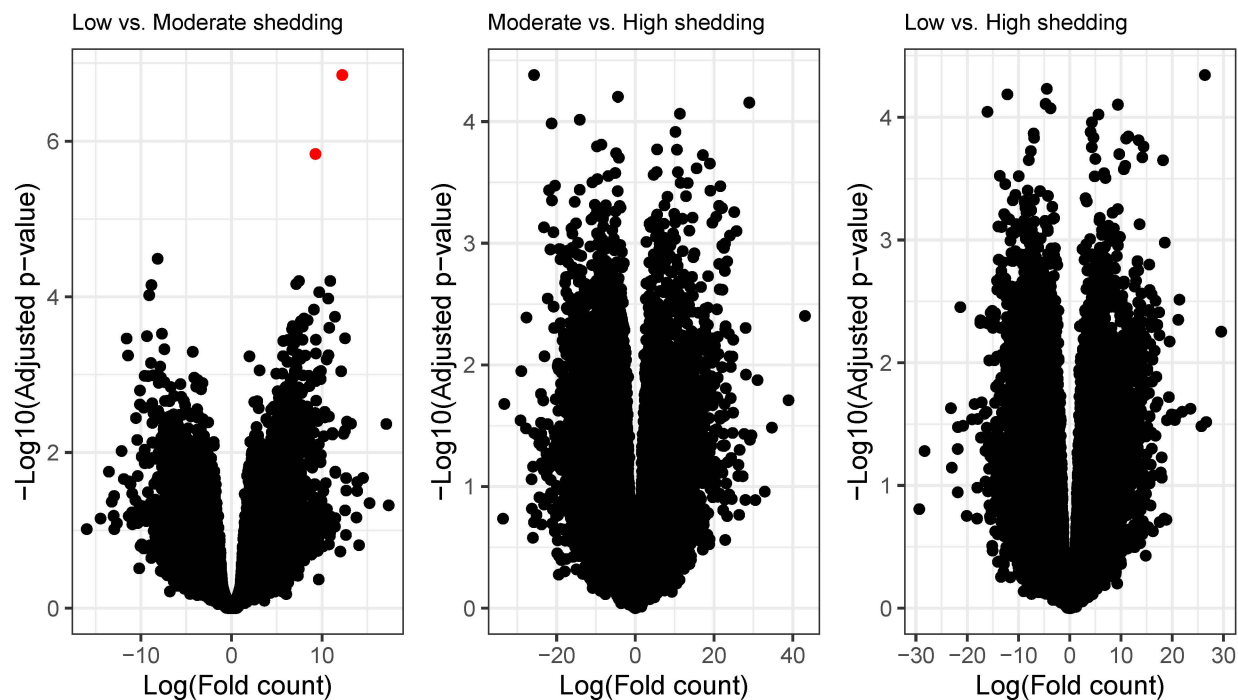


Table 2: Annotations for differentially expressed transcripts. ns denotes non-significant transcripts for each comparison and numerical values are the $\log(\text{fold change})$ difference

transcript_id	SwissProt_GeneName	LvM	MvH	LvH
DN347_c0_g1_i15	ERP44_HUMAN	12.23	ns	ns
DN1233_c0_g1_i7	SPT20_MOUSE	9.28	ns	ns

Table 3: Transcript functions

	SwissProt_GeneName	SwissProt_GeneFunction	KEGG_ID	KO_ID
DN347_c0_g1_i15	ERP44_HUMAN	Endoplasmic reticulum resident protein 44;	KEGG:hsa:23071	KO:K17264
DN1233_c0_g1_i7	SPT20_MOUSE	Spermatogenesis-associated protein 20;	KEGG:mmu:217116	NA

Table 4: Gene Ontology enrichment analysis: GO terms with p-values <0.05 were determined as over-represented (enriched)

GO.ID	Term	Annotated	Significant	Expected	elimFisher	pVal	Domain	Comparison
GO:0003756	protein disulfide isomerase activity	44	1	0	0.0024	0.0024	MF	LvM.I5
GO:0035580	specific granule lumen	51	1	0	0.0025	0.0025	CC	LvM.I5