

¹ Host Turkey B-cell Transcriptomics During THEV Infection
² Highlights Upregulated Cell Death and Breakdown Pathways
³ That May Mediate Immunosuppression

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16 **ABSTRACT**

17 **INTRODUCTION**

18 Turkey hemorrhagic enteritis virus (THEV), belonging to the family *Adenoviridae*, genus *Siadenovirus*,
19 infects turkeys, chickens, and pheasants (1, 2). Infecting its hosts via the feco-oral route, THEV causes
20 hemorrhagic enteritis (HE) in turkeys, a debilitating disease affecting predominantly 6-12-week-old turkey
21 pouls characterized by immunosuppression (IMS), depression, splenomegaly, intestinal lesions leading to
22 bloody droppings, and up to 80% mortality (3–6). The clinical disease usually persists in affected flocks for
23 about 7-10 days. However, secondary bacterial infections may extend the duration of illness and mortality for
24 an additional 2-3 weeks due to the immunosuppressive nature of the virus, exacerbating the economic losses
25 (5, 7). Low pathogenic (avirulent) strains of THEV have been isolated, which show subclinical infections
26 but retain the immunosuppressive effects. Since its isolation from a pheasant spleen, the Virginia Avirulent
27 Strain (VAS) has been used effectively as a live vaccine despite the immunosuppressive side-effects, but
28 the vaccinated birds are rendered more susceptible to opportunistic infections and death than unvaccinated
29 cohorts leading to significant economic losses (4, 5, 8–10).

30 It is well-established that THEV primarily infects and replicates in turkey B-cells of the bursa and spleen and
31 somewhat in macrophages, inducing apoptosis and necrosis. Consequently, a significant drop in number of
32 B-cells (specifically, IgM+ B-cells) and macrophages ensue along with increased T-cell counts with abnormal
33 T-cell subpopulation (CD4+ and CD8+) ratios. The cell death seen in the B-cells and macrophages is
34 generally proposed as the major cause of THEV-induced IMS as both humoral and cell-mediated immunity
35 are impaired (5, 6, 8, 11). It is also thought that the virus replication in the spleen attracts T-cells and
36 peripheral blood macrophages to the spleen where the T-cells are activated by cytokines from activated
37 macrophages and vice versa. The activated T-cells undergo clonal expansion and secrete interferons: type I
38 (IFN- α and IFN- β) and type II (IFN- γ) as well as tumor necrosis factor (TNF) while activated macrophages
39 secrete interleukin 6 (IL-6), TNF, and nitric oxide (NO), an antiviral agent with immunosuppressive properties.
40 The inflammatory cytokines released by T-cells and macrophages (e.g., TNF and IL-6) may also induce
41 apoptosis in bystander splenocytes, exacerbating the already numerous apoptotic and necrotic splenocytes,
42 culminating in IMS (8, 11) (see **Figure 1**). However, the precise molecular mechanisms of THEV-induced
43 IMS or pathways involved are poorly understood (6). Elucidating the specific mechanisms and pathways of
44 THEV-induced IMS is the most crucial step in THEV research as it will present a means of mitigating the IMS.
45 Next generation sequencing (NGS) is a groundbreaking technology that has significantly enhanced our
46 understanding of DNA and RNA structure and function and facilitated exceptional advancements in all
47 domains of biology and the Life Sciences (12). mRNA sequencing (RNA-seq), an NGS approach to
48 transcriptomic studies, is a versatile, high throughput, and cost-effective technology that allows a broad scan

49 of the entire transcriptome, thereby uncovering the active genes and molecular pathways and processes.
50 This technology has been leveraged in an ever increasing number of studies to elucidate active cellular
51 processes under a wide range of treatment conditions, including the transcriptomics of viral infections (12–16).
52 In RNA-seq studies, differentially expressed genes (DEGs) identified under different experimental conditions
53 are key to unlocking the interesting biology or mechanism under study. Identified DEGs are typically used for
54 functional enrichment analysis in large curated knowledgebases which connect genes to specific biological
55 processes, functions, and pathways such as gene ontology (GO) and Kyoto Encyclopedia of Genes and
56 Genomes (KEGG) pathways, shedding light on the biological question under study (17, 18).
57 To the best of our knowledge, no study has leveraged the wealth of information offered by RNA-seq to
58 elucidate the molecular mechanisms and pathways leading to THEV-induced IMS. To effectively counteract
59 the immunosuppressive effect of the vaccine, it is essential to unravel the host mechanisms/pathways
60 influenced by the virus to bring about IMS. In this study, we present the first transcriptomic profile of a
61 THEV infection using paired-end RNA-seq in a turkey B-cell line (MDTC-RP19), highlighting key host genes,
62 cellular/molecular processes and pathways affected during a THEV infection. Our RNA-seq yielded 149 bp
63 long high quality (mean PHRED Score of 36) sequences from each end of cDNA fragments, which were
64 mapped to the genome of domestic turkey (*Meleagris gallopavo*).

65 **RESULTS**

66 **Sequencing Results**

67 To identify the host transcriptome profile during THEV infection, MDTC-RP19 cells were THEV-infected
68 or mock-infected in triplicates or duplicates, respectively, and collected in like manner at 4-, 12-, 24-, and
69 72-hours post infection (hpi). mRNAs extracted from mock- or THEV-infected cells were sequenced on the
70 Illumina platform, yielding a total of **776.1** million raw reads (149 bp in length) across all samples (statistics
71 for the sequencing reads obtained from each RNA library are presented in **Table 1**). After trimming off
72 low-quality reads, the remaining **742.8** million total paired-end trimmed reads (approximately, **34.7-47.9**
73 million reads per sample) were mapped to the genome of *Meleagris gallopavo* obtained from the National
74 Center for Biotechnology Information (NCBI). The percentage of reads mapping to the host genome across
75 all samples ranged from **32.4-89.2%**. Although our sequencing reads have excellent quality scores (see
76 **Table 1**) at all time points, the DEGs identified at 4- and 72-hpi did not yield any results in the functional
77 enrichment analyses (i.e, GO term and KEGG pathway analysis); hence, they were excluded from all
78 subsequent analyses. In the remaining samples from 12- and 24-hpi, there is a high correlation was seen
79 between biological replicates (**Figure 2A** and **B**)

80 **DEGs of THEV-infected Versus Mock-infected Cells**

81 Gene expression levels were estimated with the StringTie software (19) in Fragments per kilobase of
82 transcript per million (FPKM) units. The analysis of DEGs was performed with the DESeq2 R package (20)
83 which employs negative binomial distribution model for read count comparisons. Using a P_{adjusted} -value
84 cutoff ≤ 0.05 as the inclusion criteria, a total of **2,343** and **3,295** genes were identified as differentially
85 expressed at 12-hpi and 24-hpi, respectively. ~~DEG analyses results at 12 and 24 hpi are presented in~~
86 ~~Supplementary Tables 1 and 2~~, respectively. At 12-hpi, **1,079** genes were upregulated and **1,264** genes
87 downregulated, whereas **1,512** genes were upregulated and **1,783** genes downregulated at 24-hpi (**Figure**
88 **2C**, and **Figure 3A-C**). The log₂fold-change(FC) values at 12-hpi ranged between **-1.4** and **+1.7** for **TMEM156**
89 (**Transmembrane Protein 156**) and **LIPG** (**Lipase G**), respectively. At 24-hpi, the log₂FC values ranged
90 between **-2.0** and **+2.6** for **C1QTNF12** (**C1q And TNF Related 12**) and **KCNG1** (**Potassium Voltage-Gated**
91 **Channel Modifier Subfamily G Member 1**), respectively.

92 **Functional Enrichment Analyses (GO, KEGG pathway, and interaction network analyses)**

93 Gene ontology (GO) enrichment analysis was performed for 12- and 24-hpi DEGs with the DAVID (Database
94 for Annotation, Visualization and Integrated Discovery; version 2021) online resource (21) and the gprofiler2
95 (version **0.2.3**) R package (22), which output results in three GO categories – cellular components (CP),

96 biological processes (BP), and molecular functions (MF). Results with P_{adjusted} -value ≤ 0.05 were considered
97 functionally enriched. The GO enrichment analyses results at 12-hpi and 24-hpi showed significant intersec-
98 tions among all three GO categories. At both time points, cellular breakdown processes were upregulated
99 while cellular maintenance processes and structures were downregulated in all three GO categories (**Table**
100 **2A-B** and **Table 3A-B**).

101 For upregulated DEGs at 12-hpi, GO terms annotated under the BP category broadly cluster into: apoptosis
102 and autophagy, cellular metabolism (catabolic processes), sterol biosynthesis, response to stimuli, and
103 protein processing (**Figure 4A** and **Table 2A**). Under the CC category, the GO terms relate primarily with
104 cytoplasmic vacuolation while the GO terms under the MF category broadly fit under protein binding and
105 kinase activity (**Table 2A**). For 12-hpi downregulated DEGs, the GO terms in BP category generally fall
106 under: translation, protein biosynthesis and folding, ribosome biogenesis, nitrogen compound metabolism,
107 nucleic acid synthesis, repair, metabolism, processing, and replication; and energy metabolism. Also,
108 immunoglobulin production and isotype switching was downregulated (**Figure 4C** and **Table 2B**). As for
109 the CC category GO terms, they broadly group into: ribosome, mitochondria, respirosome, nucleus, and
110 spliceosome while the MF category GO terms generally belong to: translation regulator activity, protein
111 folding chaperone, catalytic activity (acting on a nucleic acids), and ATP hydrolysis activity (**Table 2B**).

112 At 24-hpi, the GO terms under the BP GO category for the upregulated DEGs are connected with: apoptosis
113 and autophagy, lipid and sterol biosynthesis, catabolic process, protein ubiquitination and proteolysis, cell
114 signalling, and cell metabolism. Additionally, host defense response and genes that negatively regulate
115 cytokine production were upregulated (**Figure 4B** and **Table 3A**). The GO terms of the CC category, similar to
116 those identified at 12-hpi, are also related with cytoplasmic vacuolation and the lysosome. The MF category
117 GO terms group into: protein ubiquitination activity, kinase and acyltransferase activity, and macromolecule
118 binding activity (**Table 3A**). The GO terms for the downregulated DEGs are markedly similar to those at
119 12-hpi in all three GO categories. The BP category GO terms broadly group into: translation, peptide
120 biosynthesis and folding, ribosome biogenesis, aerobic respiration and ATP synthesis, and cell cycle process
121 and nucleic acid replication and processing (**Figure 4D** and **Table 3B**). The GO terms of the CC category
122 group under: ribosome, organelle, mitochondrion, nucleus and chromosomes while the MF category GO
123 terms group into: structural constituent of ribosome and translation regulator activity, catalytic activity acting
124 on a nucleic acid and nucleic acid binding, aminoacyl-tRNA ligase activity, and NAD binding (**Table 3B**).

125 KEGG analysis on the DEGs was performed using both the gprofiler2 R package (22) and the DAVID online
126 resource. Both analysis resources gave similar results but the results from DAVID (**Table 4A**) includes more
127 information than the gprofiler2 results (**Table 4B**). The KEGG pathway analysis was congruent with the GO

128 results, revealing that generally, cell maintenance and upkeep pathways were downregulated while cell death
129 and breakdown pathways were upregulated. Cell maintenance pathways such as DNA replication and repair,
130 ribosome biogenesis, spliceosome, and oxidative phosphorylation were downregulated at 12-hpi. Similar
131 pathways were downregulated at 24-hpi. Cell breakdown pathways such as: autophagy, response to virus
132 (Influenza A), and steroid biosynthesis were upregulated at 12-hpi similar to 24-hpi, where pathways such
133 as: autophagy, ubiquitin-mediated proteolysis, lysosome, protein processing in endoplasmic reticulum, and
134 steroid biosynthesis were upregulated.

135 It is well-established that THEV induces cell death (apoptosis and necrosis) in infected B-cells, which is linked
136 to the IMS associated with THEV (8, 11, 23). Hence, we are particularly interested in cellular processes and
137 pathways associated with cell death and pathways that may affect the survivability of the host cells, thereby
138 accounting for THEV-induced IMS. We highlight the upregulated cell death (apoptosis and autophagy)
139 pathways, cellular metabolism, and responses to stimuli (especially ER-stress response) pathways identified
140 by our GO and KEGG analyses as the likely key aspects of THEV-host cell interaction leading to IMS.

141 **Cell Death and Breakdown Pathways Upregulated by THEV**

142 Many virus families, including adenoviruses, herpesviruses, poxviruses, baculoviruses, parvoviruses, retro-
143 viruses, rhabdoviruses, paramyxoviruses, orthomyxoviruses, togaviruses, and picornaviruses are known to
144 trigger apoptosis in infected host cells either by a direct action of a viral protein or due to the host antiviral
145 response (24–26). The Mastadenovirus family possess the protein, E1B 19K to inhibit host cell apoptosis
146 long enough to complete their replication cycle (24, 26, 27). However, no such protein is known in THEV. A
147 recent paper showed several novel transcripts and open reading frames (ORFs) in the genome of THEV
148 which may offer a similar anti-apoptotic functions but the functions of these novel ORFs are yet to be shown
149 (28). Our data shows that apoptotic and autophagic pathways are upregulated during THEV infection,
150 supporting previous findings of apoptosis and necrosis of THEV-infected cells (8, 11, 23). For example, . . . ,
151 which are proapoptotic, were upregulated. We also see several cell upkeep processes downregulated which
152 can trigger apoptosis. For instance, several pathways related DNA repair are downregulated Severe
153 DNA damage is an known mechanism of apoptosis induction.

154 **Cellular Metabolism Changes During THEV Infection**

155 Many viruses, such as hepatitis C virus, human cytomegalovirus, influenza virus, and rhinovirus, have been
156 documented to manipulate the cellular metabolism process for their use

157 **Cellular Responses to Stimuli during THEV infection**

158

159 **DISCUSSION**

160 We may not have seen a measurable immune response/pathway enrichment in the infected host cells
161 because the these B-cells may likely require other immune cells such as macrophages and T-cells for
162 activation/mount an immune response. Secondly, the curated data in the GO, and KEGG databases are
163 most complete for human and other model organisms; hence, there may not be enough information curated
164 for turkeys to highlight the anything that is not very strong immune response.

165 **CONCLUSIONS**

166 **MATERIALS AND METHODS**

167 **Cell culture and THEV Infection**

168 The Turkey B-cell line (MDTC-RP19, ATCC CRL-8135) was grown as a suspension culture in 1:1 complete
169 Leibovitz's L-15/McCoy's 5A medium with 10% fetal bovine serum (FBS), 20% chicken serum (ChS), 5%
170 tryptose phosphate broth (TPB), and 1% antibiotic solution (100 U/mL Penicillin and 100 μ g/mL Streptomycin),
171 at 41°C in a humidified atmosphere with 5% CO₂. Infected cells were maintained in 1:1 serum-reduced
172 Leibovitz's L15/McCoy's 5A media (SRLM) with 2.5% FBS, 5% ChS, 1.2% TPB, and 1% antibiotic solution. A
173 commercially available THEV vaccine was purchased from Hygieia Biological Labs (VAS strain). The stock
174 virus was titrated using an in-house qPCR assay with titer expressed as genome copy number (GCN)/mL,
175 similar to Mahshoub *et al* (29). Cells were THEV-infected or mock-infected in triplicates or duplicates,
176 respectively at a multiplicity of infection (MOI) of 100 GCN/cell, incubated at 41°C for 1 hour, and washed
177 three times with phosphate buffered saline (PBS) to get rid of free virus particles. At each time point (4-, 12-,
178 24-, and 72-hpi), triplicate (THEV-infected) and duplicate (mock-infected) samples were harvested for total
179 RNA extraction.

180 **RNA extraction and Sequencing**

181 Total RNA was extracted from infected cells using the Thermo Fisher RNAqueous™-4PCR Total RNA Isolation
182 Kit (which includes a DNase I digestion step) per manufacturer's instructions. An agarose gel electrophoresis
183 was performed to check RNA integrity. The RNA quantity and purity was initially assessed using nanodrop,
184 and RNA was used only if the A260/A280 ratio was 2.0 ± 0.05 and the A260/A230 ratio was >2 and <2.2.
185 Extracted total RNA samples were sent to LC Sciences, Houston TX for poly-A-tailed mRNA sequencing.
186 RNA integrity was checked with Agilent Technologies 2100 Bioanalyzer High Sensitivity DNA Chip and
187 poly(A) RNA-seq library was prepared following Illumina's TruSeq-stranded-mRNA sample preparation
188 protocol. Paired-end sequencing, generating 150 bp reads was performed on the Illumina NovaSeq 6000
189 sequencing system. The paired-end 150bp sequences obtained during this study and all expression data
190 have been submitted to the Gene Expression Omnibus database, under accession no #####

191 **Quality Control and Mapping Process**

192 Sequencing reads were processed following a well-established protocol described by Pertea *et al* (19),
193 using Snakemake - version 7.32.4 (30), a popular workflow management system to drive the pipeline.
194 Briefly, raw sequencing reads were trimmed with Cutadapt - version 1.10 (31) and the quality of trimmed
195 reads evaluated using the FastQC software, version 0.12.1 (Bioinformatics Group at the Babraham Institute,
196 Cambridge, United Kingdom; www.bioinformatics.babraham.ac.uk), achieving an overall Mean Sequence
197 Quality (PHRED Score) of 36. Trimmed reads were mapped the reference *Meleagris gallopavo* genome

198 (https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/146/605/GCF_000146605.3_Turkey_5.1/GCF_000146
199 605.3_Turkey_5.1_genomic.fna.gz) with Hisat2 - version 2.2.1 (19) using the accompanying gene transfer
200 format (GTF) annotation file (https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/146/605/GCF_000146605.3
201 _Turkey_5.1/GCF_000146605.3_Turkey_5.1_genomic.gtf.gz) to build a genomic index. Samtools - version
202 1.19.2 was used to convert the output Sequence Alignment Map (SAM) file to the more manageable Binary
203 Alignment Map (BAM) format. The StringTie (v2.2.1) software (19), set to expression estimation mode was
204 used to generate normalized gene expression estimates from the BAM files for genes in the reference GTF
205 file after which the prepDE.py3 script was used to extract read count information from the StringTie gene
206 expression files, providing an expression-count matrix for downstream DEG analysis.

207 **DEG Analysis and Functional Enrichment Analysis**

208 DEG analysis between mock- and THEV-infected samples was performed using the very popular DESeq2
209 (20), which employs a Negative Binomial distribution model for read count comparisons. Genes with P_{adjusted} -
210 value ≤ 0.05 were considered as differentially expressed. The read count data are deposited at Gene
211 Expression Omnibus (GEO) under accession number ###. The functional profiling of DEGs (GO and KEGG
212 analyses) were performed based on GO databases and KEGG databases using the R package gprofiler2
213 (22) with *Meleagris gallopavo* as the reference organism. Results with P_{adjusted} -value ≤ 0.05 were included
214 as functionally enriched. Additionally, the DAVID (Database for Annotation, Visualization and Integrated
215 Discovery; version 2021) online analysis tool was used for KEGG pathway analysis. All visualization plots
216 were made using ggplot2, pheatmap, and ggvenn R packages (32–34).

217 **Validation of DEGs by Reverse Transcriptase Quantitative PCR (RT-qPCR)**

218 **Statistical Analysis**

²¹⁹ **DATA AVAILABILITY**

220 **CODE AVAILABILITY**

221 **ACKNOWLEDGMENTS**

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257 TABLES AND FIGURES

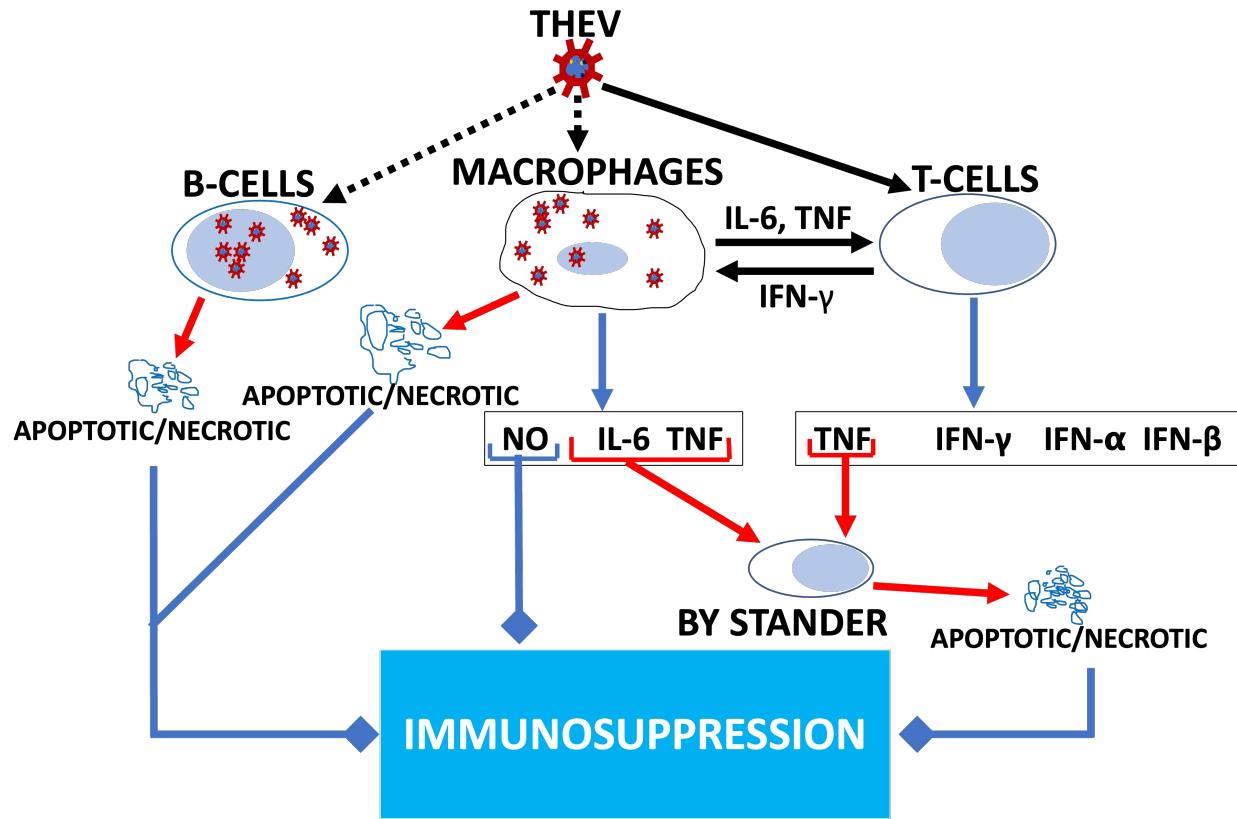


Figure 1: Model of THEV-induced immunosuppression in turkeys. THEV infection of target cells is indicated with black dotted arrows. Black unbroken arrows indicate cell activation. Red arrows indicate signals leading to apoptosis. Blue arrows indicate all cytokines released by the cell. Blue arrows with square heads indicate an event leading to IMS. Adapted from Rautenschlein *et al.* (8).

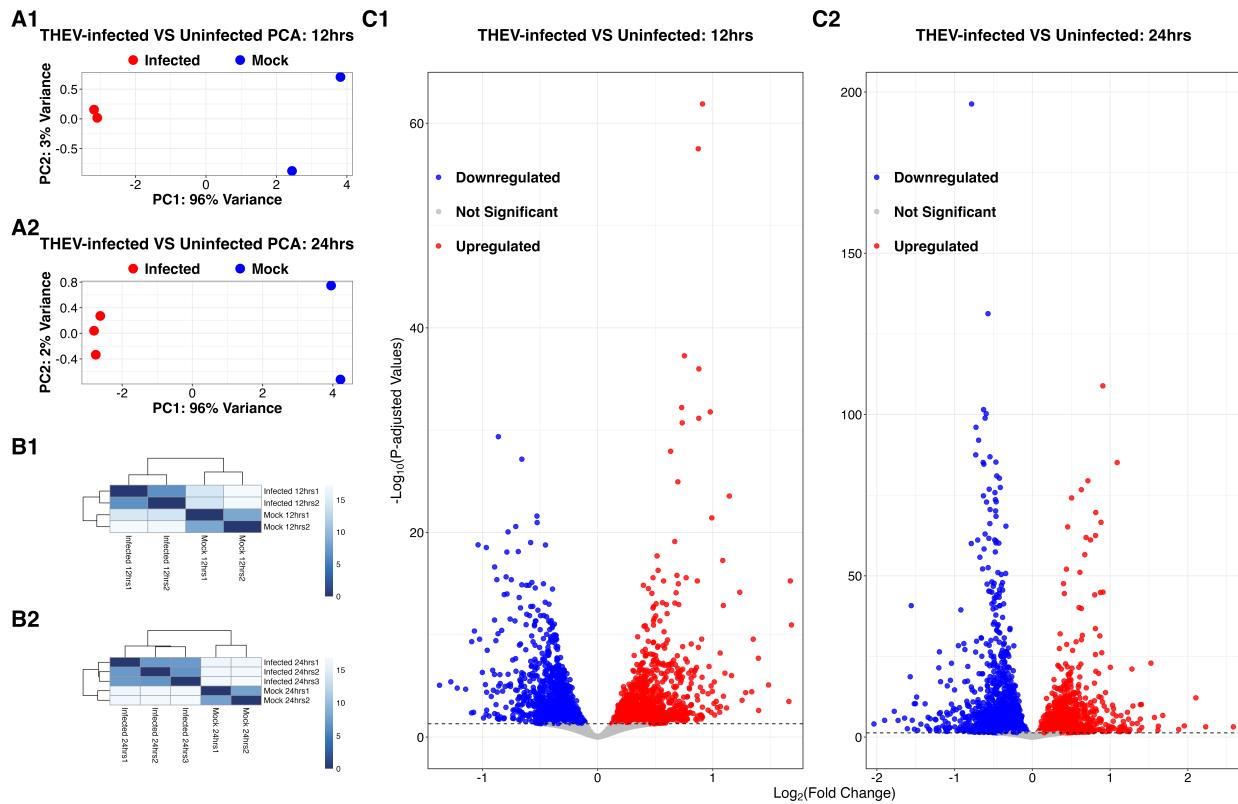


Figure 2. (A) Principal component analysis (PCA) of turkey B-cells during THEV infection. At 12-hpi (**A1**), the results indicate that the first (PC1) and second (PC2) principal components account for 96% and 3% of the variation in the samples, respectively. Whereas PC1 and PC2 account for 96% and 2% of the variation, respectively at 24-hpi (**A2**). **(B) Poisson distance matrices illustrating the RNA-seq library integrity within treatment (infected versus mock) groups.** The color scale represents the distances between biological replicates for both 12-hpi samples (**B1**) and 24-hpi samples (**B2**). Dark colors represent high correlation (similarity) between the samples involved. **(C) Volcano plots of DEGs between THEV-infected versus mock-infected cells at 12- and 24-hpi.** Red, blue, and grey dots represent upregulated, downregulated, and non-significant genes, respectively for both 12-hpi samples (**C1**) and 24-hpi samples (**C2**).

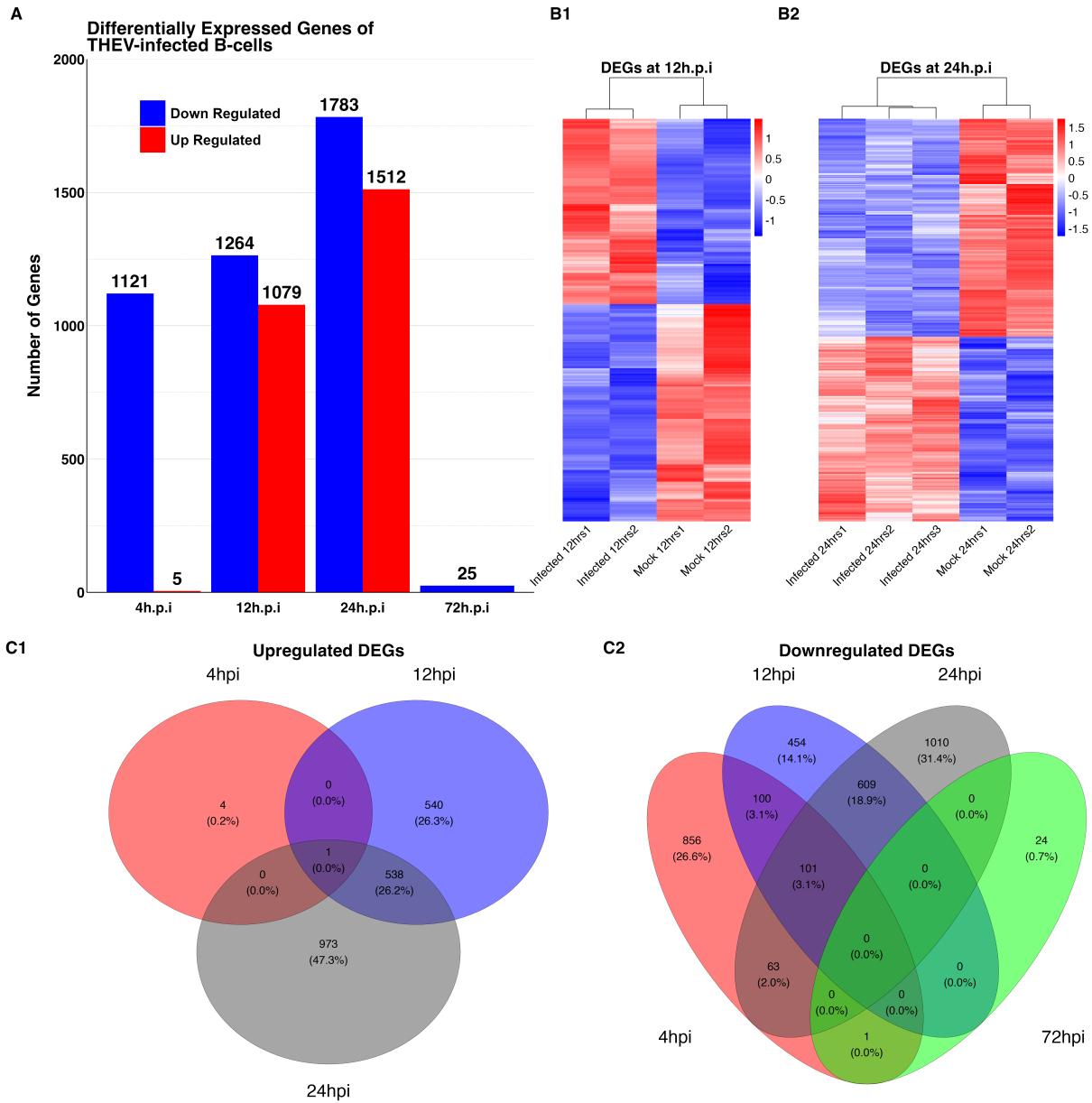


Figure 3: Differentially expressed genes (DEGs) of THEV-infected versus mock-infected samples at different time points. (A) Bar plot of number DEGs identified. Red represents upregulated genes and blue represents downregulated genes. (B) Heatmaps of scaled expression data (Z-scores) of DEGs. DEGs identified at 12-hpi are shown in (B1) and DEGs at 24-hpi in (B2). (C) Venn diagrams showing the number of DEGs identified at different time points. For the upregulated genes (C1), the red circle represents genes at 4-hpi, the blue circle, 12-hpi, and the grey circle, 24-hpi. For the downregulated genes (C2), the green circle represents genes at 72-hpi, while all the other time points retain the colors from (C1).

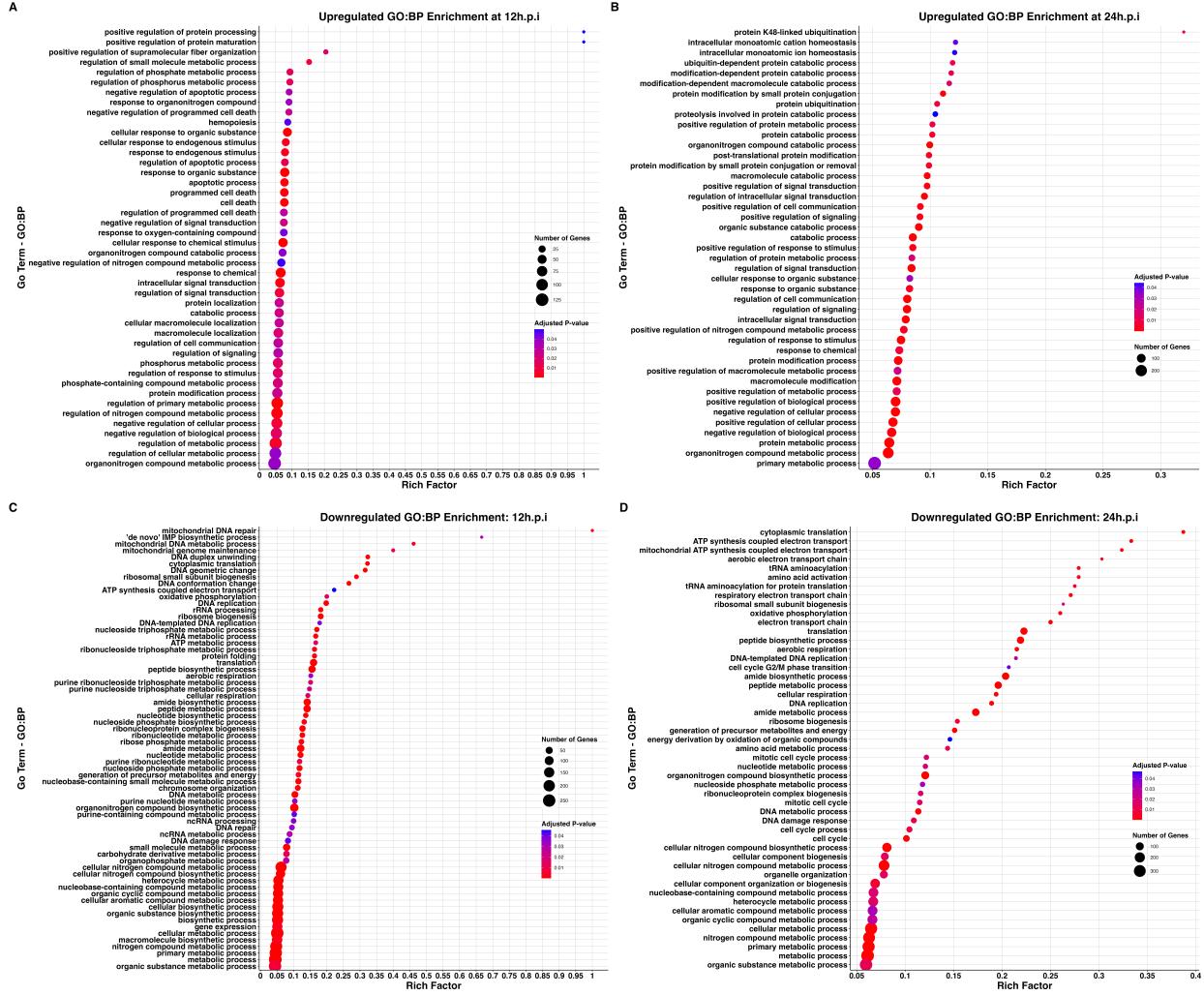


Figure 4: Dotplot of Enriched Gene Ontology Biological Processes (BP). Significant BP GO terms identified for upregulated DEGs at 12-hpi and 24-hpi are shown in (A) and (B), respectively. Significant BP GO terms for downregulated DEGs at 12-hpi and 24-hpi are shown in (C) and (D), respectively. The y-axis indicates GO terms and the x-axis represents the rich factor, which indicates the ratio of the number of DEGs annotated to the term to the total number of genes annotated to the term. The diameter indicates the number of genes overlapping the gene ontology term and the color indicates the enrichment P-value.

Table 1: Summary of sequencing, quality control, and mapping processes

Sample	Raw Reads ^M	Trimmed Reads ^M	Mapped Reads ^M	Uniquely		Non-uniquely		Q20%	Q30%	GC Content (%)
				Mapped Reads ^M	Mapped Reads ^M	Mapped Reads ^M	Mapped Reads ^M			
I_12hrsS1 ^{Inf}	40.6	39.0	34.7 (88.92%)	33.1 (84.78%)	1.6 (4.14%)	99.95	97.23	47.5		
I_12hrsS3 ^{Inf}	38.8	37.3	33.1 (88.78%)	31.7 (84.95%)	1.4 (3.83%)	99.95	97.53	47.5		
I_24hrsS1 ^{Inf}	42.7	41.0	36.2 (88.13%)	34.5 (84.2%)	1.6 (3.93%)	99.95	96.95	46.5		
I_24hrsS2 ^{Inf}	42.0	40.4	35.6 (88.1%)	33.9 (83.83%)	1.7 (4.27%)	99.94	97.05	46.5		
I_24hrsS3 ^{Inf}	40.5	38.9	34.2 (88.01%)	32.7 (84.12%)	1.5 (3.89%)	99.95	97.08	47.0		
I_4hrsS1 ^{Inf}	39.1	37.4	33 (88.16%)	31.2 (83.43%)	1.8 (4.73%)	99.93	97.04	48.5		
I_4hrsS2 ^{Inf}	41.3	39.6	35.3 (89.24%)	33.6 (84.92%)	1.7 (4.33%)	99.95	97.15	47.0		
I_4hrsS3 ^{Inf}	41.5	39.8	35.5 (89.2%)	33.2 (83.29%)	2.4 (5.91%)	99.95	97.11	47.5		
I_72hrsS1 ^{Inf}	41.2	39.8	28.3 (71.09%)	26.9 (67.7%)	1.3 (3.38%)	99.96	97.23	44.5		
I_72hrsS2 ^{Inf}	39.3	38.0	27 (71.11%)	25.8 (67.86%)	1.2 (3.25%)	99.96	97.34	44.5		
I_72hrsS3 ^{Inf}	39.9	37.1	28.3 (76.36%)	26.1 (70.3%)	2.2 (6.05%)	99.87	96.14	52.5		
U_12hrsN1 ^{Mk}	42.1	40.4	35.9 (88.72%)	34.1 (84.39%)	1.7 (4.33%)	99.95	97.04	47.5		
U_12hrsN2 ^{Mk}	41.0	39.3	34.7 (88.4%)	33.2 (84.53%)	1.5 (3.86%)	99.94	97.08	47.5		
U_24hrsN1 ^{Mk}	38.4	37.0	32.7 (88.46%)	31.4 (84.74%)	1.4 (3.72%)	99.96	97.48	47.5		
U_24hrsN2 ^{Mk}	39.9	38.4	34 (88.58%)	32.6 (84.96%)	1.4 (3.61%)	99.95	96.95	47.0		
U_4hrsN1 ^{Mk}	39.4	37.9	33.7 (88.9%)	32 (84.41%)	1.7 (4.49%)	99.96	97.36	47.0		
U_4hrsN2 ^{Mk}	37.6	34.7	22 (63.43%)	18.5 (53.18%)	3.6 (10.25%)	99.80	94.96	61.0		
U_72hrsN1 ^{Mk}	50.3	47.9	15.5 (32.4%)	11.7 (24.5%)	3.8 (7.9%)	99.88	96.54	56.0		

Sample	Raw Reads ^M	Trimmed Reads ^M	Mapped Reads ^M	Uniquely		Non-uniquely		Q20%	Q30%	GC Content (%)
				Mapped Reads ^M	Mapped Reads ^M	Mapped Reads ^M	Mapped Reads ^M			
U_72hrsN2 ^{Mk}	40.5	38.9	34.5 (88.82%)	32.7 (84.14%)	1.8 (4.68%)	99.95	97.04			46.5

^MAll values for number of reads are in millions;

^{Inf}These are infected samples indicated by the letter 'I' and 'S' in sample names

^{Mk}These are mock-infected samples indicated by the letters 'U' and 'N' in sample names

Table 2A: Gene ontology analysis of Significantly Upregulated DEGs identified at 12-hpi

GO Category	GO:Term	Fold Enrichment	Fold	Number of	P-value
			(Adjusted)	DEGs	(Adjusted)
Biological Process					
GO:BP	regulation of metabolic process	1.47	279	6.08e-09	
GO:BP	regulation of cellular metabolic process	1.48	252	2.56e-08	
GO:BP	programmed cell death	2.85	51	4.99e-08	
GO:BP	cell death	2.85	51	4.99e-08	
GO:BP	negative regulation of cellular process	1.59	174	1.90e-07	
GO:BP	negative regulation of biological process	1.56	187	1.90e-07	
GO:BP	apoptotic process	2.75	47	6.09e-07	
GO:BP	regulation of macromolecule metabolic process	1.42	248	9.05e-07	
GO:BP	protein phosphorylation	2.33	61	9.07e-07	
GO:BP	phosphate-containing compound metabolic process	1.63	145	1.11e-06	

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	phosphorus metabolic process	1.63	146	1.11e-06
GO:BP	regulation of primary metabolic process	1.40	226	1.02e-05
GO:BP	secondary alcohol biosynthetic process	7.67	13	1.58e-05
GO:BP	regulation of cellular biosynthetic process	1.41	210	2.24e-05
GO:BP	sterol biosynthetic process	7.24	13	2.79e-05
GO:BP	regulation of apoptotic process	2.15	57	2.79e-05
GO:BP	protein modification process	1.55	138	3.56e-05
GO:BP	regulation of biosynthetic process	1.40	210	3.56e-05
GO:BP	macromolecule localization	1.58	128	3.56e-05
GO:BP	small molecule biosynthetic process	2.38	45	3.75e-05
GO:BP	phytosteroid biosynthetic process	12.04	9	3.75e-05
GO:BP	phytosteroid metabolic process	12.04	9	3.75e-05
GO:BP	regulation of macromolecule biosynthetic process	1.39	205	6.25e-05
GO:BP	regulation of programmed cell death	2.07	57	6.77e-05
GO:BP	negative regulation of cellular metabolic process	1.79	80	9.46e-05
GO:BP	regulation of gene expression	1.38	201	1.06e-04
GO:BP	primary metabolic process	1.22	380	1.08e-04
GO:BP	negative regulation of metabolic process	1.70	91	1.10e-04
GO:BP	cellular response to stress	1.77	81	1.11e-04
GO:BP	phosphorylation	1.80	74	1.96e-04

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	alcohol biosynthetic process	3.77	19	3.45e-04
GO:BP	metabolic process	1.19	426	3.93e-04
GO:BP	organonitrogen compound metabolic process	1.29	260	3.93e-04
GO:BP	protein localization	1.58	104	4.21e-04
GO:BP	regulation of cellular process	1.16	473	4.21e-04
GO:BP	cellular macromolecule localization	1.58	104	4.21e-04
GO:BP	negative regulation of programmed cell death	2.35	37	4.29e-04
GO:BP	cellular localization	1.45	145	4.34e-04
GO:BP	positive regulation of metabolic process	1.53	116	4.34e-04
GO:BP	negative regulation of apoptotic process	2.37	36	4.54e-04
GO:BP	regulation of biological process	1.15	497	5.83e-04
GO:BP	intracellular protein transport	2.00	50	5.94e-04
GO:BP	establishment of localization in cell	1.56	104	5.94e-04
GO:BP	ergosterol biosynthetic process	12.77	7	5.94e-04
GO:BP	ergosterol metabolic process	12.77	7	5.94e-04
GO:BP	negative regulation of macromolecule metabolic process	1.66	82	7.20e-04
GO:BP	cholesterol biosynthetic process	6.92	10	7.48e-04
GO:BP	apoptotic signaling pathway	3.32	20	8.19e-04
GO:BP	biological regulation	1.14	517	8.20e-04
GO:BP	mitotic cell cycle process	2.14	41	8.20e-04

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	regulation of catabolic process	2.01	47	8.20e-04
GO:BP	steroid biosynthetic process	3.96	16	8.52e-04
GO:BP	negative regulation of gene expression	2.16	40	8.52e-04
GO:BP	cellular metabolic process	1.23	307	8.52e-04
GO:BP	positive regulation of cellular metabolic process	1.56	98	8.52e-04
GO:BP	negative regulation of cellular biosynthetic process	1.74	68	8.52e-04
GO:BP	macromolecule modification	1.43	138	9.09e-04
GO:BP	positive regulation of apoptotic process	2.85	24	9.34e-04
GO:BP	negative regulation of biosynthetic process	1.73	68	1.03e-03
GO:BP	catabolic process	1.51	108	1.03e-03
GO:BP	protein localization to organelle	1.90	52	1.15e-03
GO:BP	response to chemical	1.56	95	1.24e-03
GO:BP	positive regulation of biological process	1.33	193	1.29e-03
GO:BP	regulation of nucleobase-containing compound metabolic process	1.36	167	1.29e-03
GO:BP	cell cycle	1.68	72	1.34e-03
GO:BP	intracellular signal transduction	1.54	97	1.48e-03
GO:BP	positive regulation of programmed cell death	2.74	24	1.58e-03
GO:BP	mitotic cell cycle	1.94	47	1.70e-03
GO:BP	macromolecule catabolic process	1.76	60	1.77e-03
GO:BP	positive regulation of cellular process	1.34	173	1.83e-03

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	sterol metabolic process	3.86	15	1.83e-03
GO:BP	lipid biosynthetic process	1.94	46	1.94e-03
GO:BP	negative regulation of macromolecule biosynthetic process	1.70	65	2.25e-03
GO:BP	regulation of response to stress	1.91	46	2.54e-03
GO:BP	cellular lipid metabolic process	1.67	67	3.03e-03
GO:BP	organic hydroxy compound biosynthetic process	2.93	20	3.11e-03
GO:BP	cellular lipid biosynthetic process	9.36	7	3.16e-03
GO:BP	regulation of response to stimulus	1.39	137	3.49e-03
GO:BP	establishment of protein localization	1.61	73	3.79e-03
GO:BP	response to stress	1.44	112	3.79e-03
GO:BP	nitrogen compound transport	1.57	79	4.15e-03
GO:BP	response to oxygen-containing compound	1.90	44	4.16e-03
GO:BP	process utilizing autophagic mechanism	2.59	23	4.43e-03
GO:BP	autophagy	2.59	23	4.43e-03
GO:BP	regulation of intracellular signal transduction	1.60	73	4.75e-03
GO:BP	secondary alcohol metabolic process	3.70	14	4.85e-03
GO:BP	regulation of signal transduction	1.44	110	4.85e-03
GO:BP	cell cycle process	1.70	59	4.85e-03
GO:BP	regulation of developmental process	1.59	73	4.88e-03
GO:BP	macroautophagy	2.98	18	5.47e-03

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	response to lipid	2.41	25	5.91e-03
GO:BP	positive regulation of macromolecule metabolic process	1.46	100	5.97e-03
GO:BP	regulation of RNA metabolic process	1.34	154	5.97e-03
GO:BP	macromolecule metabolic process	1.21	286	6.45e-03
GO:BP	positive regulation of catabolic process	2.30	27	6.45e-03
GO:BP	regulation of DNA-templated transcription	1.35	142	7.41e-03
GO:BP	establishment of protein localization to organelle	2.04	34	7.41e-03
GO:BP	lipid metabolic process	1.53	79	7.41e-03
GO:BP	response to organonitrogen compound	2.19	29	7.59e-03
GO:BP	regulation of RNA biosynthetic process	1.35	142	7.59e-03
GO:BP	endoderm development	6.42	8	7.66e-03
GO:BP	mRNA transcription	7.80	7	7.79e-03
GO:BP	regulation of transcription by RNA polymerase II	1.41	111	7.98e-03
GO:BP	cellular response to lipid	2.66	20	8.44e-03
GO:BP	protein metabolic process	1.27	198	8.44e-03
GO:BP	nuclear-transcribed mRNA catabolic process, deadenylation-independent decay	14.33	5	8.47e-03
GO:BP	deadenylation-independent decapping of nuclear-transcribed mRNA	14.33	5	8.47e-03
GO:BP	gland development	3.06	16	9.41e-03
GO:BP	vesicle-mediated transport	1.51	80	9.41e-03

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	multicellular organismal-level homeostasis	2.48	22	9.41e-03
GO:BP	embryonic morphogenesis	2.36	24	9.41e-03
GO:BP	regulation of autophagy	2.61	20	1.02e-02
GO:BP	intracellular transport	1.51	79	1.02e-02
GO:BP	organophosphate metabolic process	1.59	65	1.09e-02
GO:BP	cholesterol metabolic process	3.76	12	1.20e-02
GO:BP	small molecule metabolic process	1.44	93	1.24e-02
GO:BP	regulation of signaling	1.37	121	1.25e-02
GO:BP	localization	1.24	219	1.25e-02
GO:BP	homeostasis of number of cells	3.27	14	1.27e-02
GO:BP	cellular response to oxygen levels	5.02	9	1.27e-02
GO:BP	intrinsic apoptotic signaling pathway	3.70	12	1.31e-02
GO:BP	cell division	2.20	26	1.31e-02
GO:BP	regulation of cell communication	1.36	120	1.31e-02
GO:BP	cellular component disassembly	2.46	21	1.31e-02
GO:BP	protein transport	1.58	62	1.45e-02
GO:BP	establishment or maintenance of cell polarity	2.51	20	1.48e-02
GO:BP	DNA-templated transcription	2.17	26	1.53e-02
GO:BP	developmental growth	2.58	19	1.53e-02
GO:BP	growth	2.58	19	1.53e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	hemopoiesis	2.16	26	1.69e-02
GO:BP	biological process involved in interspecies interaction between organisms	1.80	40	1.74e-02
GO:BP	negative regulation of intracellular signal transduction	2.07	28	1.78e-02
GO:BP	extrinsic apoptotic signaling pathway	4.18	10	1.89e-02
GO:BP	cellular response to oxygen-containing compound	1.92	33	1.98e-02
GO:BP	regulation of cellular catabolic process	2.35	21	2.18e-02
GO:BP	response to nitrogen compound	1.97	30	2.46e-02
GO:BP	steroid metabolic process	2.54	18	2.46e-02
GO:BP	establishment of localization	1.24	195	2.46e-02
GO:BP	cellular response to chemical stimulus	1.56	60	2.49e-02
GO:BP	regulation of cytokine production	2.21	23	2.61e-02
GO:BP	regulation of epithelial cell apoptotic process	5.02	8	2.79e-02
GO:BP	intracellular lipid transport	5.02	8	2.79e-02
GO:BP	cellular response to hypoxia	5.02	8	2.79e-02
GO:BP	nuclear transport	2.24	22	2.79e-02
GO:BP	nucleocytoplasmic transport	2.24	22	2.79e-02
GO:BP	positive regulation of signal transduction	1.62	51	2.85e-02
GO:BP	regulation of phosphate metabolic process	1.79	37	2.89e-02
GO:BP	regulation of phosphorus metabolic process	1.79	37	2.89e-02
GO:BP	cellular response to lipopolysaccharide	3.56	11	2.92e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	androgen receptor signaling pathway	10.03	5	3.18e-02
GO:BP	motor neuron apoptotic process	10.03	5	3.18e-02
GO:BP	cellular response to decreased oxygen levels	4.86	8	3.18e-02
GO:BP	transport	1.24	183	3.18e-02
GO:BP	purine nucleoside bisphosphate metabolic process	3.03	13	3.39e-02
GO:BP	ribonucleoside bisphosphate metabolic process	3.03	13	3.39e-02
GO:BP	nucleoside bisphosphate metabolic process	3.03	13	3.39e-02
GO:BP	appendage development	4.20	9	3.40e-02
GO:BP	limb development	4.20	9	3.40e-02
GO:BP	embryo development	1.93	29	3.43e-02
GO:BP	cellular response to biotic stimulus	3.21	12	3.47e-02
GO:BP	regulation of leukocyte differentiation	3.00	13	3.64e-02
GO:BP	regulation of cell cycle	1.67	43	3.66e-02
GO:BP	tissue development	1.58	51	4.22e-02
GO:BP	limb morphogenesis	4.59	8	4.22e-02
GO:BP	appendage morphogenesis	4.59	8	4.22e-02
GO:BP	mitotic cell cycle phase transition	3.34	11	4.22e-02
GO:BP	cellular response to molecule of bacterial origin	3.34	11	4.22e-02
GO:BP	positive regulation of cell communication	1.55	55	4.22e-02
GO:BP	positive regulation of signaling	1.55	55	4.22e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	cellular catabolic process	1.64	44	4.22e-02
GO:BP	nucleobase-containing compound catabolic process	2.05	24	4.40e-02
GO:BP	protein catabolic process	1.66	42	4.40e-02
GO:BP	cell cycle phase transition	3.29	11	4.63e-02
GO:BP	regulation of cell cycle process	1.79	33	4.65e-02
GO:BP	regulation of anatomical structure morphogenesis	1.81	32	4.74e-02
GO:BP	regulation of mitotic cell cycle phase transition	2.34	18	4.74e-02
GO:BP	positive regulation of cellular biosynthetic process	1.44	72	4.95e-02
GO:BP	regulation of protein metabolic process	1.50	59	4.97e-02

Cellular Component

GO:CC	intracellular anatomical structure	1.19	774	8.23e-20
GO:CC	cytoplasm	1.28	590	7.06e-17
GO:CC	intracellular membrane-bounded organelle	1.29	578	1.08e-16
GO:CC	membrane-bounded organelle	1.26	595	7.52e-16
GO:CC	intracellular organelle	1.23	655	7.52e-16
GO:CC	organelle	1.21	666	2.49e-14
GO:CC	nucleus	1.42	371	1.33e-13
GO:CC	cytosol	1.69	166	6.96e-10
GO:CC	organelle membrane	1.59	154	3.53e-07
GO:CC	endomembrane system	1.48	200	3.53e-07

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:CC	nucleoplasm	1.75	104	1.57e-06
GO:CC	bounding membrane of organelle	1.70	92	3.49e-05
GO:CC	intracellular organelle lumen	1.51	135	4.91e-05
GO:CC	organelle lumen	1.51	135	4.91e-05
GO:CC	membrane-enclosed lumen	1.51	135	4.91e-05
GO:CC	nuclear lumen	1.55	119	6.06e-05
GO:CC	cytoplasmic vesicle	1.57	88	1.12e-03
GO:CC	intracellular vesicle	1.55	88	1.62e-03
GO:CC	vesicle	1.51	95	1.94e-03
GO:CC	endoplasmic reticulum	1.54	86	2.07e-03
GO:CC	perinuclear region of cytoplasm	2.51	25	2.11e-03
GO:CC	chromatin	1.84	40	9.58e-03
GO:CC	chromosome	1.58	63	1.10e-02
GO:CC	organelle subcompartment	1.56	65	1.21e-02
GO:CC	endosome	1.69	48	1.37e-02
GO:CC	Golgi apparatus	1.52	69	1.40e-02
GO:CC	protein-DNA complex	1.76	42	1.40e-02
GO:CC	vesicle membrane	1.74	43	1.40e-02
GO:CC	transcription regulator complex	1.99	30	1.40e-02
GO:CC	vacuole	1.82	34	2.73e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:CC	phagophore assembly site	4.73	8	2.83e-02
GO:CC	spindle	2.04	25	2.85e-02
GO:CC	cytoplasmic vesicle membrane	1.69	41	2.85e-02
GO:CC	endosome membrane	2.02	25	3.21e-02
GO:CC	early endosome	2.11	22	3.70e-02
Molecular Function				
GO:MF	enzyme binding	2.20	102	8.60e-11
GO:MF	protein binding	1.27	427	8.52e-08
GO:MF	protein-macromolecule adaptor activity	1.98	67	5.57e-05
GO:MF	molecular adaptor activity	1.90	73	5.57e-05
GO:MF	identical protein binding	2.07	54	1.96e-04
GO:MF	binding	1.09	714	4.02e-04
GO:MF	kinase activity	1.58	86	4.95e-03
GO:MF	transferase activity, transferring phosphorus-containing groups	1.51	96	5.83e-03
GO:MF	kinase binding	2.14	35	5.83e-03
GO:MF	phosphotransferase activity, alcohol group as acceptor	1.59	80	5.83e-03
GO:MF	DNA-binding transcription factor binding	2.73	22	5.83e-03
GO:MF	small molecule binding	1.19	338	5.83e-03
GO:MF	protein domain specific binding	2.51	25	5.83e-03
GO:MF	transcription factor binding	2.38	27	6.59e-03

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:MF	RNA polymerase II-specific DNA-binding transcription factor binding	2.94	18	1.05e-02
GO:MF	ion binding	1.19	325	1.05e-02
GO:MF	manganese ion binding	5.62	9	1.05e-02
GO:MF	transferase activity	1.30	176	1.05e-02
GO:MF	transcription coregulator activity	1.93	38	1.18e-02
GO:MF	protein kinase binding	2.10	31	1.18e-02
GO:MF	protein kinase activity	1.59	67	1.20e-02
GO:MF	enzyme regulator activity	1.50	82	1.38e-02
GO:MF	nuclear androgen receptor binding	12.88	5	1.83e-02
GO:MF	protein homodimerization activity	2.29	23	2.51e-02
GO:MF	ATP binding	1.33	128	2.71e-02
GO:MF	adenyl ribonucleotide binding	1.33	130	2.71e-02
GO:MF	myosin phosphatase activity	4.64	9	2.71e-02
GO:MF	signaling adaptor activity	3.44	12	3.01e-02
GO:MF	R-SMAD binding	10.31	5	4.03e-02
GO:MF	protein serine/threonine kinase activity	1.68	44	4.27e-02
GO:MF	purine ribonucleoside triphosphate binding	1.28	148	4.38e-02
GO:MF	adenyl nucleotide binding	1.30	133	4.38e-02

Table 2B: Gene ontology analysis of Significantly Downregulated DEGs identified at 12-hpi

GO Category	GO:Term	Fold Enrichment	Number of DEGs	P-value (Adjusted)
Biological Process				
GO:BP	gene expression	3.07	289	4.61e-70
GO:BP	macromolecule biosynthetic process	2.69	313	8.24e-63
GO:BP	biosynthetic process	2.25	377	3.04e-57
GO:BP	translation	6.31	110	7.08e-55
GO:BP	cellular biosynthetic process	2.29	329	4.05e-50
GO:BP	ribonucleoprotein complex biogenesis	5.52	108	1.71e-47
GO:BP	metabolic process	1.57	618	9.00e-47
GO:BP	cellular metabolic process	1.77	482	3.42e-45
GO:BP	macromolecule metabolic process	1.79	466	6.20e-45
GO:BP	nucleobase-containing compound metabolic process	2.41	276	9.74e-45
GO:BP	primary metabolic process	1.63	556	1.30e-44
GO:BP	nucleic acid metabolic process	2.56	226	1.57e-39
GO:BP	ribosome biogenesis	5.80	86	2.32e-39
GO:BP	organonitrogen compound biosynthetic process	2.74	170	3.69e-32
GO:BP	nucleobase-containing compound biosynthetic process	2.57	178	2.25e-30
GO:BP	rRNA processing	5.97	62	1.61e-28
GO:BP	rRNA metabolic process	5.57	63	4.00e-27
GO:BP	RNA processing	3.04	120	6.65e-26

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	RNA metabolic process	2.49	152	6.25e-24
GO:BP	nucleic acid biosynthetic process	2.57	142	1.38e-23
GO:BP	RNA biosynthetic process	2.55	135	4.64e-22
GO:BP	ribosomal large subunit biogenesis	8.18	34	8.01e-20
GO:BP	protein-RNA complex assembly	5.76	40	3.24e-17
GO:BP	cytoplasmic translation	9.15	27	7.21e-17
GO:BP	protein-RNA complex organization	5.54	40	1.35e-16
GO:BP	ribosomal small subunit biogenesis	7.36	31	2.14e-16
GO:BP	DNA replication	4.95	39	2.28e-14
GO:BP	organonitrogen compound metabolic process	1.50	331	2.81e-14
GO:BP	DNA metabolic process	2.74	82	3.18e-14
GO:BP	cellular component biogenesis	1.83	182	5.57e-14
GO:BP	DNA-templated DNA replication	5.29	33	8.34e-13
GO:BP	protein metabolic process	1.52	261	2.39e-11
GO:BP	ribosome assembly	8.13	20	6.51e-11
GO:BP	aerobic respiration	5.10	29	1.17e-10
GO:BP	protein folding	4.00	35	6.76e-10
GO:BP	oxidative phosphorylation	6.29	22	1.17e-09
GO:BP	protein-containing complex organization	1.95	112	1.17e-09
GO:BP	protein-containing complex assembly	2.19	83	2.81e-09

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	cellular respiration	4.50	29	2.81e-09
GO:BP	DNA damage response	2.35	69	7.26e-09
GO:BP	maturation of LSU-rRNA	8.13	16	1.88e-08
GO:BP	ATP synthesis coupled electron transport	6.10	18	1.95e-07
GO:BP	nucleoside triphosphate metabolic process	3.95	27	2.73e-07
GO:BP	cellular process	1.10	827	3.50e-07
GO:BP	maturation of SSU-rRNA	6.22	17	4.15e-07
GO:BP	electron transport chain	5.08	20	5.49e-07
GO:BP	mitochondrial ATP synthesis coupled electron transport	6.10	17	5.49e-07
GO:BP	ribonucleoside triphosphate metabolic process	4.14	24	8.49e-07
GO:BP	generation of precursor metabolites and energy	2.77	40	1.13e-06
GO:BP	regulation of DNA replication	6.23	16	1.18e-06
GO:BP	DNA repair	2.39	51	1.44e-06
GO:BP	aerobic electron transport chain	5.97	16	2.15e-06
GO:BP	respiratory electron transport chain	4.99	18	4.43e-06
GO:BP	cellular response to stress	1.79	90	5.95e-06
GO:BP	ribosomal large subunit assembly	10.16	10	9.32e-06
GO:BP	maturation of 5.8S rRNA	6.79	13	1.21e-05
GO:BP	nucleoside triphosphate biosynthetic process	5.23	16	1.41e-05
GO:BP	energy derivation by oxidation of organic compounds	3.00	30	1.49e-05

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	ATP metabolic process	4.29	19	1.86e-05
GO:BP	mitochondrion organization	2.51	39	1.97e-05
GO:BP	purine ribonucleoside triphosphate metabolic process	3.88	21	2.09e-05
GO:BP	mRNA processing	2.50	39	2.09e-05
GO:BP	RNA localization	3.69	22	2.39e-05
GO:BP	regulation of DNA metabolic process	2.92	30	2.42e-05
GO:BP	tRNA metabolic process	2.81	31	3.49e-05
GO:BP	mRNA metabolic process	2.21	47	4.07e-05
GO:BP	purine nucleoside triphosphate metabolic process	3.69	21	4.37e-05
GO:BP	ribonucleoside triphosphate biosynthetic process	5.45	14	5.12e-05
GO:BP	nuclear transport	2.79	30	5.99e-05
GO:BP	nucleocytoplasmic transport	2.79	30	5.99e-05
GO:BP	'de novo' post-translational protein folding	8.31	10	6.05e-05
GO:BP	mitochondrial transport	3.47	22	6.14e-05
GO:BP	nucleobase-containing small molecule metabolic process	2.04	53	7.60e-05
GO:BP	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	6.27	12	8.09e-05
GO:BP	'de novo' protein folding	7.95	10	8.96e-05
GO:BP	cellular component organization or biogenesis	1.26	310	9.53e-05
GO:BP	nucleoside monophosphate biosynthetic process	5.12	14	9.79e-05

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	cell cycle checkpoint signaling	3.59	20	1.16e-04
GO:BP	regulation of cell cycle process	2.18	44	1.16e-04
GO:BP	RNA splicing	2.51	33	1.35e-04
GO:BP	regulation of cell cycle	1.95	55	1.68e-04
GO:BP	nucleotide metabolic process	2.10	46	1.68e-04
GO:BP	translational initiation	5.78	12	1.79e-04
GO:BP	nucleobase-containing compound transport	3.22	22	1.83e-04
GO:BP	mRNA splicing, via spliceosome	2.70	28	2.22e-04
GO:BP	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	2.70	28	2.22e-04
GO:BP	RNA splicing, via transesterification reactions	2.70	28	2.22e-04
GO:BP	nucleotide biosynthetic process	2.53	31	2.28e-04
GO:BP	protein maturation	2.16	42	2.32e-04
GO:BP	establishment of RNA localization	3.70	18	2.32e-04
GO:BP	mitochondrial transmembrane transport	3.70	18	2.32e-04
GO:BP	nucleic acid transport	3.70	18	2.32e-04
GO:BP	RNA transport	3.70	18	2.32e-04
GO:BP	nucleoside phosphate biosynthetic process	2.50	31	2.80e-04
GO:BP	nuclear export	3.33	20	3.06e-04
GO:BP	nucleoside monophosphate metabolic process	4.57	14	3.08e-04

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	chaperone cofactor-dependent protein refolding	7.84	9	3.37e-04
GO:BP	regulation of protein stability	3.41	19	3.76e-04
GO:BP	formation of cytoplasmic translation initiation complex	11.64	7	3.80e-04
GO:BP	cytoplasmic translational initiation	7.48	9	4.85e-04
GO:BP	nucleoside phosphate metabolic process	2.00	46	4.85e-04
GO:BP	protein stabilization	3.85	16	4.94e-04
GO:BP	chromosome organization	2.15	38	6.51e-04
GO:BP	DNA integrity checkpoint signaling	3.75	16	6.72e-04
GO:BP	regulation of cell cycle phase transition	2.42	30	6.83e-04
GO:BP	ribose phosphate metabolic process	2.19	36	7.72e-04
GO:BP	ribonucleoside monophosphate biosynthetic process	4.88	12	8.23e-04
GO:BP	small molecule metabolic process	1.50	106	8.46e-04
GO:BP	response to stress	1.45	123	9.23e-04
GO:BP	proton motive force-driven ATP synthesis	6.86	9	9.28e-04
GO:BP	mitochondrial DNA metabolic process	9.85	7	1.15e-03
GO:BP	ATP biosynthetic process	6.58	9	1.26e-03
GO:BP	mitochondrial electron transport, NADH to ubiquinone	6.58	9	1.26e-03
GO:BP	viral gene expression	18.29	5	1.45e-03
GO:BP	chaperone-mediated protein folding	5.03	11	1.45e-03
GO:BP	purine ribonucleoside triphosphate biosynthetic process	5.03	11	1.45e-03

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	nuclear DNA replication	6.33	9	1.67e-03
GO:BP	cell cycle DNA replication	6.33	9	1.67e-03
GO:BP	purine nucleoside triphosphate biosynthetic process	4.91	11	1.78e-03
GO:BP	DNA strand elongation involved in DNA replication	7.32	8	1.93e-03
GO:BP	ribose phosphate biosynthetic process	2.55	24	2.07e-03
GO:BP	ribonucleoside monophosphate metabolic process	4.39	12	2.07e-03
GO:BP	ribonucleotide metabolic process	2.12	34	2.14e-03
GO:BP	DNA strand elongation	6.97	8	2.67e-03
GO:BP	ribosomal small subunit assembly	8.54	7	2.70e-03
GO:BP	RNA export from nucleus	3.77	13	4.16e-03
GO:BP	DNA replication checkpoint signaling	6.36	8	5.00e-03
GO:BP	import into the mitochondrion	3.92	12	5.82e-03
GO:BP	rRNA modification	5.14	9	7.66e-03
GO:BP	positive regulation of signal transduction by p53 class mediator	13.06	5	8.24e-03
GO:BP	GMP biosynthetic process	9.15	6	8.32e-03
GO:BP	ribonucleotide biosynthetic process	2.42	22	8.55e-03
GO:BP	protein targeting to mitochondrion	3.66	12	1.06e-02
GO:BP	establishment of protein localization to organelle	1.91	35	1.13e-02
GO:BP	negative regulation of cell cycle phase transition	2.49	20	1.22e-02
GO:BP	'de novo' IMP biosynthetic process	11.43	5	1.51e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	non-membrane-bounded organelle assembly	1.99	30	1.66e-02
GO:BP	negative regulation of cell cycle	2.19	24	1.71e-02
GO:BP	DNA replication initiation	5.23	8	1.71e-02
GO:BP	XMP biosynthetic process	18.29	4	1.71e-02
GO:BP	'de novo' XMP biosynthetic process	18.29	4	1.71e-02
GO:BP	viral translation	18.29	4	1.71e-02
GO:BP	XMP metabolic process	18.29	4	1.71e-02
GO:BP	negative regulation of DNA metabolic process	3.43	12	1.71e-02
GO:BP	AMP biosynthetic process	7.84	6	1.71e-02
GO:BP	GMP metabolic process	7.84	6	1.71e-02
GO:BP	regulation of DNA-templated DNA replication	7.84	6	1.71e-02
GO:BP	mitochondrial genome maintenance	6.10	7	1.85e-02
GO:BP	regulation of signal transduction by p53 class mediator	6.10	7	1.85e-02
GO:BP	mitotic cell cycle	1.69	45	2.01e-02
GO:BP	mitotic cell cycle checkpoint signaling	3.13	13	2.10e-02
GO:BP	positive regulation of translation	3.59	11	2.11e-02
GO:BP	carbohydrate derivative biosynthetic process	1.64	49	2.14e-02
GO:BP	protein import into nucleus	2.80	15	2.20e-02
GO:BP	DNA geometric change	4.33	9	2.22e-02
GO:BP	'de novo' AMP biosynthetic process	10.16	5	2.26e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	cellular component assembly	1.34	117	2.26e-02
GO:BP	double-strand break repair via break-induced replication	7.32	6	2.28e-02
GO:BP	immunoglobulin production involved in immunoglobulin-mediated immune response	5.82	7	2.28e-02
GO:BP	carbohydrate derivative metabolic process	1.49	69	2.28e-02
GO:BP	negative regulation of cell cycle process	2.26	21	2.46e-02
GO:BP	purine ribonucleotide metabolic process	1.94	29	2.52e-02
GO:BP	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	5.57	7	2.86e-02
GO:BP	regulation of apoptotic signaling pathway	2.29	20	2.86e-02
GO:BP	tRNA aminoacylation	3.41	11	2.94e-02
GO:BP	regulation of G2/M transition of mitotic cell cycle	3.41	11	2.94e-02
GO:BP	protein localization to nucleus	2.49	17	3.01e-02
GO:BP	import into nucleus	2.69	15	3.01e-02
GO:BP	macromolecule methylation	2.81	14	3.04e-02
GO:BP	cell cycle	1.47	69	3.10e-02
GO:BP	regulation of translation	2.26	20	3.13e-02
GO:BP	telomere maintenance	3.35	11	3.13e-02
GO:BP	mitochondrial DNA replication	9.15	5	3.13e-02
GO:BP	somatic recombination of immunoglobulin genes involved in immune response	9.15	5	3.13e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	somatic diversification of immunoglobulins involved in immune response	9.15	5	3.13e-02
GO:BP	isotype switching	9.15	5	3.13e-02
GO:BP	positive regulation of gene expression	1.74	37	3.13e-02
GO:BP	NADH dehydrogenase complex assembly	4.57	8	3.13e-02
GO:BP	mitochondrial respiratory chain complex I assembly	4.57	8	3.13e-02
GO:BP	purine nucleoside monophosphate biosynthetic process	4.57	8	3.13e-02
GO:BP	purine ribonucleoside monophosphate biosynthetic process	4.57	8	3.13e-02
GO:BP	tRNA transport	14.63	4	3.24e-02
GO:BP	RNA modification	2.30	19	3.26e-02
GO:BP	establishment of protein localization to mitochondrion	3.09	12	3.30e-02
GO:BP	DNA recombination	2.07	23	3.64e-02
GO:BP	DNA-templated DNA replication maintenance of fidelity	4.43	8	3.69e-02
GO:BP	protein targeting	2.11	22	3.80e-02
GO:BP	amino acid activation	3.25	11	3.83e-02
GO:BP	protein localization to mitochondrion	3.01	12	4.05e-02
GO:BP	telomere organization	3.19	11	4.28e-02
GO:BP	translational elongation	4.30	8	4.31e-02
GO:BP	regulation of DNA strand elongation	8.31	5	4.39e-02
GO:BP	mitotic cell cycle process	1.71	36	4.39e-02
GO:BP	purine nucleotide metabolic process	1.76	33	4.40e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	regulation of apoptotic process	1.58	46	4.77e-02
GO:BP	mitochondrial gene expression	2.93	12	4.86e-02
GO:BP	cell cycle process	1.50	57	4.88e-02
GO:BP	organelle organization	1.23	174	4.94e-02
Cellular Component				
GO:CC	ribonucleoprotein complex	5.28	181	7.13e-79
GO:CC	ribosome	8.45	100	9.07e-64
GO:CC	ribosomal subunit	9.31	90	8.18e-62
GO:CC	cytosolic ribosome	10.70	69	3.41e-52
GO:CC	intracellular anatomical structure	1.26	951	6.67e-51
GO:CC	membrane-enclosed lumen	2.62	271	6.67e-51
GO:CC	intracellular organelle lumen	2.62	271	6.67e-51
GO:CC	organelle lumen	2.62	271	6.67e-51
GO:CC	nucleolus	4.68	111	8.60e-42
GO:CC	intracellular organelle	1.33	823	1.15e-41
GO:CC	protein-containing complex	1.73	467	5.00e-40
GO:CC	organelle	1.30	829	4.21e-37
GO:CC	nuclear lumen	2.49	221	4.84e-37
GO:CC	intracellular membrane-bounded organelle	1.39	719	2.65e-36
GO:CC	non-membrane-bounded organelle	1.85	362	1.14e-34

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:CC	intracellular non-membrane-bounded organelle	1.85	361	2.45e-34
GO:CC	large ribosomal subunit	8.79	52	1.03e-33
GO:CC	membrane-bounded organelle	1.34	729	1.48e-31
GO:CC	cytosolic large ribosomal subunit	10.51	40	1.85e-29
GO:CC	mitochondrion	2.46	177	2.97e-28
GO:CC	cytosol	2.09	237	4.82e-28
GO:CC	small ribosomal subunit	10.00	37	3.59e-26
GO:CC	nucleus	1.53	462	4.75e-26
GO:CC	preribosome	8.06	43	6.98e-26
GO:CC	cytosolic small ribosomal subunit	12.20	29	1.62e-23
GO:CC	cytoplasm	1.29	685	9.10e-22
GO:CC	mitochondrial protein-containing complex	4.57	55	9.42e-20
GO:CC	nuclear protein-containing complex	2.21	137	2.38e-17
GO:CC	organelle envelope	2.56	101	8.81e-17
GO:CC	small-subunit processome	8.20	26	1.78e-15
GO:CC	mitochondrial matrix	3.99	42	9.69e-13
GO:CC	nucleoplasm	1.94	133	3.47e-12
GO:CC	mitochondrial envelope	2.71	68	3.51e-12
GO:CC	mitochondrial inner membrane	3.34	50	3.51e-12
GO:CC	organelle inner membrane	3.14	54	4.23e-12

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:CC	90S preribosome	8.05	20	1.61e-11
GO:CC	inner mitochondrial membrane protein complex	4.50	29	6.05e-10
GO:CC	mitochondrial membrane	2.58	60	8.01e-10
GO:CC	chromosome	1.98	91	1.20e-08
GO:CC	organellar ribosome	5.03	21	5.82e-08
GO:CC	mitochondrial ribosome	5.03	21	5.82e-08
GO:CC	catalytic complex	1.63	136	2.38e-07
GO:CC	translation preinitiation complex	13.10	9	1.03e-06
GO:CC	eukaryotic 48S preinitiation complex	15.14	8	1.98e-06
GO:CC	eukaryotic translation initiation factor 3 complex	12.17	9	2.20e-06
GO:CC	protein folding chaperone complex	7.33	12	4.35e-06
GO:CC	eukaryotic 43S preinitiation complex	12.62	8	1.11e-05
GO:CC	preribosome, large subunit precursor	8.60	10	1.27e-05
GO:CC	nuclear chromosome	3.03	25	3.48e-05
GO:CC	spliceosomal complex	2.63	29	8.28e-05
GO:CC	replication fork	4.82	13	1.51e-04
GO:CC	mitochondrial large ribosomal subunit	4.73	13	1.79e-04
GO:CC	organellar large ribosomal subunit	4.73	13	1.79e-04
GO:CC	nuclear envelope	2.30	34	1.90e-04
GO:CC	oxidoreductase complex	4.27	14	2.31e-04

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:CC	protein-DNA complex	1.89	52	2.33e-04
GO:CC	U2-type spliceosomal complex	4.32	13	4.48e-04
GO:CC	sno(s)RNA-containing ribonucleoprotein complex	7.57	8	6.08e-04
GO:CC	mitochondrial proton-transporting ATP synthase complex	6.08	9	8.94e-04
GO:CC	proton-transporting ATP synthase complex	5.87	9	1.16e-03
GO:CC	Ctf18 RFC-like complex	15.77	5	1.30e-03
GO:CC	catalytic step 2 spliceosome	3.40	14	2.49e-03
GO:CC	chaperonin-containing T-complex	7.36	7	2.67e-03
GO:CC	mitochondrial small ribosomal subunit	6.06	8	2.67e-03
GO:CC	organellar small ribosomal subunit	6.06	8	2.67e-03
GO:CC	Sm-like protein family complex	3.57	13	2.69e-03
GO:CC	nuclear pore	3.51	13	3.05e-03
GO:CC	respiratory chain complex	5.82	8	3.33e-03
GO:CC	spliceosomal snRNP complex	3.86	11	4.98e-03
GO:CC	mitochondrial intermembrane space	4.73	9	5.04e-03
GO:CC	respirasome	5.22	8	6.59e-03
GO:CC	small nuclear ribonucleoprotein complex	3.65	11	7.47e-03
GO:CC	organelle envelope lumen	4.37	9	8.53e-03
GO:CC	endopeptidase complex	3.11	13	8.59e-03
GO:CC	spliceosomal tri-snRNP complex	4.88	8	9.58e-03

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:CC	proton-transporting ATP synthase complex, coupling factor F(o)	7.10	6	1.05e-02
GO:CC	preribosome, small subunit precursor	7.10	6	1.05e-02
GO:CC	peptidase complex	2.70	15	1.18e-02
GO:CC	DNA replication preinitiation complex	9.46	5	1.18e-02
GO:CC	eukaryotic translation initiation factor 3 complex, eIF3m	15.14	4	1.26e-02
GO:CC	U2-type prespliceosome	6.31	6	1.77e-02
GO:CC	prespliceosome	6.31	6	1.77e-02
GO:CC	cytochrome complex	5.10	7	1.77e-02
GO:CC	fibrillar center	3.44	10	1.94e-02
GO:CC	chromatin	1.64	41	2.10e-02
GO:CC	Arp2/3 protein complex	7.89	5	2.33e-02
GO:CC	Ino80 complex	7.89	5	2.33e-02
GO:CC	nuclear membrane	2.38	16	2.43e-02
GO:CC	proton-transporting two-sector ATPase complex	3.26	10	2.66e-02
GO:CC	INO80-type complex	5.68	6	2.68e-02
GO:CC	MCM complex	7.28	5	3.08e-02
GO:CC	organelle membrane	1.25	140	3.13e-02
GO:CC	rough endoplasmic reticulum	3.88	8	3.13e-02
GO:CC	mitochondrial respirasome	5.16	6	3.92e-02
GO:CC	exosome (RNase complex)	5.16	6	3.92e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:CC	mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)	6.76	5	3.92e-02
Molecular Function				
GO:MF	structural constituent of ribosome	9.21	88	5.28e-59
GO:MF	RNA binding	3.20	181	1.08e-43
GO:MF	nucleic acid binding	1.74	292	1.36e-21
GO:MF	structural molecule activity	2.69	109	8.75e-19
GO:MF	organic cyclic compound binding	1.43	438	2.05e-17
GO:MF	rRNA binding	7.82	21	8.21e-11
GO:MF	translation regulator activity	4.84	29	8.60e-10
GO:MF	snoRNA binding	10.84	14	7.89e-09
GO:MF	translation factor activity, RNA binding	5.36	23	1.83e-08
GO:MF	translation regulator activity, nucleic acid binding	4.94	24	3.61e-08
GO:MF	unfolded protein binding	4.65	25	4.96e-08
GO:MF	catalytic activity, acting on a nucleic acid	2.13	71	3.41e-07
GO:MF	identical protein binding	2.09	58	2.05e-05
GO:MF	translation initiation factor activity	5.58	15	2.21e-05
GO:MF	ATP-dependent protein folding chaperone	4.92	15	1.11e-04
GO:MF	protein folding chaperone	4.01	17	2.99e-04
GO:MF	catalytic activity, acting on DNA	2.37	32	1.02e-03

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:MF	mRNA binding	2.26	35	1.02e-03
GO:MF	DNA helicase activity	4.66	13	1.02e-03
GO:MF	catalytic activity, acting on RNA	2.07	41	1.27e-03
GO:MF	single-stranded DNA binding	3.64	16	1.61e-03
GO:MF	hydrolase activity, acting on acid anhydrides	1.66	71	1.87e-03
GO:MF	ribonucleoprotein complex binding	3.39	17	1.91e-03
GO:MF	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor	7.74	8	2.16e-03
GO:MF	pyrophosphatase activity	1.65	70	2.23e-03
GO:MF	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	1.64	70	2.65e-03
GO:MF	ribosome binding	3.99	13	3.66e-03
GO:MF	single-stranded DNA helicase activity	7.04	8	3.73e-03
GO:MF	oxidoreductase activity, acting on NAD(P)H	4.63	11	4.18e-03
GO:MF	ATP-dependent activity, acting on DNA	2.75	20	4.94e-03
GO:MF	helicase activity	2.66	21	4.94e-03
GO:MF	catalytic activity, acting on a tRNA	2.83	19	4.94e-03
GO:MF	translation elongation factor activity	7.53	7	7.78e-03
GO:MF	NADH dehydrogenase (ubiquinone) activity	9.68	6	7.91e-03
GO:MF	heat shock protein binding	3.45	13	1.17e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:MF	protein-folding chaperone binding	3.45	13	1.17e-02
GO:MF	oxidoreductase activity	1.55	68	1.17e-02
GO:MF	proton transmembrane transporter activity	2.79	17	1.23e-02
GO:MF	oxidoreduction-driven active transmembrane transporter activity	6.77	7	1.26e-02
GO:MF	ribonucleoside triphosphate phosphatase activity	1.57	61	1.65e-02
GO:MF	ATP hydrolysis activity	1.81	38	1.92e-02
GO:MF	electron transfer activity	5.16	8	2.07e-02
GO:MF	isomerase activity	2.25	21	3.26e-02
GO:MF	poly(U) RNA binding	9.68	5	3.33e-02
GO:MF	nucleotide binding	1.24	173	3.69e-02
GO:MF	nucleoside phosphate binding	1.24	173	3.69e-02
GO:MF	structural constituent of nuclear pore	5.42	7	3.82e-02
GO:MF	heterocyclic compound binding	1.23	180	4.54e-02

Table 3A: Gene ontology analysis of Significantly Upregulated DEGs identified at 24-hpi

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
Biological Process				
GO:BP	primary metabolic process	1.32	558	9.52e-14
GO:BP	protein metabolic process	1.48	313	1.04e-10

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	protein modification process	1.68	202	1.04e-10
GO:BP	macromolecule metabolic process	1.35	435	1.22e-10
GO:BP	organonitrogen compound metabolic process	1.39	381	1.64e-10
GO:BP	metabolic process	1.25	609	1.89e-10
GO:BP	macromolecule modification	1.62	212	2.68e-10
GO:BP	catabolic process	1.71	165	3.58e-09
GO:BP	secondary alcohol biosynthetic process	7.40	17	6.60e-08
GO:BP	transport	1.41	283	9.39e-08
GO:BP	establishment of localization	1.40	298	9.39e-08
GO:BP	sterol biosynthetic process	6.99	17	1.44e-07
GO:BP	macromolecule catabolic process	1.95	90	5.00e-07
GO:BP	localization	1.34	322	9.94e-07
GO:BP	organonitrogen compound catabolic process	1.84	100	1.01e-06
GO:BP	nitrogen compound transport	1.73	118	1.35e-06
GO:BP	protein catabolic process	2.07	71	2.36e-06
GO:BP	establishment of localization in cell	1.60	145	2.78e-06
GO:BP	cholesterol biosynthetic process	7.14	14	3.72e-06
GO:BP	regulation of catabolic process	2.09	66	5.48e-06
GO:BP	intracellular protein transport	2.03	69	6.74e-06
GO:BP	cellular metabolic process	1.25	422	7.24e-06

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	vesicle-mediated transport	1.66	119	8.14e-06
GO:BP	intracellular transport	1.66	118	8.14e-06
GO:BP	cellular localization	1.44	196	1.35e-05
GO:BP	ERAD pathway	6.28	14	1.77e-05
GO:BP	phytosteroid metabolic process	9.86	10	1.77e-05
GO:BP	phytosteroid biosynthetic process	9.86	10	1.77e-05
GO:BP	cellular response to stress	1.69	105	1.87e-05
GO:BP	negative regulation of gene expression	2.15	54	3.27e-05
GO:BP	macromolecule localization	1.48	162	4.06e-05
GO:BP	peptidyl-amino acid modification	2.40	42	4.49e-05
GO:BP	heparan sulfate proteoglycan biosynthetic process	7.75	11	5.17e-05
GO:BP	proteolysis involved in protein catabolic process	1.97	63	5.57e-05
GO:BP	proteasomal protein catabolic process	2.36	42	6.24e-05
GO:BP	regulation of metabolic process	1.27	329	6.35e-05
GO:BP	protein localization	1.51	135	1.30e-04
GO:BP	cellular macromolecule localization	1.51	135	1.34e-04
GO:BP	negative regulation of cellular metabolic process	1.64	99	1.56e-04
GO:BP	positive regulation of catabolic process	2.38	38	1.68e-04
GO:BP	steroid biosynthetic process	3.65	20	1.68e-04
GO:BP	intracellular pH reduction	6.12	12	1.68e-04

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	establishment of protein localization	1.63	100	1.68e-04
GO:BP	negative regulation of cellular process	1.37	203	1.70e-04
GO:BP	response to endoplasmic reticulum stress	3.24	23	1.76e-04
GO:BP	ergosterol metabolic process	10.76	8	1.76e-04
GO:BP	ergosterol biosynthetic process	10.76	8	1.76e-04
GO:BP	negative regulation of intracellular signal transduction	2.24	41	2.58e-04
GO:BP	alcohol biosynthetic process	3.22	22	3.23e-04
GO:BP	negative regulation of metabolic process	1.55	112	3.27e-04
GO:BP	sterol metabolic process	3.60	19	3.27e-04
GO:BP	regulation of intracellular signal transduction	1.60	99	3.58e-04
GO:BP	post-translational protein modification	1.73	75	4.24e-04
GO:BP	protein modification by small protein conjugation or removal	1.73	73	5.68e-04
GO:BP	negative regulation of biological process	1.33	216	5.68e-04
GO:BP	protein phosphorylation	1.80	64	5.84e-04
GO:BP	response to chemical	1.49	123	6.61e-04
GO:BP	response to stress	1.42	149	8.20e-04
GO:BP	secondary alcohol metabolic process	3.50	18	8.20e-04
GO:BP	protein transport	1.62	86	8.20e-04
GO:BP	regulation of cellular metabolic process	1.26	290	8.57e-04
GO:BP	cellular catabolic process	1.76	64	1.02e-03

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	vacuolar acidification	6.16	10	1.18e-03
GO:BP	cellular lipid metabolic process	1.60	87	1.20e-03
GO:BP	regulation of signal transduction	1.41	146	1.27e-03
GO:BP	cholesterol metabolic process	3.70	16	1.34e-03
GO:BP	regulation of protein metabolic process	1.60	85	1.41e-03
GO:BP	regulation of cellular pH	3.19	19	1.47e-03
GO:BP	lipid metabolic process	1.50	105	1.77e-03
GO:BP	cellular lipid biosynthetic process	7.89	8	1.81e-03
GO:BP	regulation of response to stress	1.78	58	1.81e-03
GO:BP	ubiquitin-dependent protein catabolic process	1.89	49	1.89e-03
GO:BP	regulation of cytokine production	2.27	32	2.03e-03
GO:BP	regulation of protein catabolic process	2.47	27	2.19e-03
GO:BP	regulation of response to stimulus	1.34	179	2.19e-03
GO:BP	proteoglycan metabolic process	3.70	15	2.31e-03
GO:BP	lipid biosynthetic process	1.77	57	2.31e-03
GO:BP	positive regulation of biological process	1.26	249	2.53e-03
GO:BP	negative regulation of cellular biosynthetic process	1.57	83	2.79e-03
GO:BP	regulation of intracellular pH	3.13	18	2.85e-03
GO:BP	modification-dependent protein catabolic process	1.84	49	2.99e-03
GO:BP	regulation of pH	2.99	19	3.08e-03

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	modification-dependent macromolecule catabolic process	1.84	49	3.12e-03
GO:BP	response to organonitrogen compound	2.06	37	3.12e-03
GO:BP	positive regulation of signal transduction	1.64	70	3.22e-03
GO:BP	negative regulation of biosynthetic process	1.56	83	3.32e-03
GO:BP	positive regulation of metabolic process	1.38	142	3.34e-03
GO:BP	peptidyl-threonine modification	5.28	10	3.48e-03
GO:BP	autophagy	2.33	28	3.55e-03
GO:BP	process utilizing autophagic mechanism	2.33	28	3.55e-03
GO:BP	homeostatic process	1.60	73	3.78e-03
GO:BP	regulation of macromolecule metabolic process	1.22	291	3.83e-03
GO:BP	protein folding	2.40	26	3.87e-03
GO:BP	steroid metabolic process	2.50	24	4.19e-03
GO:BP	proteoglycan biosynthetic process	3.85	13	4.99e-03
GO:BP	response to nitrogen compound	1.93	40	5.15e-03
GO:BP	organic hydroxy compound biosynthetic process	2.48	23	6.55e-03
GO:BP	proteolysis	1.45	101	6.55e-03
GO:BP	regulation of proteolysis involved in protein catabolic process	2.78	19	6.74e-03
GO:BP	vacuolar transport	2.47	23	7.10e-03
GO:BP	regulation of cell communication	1.33	158	7.93e-03
GO:BP	establishment of protein localization to organelle	1.85	42	7.96e-03

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	negative regulation of macromolecule biosynthetic process	1.53	79	8.47e-03
GO:BP	glycoprotein metabolic process	1.88	40	8.79e-03
GO:BP	intracellular signal transduction	1.39	119	8.90e-03
GO:BP	negative regulation of macromolecule metabolic process	1.45	97	9.56e-03
GO:BP	phosphorus metabolic process	1.31	160	9.82e-03
GO:BP	regulation of signaling	1.32	158	1.06e-02
GO:BP	sulfur compound biosynthetic process	2.75	18	1.13e-02
GO:BP	positive regulation of cell communication	1.53	74	1.13e-02
GO:BP	positive regulation of signaling	1.53	74	1.13e-02
GO:BP	endocytosis	1.83	41	1.20e-02
GO:BP	phosphate-containing compound metabolic process	1.31	158	1.20e-02
GO:BP	regulation of autophagy	2.31	24	1.20e-02
GO:BP	positive regulation of cellular process	1.24	217	1.54e-02
GO:BP	regulation of apoptotic process	1.62	58	1.54e-02
GO:BP	carbohydrate derivative metabolic process	1.47	84	1.58e-02
GO:BP	cellular biosynthetic process	1.24	220	1.58e-02
GO:BP	response to topologically incorrect protein	3.00	15	1.61e-02
GO:BP	positive regulation of protein catabolic process	2.64	18	1.71e-02
GO:BP	biosynthetic process	1.21	252	1.72e-02
GO:BP	positive regulation of protein metabolic process	1.67	50	1.78e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	positive regulation of apoptotic process	2.19	25	1.78e-02
GO:BP	regulation of lysosomal lumen pH	8.07	6	1.86e-02
GO:BP	cytosolic transport	2.78	16	2.09e-02
GO:BP	positive regulation of response to stimulus	1.43	90	2.09e-02
GO:BP	regulation of programmed cell death	1.58	59	2.12e-02
GO:BP	morphogenesis of embryonic epithelium	3.70	11	2.25e-02
GO:BP	small molecule biosynthetic process	1.72	44	2.28e-02
GO:BP	chemical homeostasis	1.61	54	2.28e-02
GO:BP	regulation of defense response	1.88	34	2.33e-02
GO:BP	embryonic morphogenesis	2.03	28	2.34e-02
GO:BP	lysosomal lumen acidification	10.57	5	2.34e-02
GO:BP	protein modification by small protein conjugation	1.59	56	2.50e-02
GO:BP	negative regulation of cytokine production	3.15	13	2.50e-02
GO:BP	cell death	1.73	42	2.50e-02
GO:BP	programmed cell death	1.73	42	2.50e-02
GO:BP	intracellular monoatomic cation homeostasis	1.82	36	2.50e-02
GO:BP	regulation of primary metabolic process	1.20	262	2.50e-02
GO:BP	protein modification by small protein removal	2.51	18	2.60e-02
GO:BP	intracellular monoatomic ion homeostasis	1.82	36	2.63e-02
GO:BP	monoatomic ion homeostasis	1.75	40	2.65e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	sulfur compound metabolic process	1.95	30	2.66e-02
GO:BP	embryonic epithelial tube formation	3.89	10	2.70e-02
GO:BP	regulation of cytoplasmic pattern recognition receptor signaling pathway	3.89	10	2.70e-02
GO:BP	positive regulation of programmed cell death	2.10	25	2.71e-02
GO:BP	monoatomic cation homeostasis	1.75	39	2.96e-02
GO:BP	positive regulation of macromolecule metabolic process	1.32	123	3.22e-02
GO:BP	epithelial tube formation	3.79	10	3.22e-02
GO:BP	regulation of cellular catabolic process	2.07	25	3.36e-02
GO:BP	tissue morphogenesis	2.10	24	3.43e-02
GO:BP	protein ubiquitination	1.60	51	3.47e-02
GO:BP	protein maturation	1.70	41	3.55e-02
GO:BP	regulation of proteasomal protein catabolic process	2.60	16	3.55e-02
GO:BP	positive regulation of intracellular signal transduction	1.61	49	3.55e-02
GO:BP	chaperone-mediated protein folding	3.70	10	3.73e-02
GO:BP	cellular homeostasis	1.64	45	3.99e-02
GO:BP	macroautophagy	2.32	19	4.03e-02
GO:BP	neural tube formation	4.03	9	4.08e-02
GO:BP	phospholipid metabolic process	1.71	39	4.17e-02
GO:BP	protein export from nucleus	4.55	8	4.17e-02
GO:BP	protein localization to organelle	1.53	57	4.32e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	vacuole organization	2.24	20	4.33e-02
GO:BP	protein localization to vacuole	2.76	14	4.39e-02
GO:BP	vesicle organization	1.89	29	4.52e-02
GO:BP	phosphorylation	1.42	79	4.67e-02
GO:BP	cellular response to topologically incorrect protein	2.87	13	4.82e-02
GO:BP	peptidyl-serine modification	2.87	13	4.82e-02
GO:BP	phospholipid biosynthetic process	2.03	24	4.91e-02
GO:BP	proteasome-mediated ubiquitin-dependent protein catabolic process	1.90	28	4.97e-02
Cellular Component				
GO:CC	cytoplasm	1.30	827	6.20e-27
GO:CC	intracellular membrane-bounded organelle	1.30	805	3.83e-25
GO:CC	membrane-bounded organelle	1.26	822	4.43e-22
GO:CC	endomembrane system	1.68	315	1.99e-20
GO:CC	intracellular anatomical structure	1.16	1,043	5.44e-20
GO:CC	organelle membrane	1.82	244	1.57e-19
GO:CC	intracellular organelle	1.19	881	2.20e-16
GO:CC	organelle	1.17	893	9.33e-14
GO:CC	endoplasmic reticulum	1.88	145	8.54e-12
GO:CC	bounding membrane of organelle	1.89	141	1.37e-11
GO:CC	cytosol	1.58	214	4.32e-10

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:CC	organelle subcompartment	1.93	111	1.94e-09
GO:CC	vacuole	2.48	64	2.52e-09
GO:CC	lysosome	2.62	52	2.58e-08
GO:CC	lytic vacuole	2.59	52	3.79e-08
GO:CC	organelle lumen	1.53	190	5.31e-08
GO:CC	intracellular organelle lumen	1.53	190	5.31e-08
GO:CC	membrane-enclosed lumen	1.53	190	5.31e-08
GO:CC	endoplasmic reticulum subcompartment	1.98	85	9.98e-08
GO:CC	nucleoplasm	1.67	137	9.98e-08
GO:CC	endoplasmic reticulum membrane	1.98	84	1.17e-07
GO:CC	nuclear outer membrane-endoplasmic reticulum membrane network	1.94	84	2.90e-07
GO:CC	nuclear lumen	1.55	164	4.35e-07
GO:CC	cytoplasmic vesicle	1.65	128	5.29e-07
GO:CC	vacuolar membrane	2.73	39	9.21e-07
GO:CC	intracellular vesicle	1.63	128	1.01e-06
GO:CC	nucleus	1.24	447	1.08e-06
GO:CC	lysosomal membrane	3.03	32	1.47e-06
GO:CC	lytic vacuole membrane	3.03	32	1.47e-06
GO:CC	vesicle	1.56	136	3.62e-06
GO:CC	Golgi apparatus	1.68	105	4.83e-06

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:CC	vesicle membrane	1.94	66	9.55e-06
GO:CC	Golgi membrane	2.28	45	1.13e-05
GO:CC	endosome	1.81	71	3.79e-05
GO:CC	perinuclear region of cytoplasm	2.47	34	6.02e-05
GO:CC	cytoplasmic vesicle membrane	1.85	62	9.07e-05
GO:CC	endosome membrane	2.16	37	4.17e-04
GO:CC	coated vesicle	2.38	26	1.90e-03
GO:CC	membrane	1.12	612	2.43e-03
GO:CC	vacuolar proton-transporting V-type ATPase complex	6.33	8	2.95e-03
GO:CC	cation-transporting ATPase complex	4.14	11	4.36e-03
GO:CC	ATPase dependent transmembrane transport complex	3.96	11	6.39e-03
GO:CC	intracellular protein-containing complex	1.47	79	1.13e-02
GO:CC	ATPase complex	2.46	19	1.18e-02
GO:CC	clathrin-coated vesicle	2.72	16	1.23e-02
GO:CC	membrane raft	2.69	16	1.35e-02
GO:CC	membrane microdomain	2.66	16	1.48e-02
GO:CC	early endosome	1.94	28	2.07e-02
GO:CC	Golgi cisterna	3.11	12	2.23e-02
GO:CC	proton-transporting V-type ATPase complex	4.52	8	2.23e-02
GO:CC	nuclear body	1.81	33	2.23e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:CC	catalytic complex	1.30	130	2.23e-02
GO:CC	nucleolus	1.62	46	2.25e-02
GO:CC	endocytic vesicle	2.26	18	3.61e-02
GO:CC	protein-containing complex	1.13	366	4.13e-02
GO:CC	Golgi apparatus subcompartment	1.83	28	4.19e-02
Molecular Function				
GO:MF	enzyme binding	1.95	120	2.10e-09
GO:MF	protein binding	1.24	551	4.61e-08
GO:MF	identical protein binding	2.17	75	2.02e-07
GO:MF	misfolded protein binding	7.40	10	9.76e-04
GO:MF	catalytic activity	1.16	522	1.47e-03
GO:MF	kinase binding	2.08	45	1.47e-03
GO:MF	transferase activity	1.30	233	2.67e-03
GO:MF	catalytic activity, acting on a protein	1.28	230	4.88e-03
GO:MF	protein kinase binding	2.04	40	4.88e-03
GO:MF	acyltransferase activity	1.63	72	7.45e-03
GO:MF	binding	1.07	924	1.02e-02
GO:MF	manganese ion binding	4.71	10	2.12e-02
GO:MF	protein domain specific binding	2.12	28	3.51e-02
GO:MF	steroid binding	3.20	14	3.61e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:MF	lipid binding	1.57	62	4.54e-02
GO:MF	ubiquitin-like protein ligase binding	2.50	19	4.88e-02

Table 3B: Gene ontology analysis of Significantly Downregulated DEGs identified at 24-hpi

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
Biological Process				
GO:BP	translation	5.77	136	3.59e-65
GO:BP	gene expression	2.26	288	1.04e-39
GO:BP	metabolic process	1.43	761	3.14e-36
GO:BP	organonitrogen compound biosynthetic process	2.54	213	1.45e-35
GO:BP	macromolecule biosynthetic process	2.03	319	5.47e-35
GO:BP	biosynthetic process	1.78	404	6.23e-33
GO:BP	cellular metabolic process	1.55	571	2.12e-32
GO:BP	nucleobase-containing compound metabolic process	1.99	308	3.62e-32
GO:BP	primary metabolic process	1.45	670	5.01e-32
GO:BP	cellular biosynthetic process	1.83	356	7.55e-31
GO:BP	macromolecule metabolic process	1.54	540	3.53e-29
GO:BP	nucleic acid metabolic process	2.02	241	3.92e-25
GO:BP	cytoplasmic translation	8.27	33	2.36e-20

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	ribonucleoprotein complex biogenesis	3.17	84	5.63e-19
GO:BP	cell cycle	2.28	145	5.63e-19
GO:BP	organonitrogen compound metabolic process	1.46	436	4.46e-17
GO:BP	aerobic respiration	5.33	41	7.30e-17
GO:BP	cell cycle process	2.35	121	1.51e-16
GO:BP	cellular respiration	4.93	43	2.46e-16
GO:BP	mitotic cell cycle	2.64	95	5.25e-16
GO:BP	oxidative phosphorylation	6.34	30	2.57e-14
GO:BP	protein-containing complex organization	1.97	153	5.98e-14
GO:BP	protein-RNA complex organization	4.20	41	8.95e-13
GO:BP	mitotic cell cycle process	2.68	76	9.49e-13
GO:BP	protein-RNA complex assembly	4.26	40	1.03e-12
GO:BP	electron transport chain	5.64	30	1.03e-12
GO:BP	RNA metabolic process	1.89	156	1.03e-12
GO:BP	generation of precursor metabolites and energy	3.07	60	1.49e-12
GO:BP	respiratory electron transport chain	5.74	28	5.17e-12
GO:BP	nucleobase-containing compound biosynthetic process	1.80	168	6.72e-12
GO:BP	ATP synthesis coupled electron transport	6.26	25	1.40e-11
GO:BP	DNA metabolic process	2.27	92	2.37e-11
GO:BP	mitochondrial ATP synthesis coupled electron transport	6.37	24	2.94e-11

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	energy derivation by oxidation of organic compounds	3.40	46	5.23e-11
GO:BP	ribosome biogenesis	2.90	58	5.23e-11
GO:BP	cellular component biogenesis	1.61	217	5.62e-11
GO:BP	aerobic electron transport chain	6.35	23	9.80e-11
GO:BP	protein-containing complex assembly	2.07	106	1.19e-10
GO:BP	cellular process	1.10	1,121	1.42e-10
GO:BP	protein metabolic process	1.41	327	6.60e-10
GO:BP	chromosome organization	2.47	59	2.36e-08
GO:BP	nucleic acid biosynthetic process	1.75	131	2.42e-08
GO:BP	amino acid metabolic process	2.61	52	4.48e-08
GO:BP	DNA repair	2.28	66	5.27e-08
GO:BP	tRNA aminoacylation	5.04	22	5.27e-08
GO:BP	DNA replication	3.29	35	9.38e-08
GO:BP	ribosome assembly	5.71	19	9.60e-08
GO:BP	DNA damage response	2.04	81	1.12e-07
GO:BP	amino acid activation	4.80	22	1.38e-07
GO:BP	regulation of cell cycle	2.05	78	2.06e-07
GO:BP	RNA processing	1.85	99	2.56e-07
GO:BP	cellular response to stress	1.74	118	2.81e-07
GO:BP	protein-DNA complex organization	2.23	62	3.95e-07

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	RNA biosynthetic process	1.71	122	4.31e-07
GO:BP	nucleoside triphosphate metabolic process	3.36	31	5.03e-07
GO:BP	tRNA aminoacylation for protein translation	4.92	20	5.03e-07
GO:BP	nuclear division	2.71	42	6.47e-07
GO:BP	cellular component assembly	1.51	179	8.36e-07
GO:BP	organelle organization	1.38	265	8.36e-07
GO:BP	DNA-templated DNA replication	3.44	29	8.52e-07
GO:BP	chromosome segregation	2.49	47	1.02e-06
GO:BP	non-membrane-bounded organelle assembly	2.40	49	1.65e-06
GO:BP	cellular component organization or biogenesis	1.25	417	3.54e-06
GO:BP	ATP metabolic process	3.84	23	4.27e-06
GO:BP	regulation of cell cycle process	2.13	58	5.99e-06
GO:BP	small molecule metabolic process	1.54	147	7.02e-06
GO:BP	cytoplasmic translational initiation	7.38	12	7.93e-06
GO:BP	ribonucleoside triphosphate metabolic process	3.32	26	1.07e-05
GO:BP	organelle fission	2.44	42	1.11e-05
GO:BP	translational initiation	5.34	15	1.59e-05
GO:BP	tricarboxylic acid cycle	5.34	15	1.59e-05
GO:BP	nucleoside triphosphate biosynthetic process	4.35	18	2.11e-05
GO:BP	ribosomal large subunit biogenesis	3.74	21	2.61e-05

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	purine nucleoside triphosphate metabolic process	3.25	25	2.63e-05
GO:BP	rRNA processing	2.56	36	2.63e-05
GO:BP	rRNA metabolic process	2.48	38	2.68e-05
GO:BP	nucleobase-containing small molecule metabolic process	1.91	67	2.86e-05
GO:BP	ribosomal small subunit biogenesis	3.69	21	3.07e-05
GO:BP	nucleotide metabolic process	2.00	59	3.40e-05
GO:BP	nucleoside phosphate metabolic process	1.96	61	3.63e-05
GO:BP	purine ribonucleoside triphosphate metabolic process	3.28	24	3.71e-05
GO:BP	chromatin organization	2.10	51	4.41e-05
GO:BP	ribose phosphate metabolic process	2.16	48	4.64e-05
GO:BP	carboxylic acid metabolic process	1.76	78	6.39e-05
GO:BP	protein-DNA complex assembly	3.28	23	6.53e-05
GO:BP	spindle organization	2.62	32	6.68e-05
GO:BP	oxoacid metabolic process	1.75	79	6.92e-05
GO:BP	regulation of cell cycle phase transition	2.32	39	8.76e-05
GO:BP	cell division	2.28	40	9.83e-05
GO:BP	mRNA metabolic process	1.95	56	1.28e-04
GO:BP	mRNA processing	2.14	45	1.28e-04
GO:BP	RNA splicing	2.25	40	1.31e-04
GO:BP	formation of cytoplasmic translation initiation complex	9.84	8	1.51e-04

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	RNA splicing, via transesterification reactions	2.42	34	1.68e-04
GO:BP	mRNA splicing, via spliceosome	2.42	34	1.68e-04
GO:BP	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	2.42	34	1.68e-04
GO:BP	meiotic cell cycle process	2.71	28	1.68e-04
GO:BP	proton motive force-driven ATP synthesis	6.20	11	1.68e-04
GO:BP	organic acid metabolic process	1.70	80	1.79e-04
GO:BP	cell cycle checkpoint signaling	3.05	23	1.96e-04
GO:BP	nuclear chromosome segregation	2.47	32	2.06e-04
GO:BP	microtubule cytoskeleton organization involved in mitosis	2.67	28	2.13e-04
GO:BP	ATP biosynthetic process	5.95	11	2.49e-04
GO:BP	response to stress	1.40	161	3.57e-04
GO:BP	ribonucleotide metabolic process	2.03	44	5.34e-04
GO:BP	tRNA metabolic process	2.28	34	5.83e-04
GO:BP	cellular component organization	1.20	381	8.36e-04
GO:BP	organelle assembly	1.63	79	8.36e-04
GO:BP	meiotic nuclear division	2.71	24	8.57e-04
GO:BP	translational elongation	4.77	12	8.57e-04
GO:BP	meiotic cell cycle	2.42	29	8.58e-04
GO:BP	L-amino acid metabolic process	2.46	28	9.12e-04

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	ribonucleoside triphosphate biosynthetic process	4.03	14	1.00e-03
GO:BP	purine ribonucleotide metabolic process	2.03	41	1.00e-03
GO:BP	purine nucleoside triphosphate biosynthetic process	4.29	13	1.08e-03
GO:BP	purine nucleotide metabolic process	1.90	48	1.11e-03
GO:BP	purine-containing compound metabolic process	1.86	50	1.20e-03
GO:BP	mitochondrial transport	2.68	23	1.42e-03
GO:BP	mitotic spindle organization	2.76	22	1.43e-03
GO:BP	sister chromatid segregation	2.91	20	1.62e-03
GO:BP	mitochondrial electron transport, NADH to ubiquinone	5.41	10	1.70e-03
GO:BP	chromatin remodeling	2.07	37	1.70e-03
GO:BP	proteinogenic amino acid metabolic process	2.46	26	1.73e-03
GO:BP	regulation of mitotic cell cycle	2.05	37	1.99e-03
GO:BP	nucleoside phosphate biosynthetic process	2.09	35	2.32e-03
GO:BP	mitotic sister chromatid segregation	2.92	19	2.39e-03
GO:BP	mitotic nuclear division	2.82	20	2.41e-03
GO:BP	mitochondrial transmembrane transport	2.89	19	2.75e-03
GO:BP	regulation of G2/M transition of mitotic cell cycle	3.44	15	2.78e-03
GO:BP	mitochondrial translation	3.64	14	2.78e-03
GO:BP	DNA recombination	2.13	32	3.19e-03
GO:BP	fatty acid beta-oxidation	3.57	14	3.37e-03

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	mitochondrial gene expression	3.07	17	3.37e-03
GO:BP	double-strand break repair	2.15	31	3.48e-03
GO:BP	2'-deoxyribonucleotide biosynthetic process	7.89	7	3.48e-03
GO:BP	deoxyribose phosphate biosynthetic process	7.89	7	3.48e-03
GO:BP	regulation of cell cycle G2/M phase transition	3.18	16	3.60e-03
GO:BP	purine ribonucleoside triphosphate biosynthetic process	4.06	12	3.66e-03
GO:BP	nucleotide biosynthetic process	2.05	34	3.69e-03
GO:BP	mitotic cell cycle checkpoint signaling	3.03	17	3.78e-03
GO:BP	regulation of DNA replication	3.74	13	3.86e-03
GO:BP	protein peptidyl-prolyl isomerization	6.37	8	3.90e-03
GO:BP	deoxyribonucleotide biosynthetic process	6.37	8	3.90e-03
GO:BP	sexual reproduction	1.74	51	4.56e-03
GO:BP	ribose phosphate biosynthetic process	2.20	28	5.00e-03
GO:BP	DNA integrity checkpoint signaling	2.95	17	5.00e-03
GO:BP	regulation of mitotic cell cycle phase transition	2.28	26	5.00e-03
GO:BP	alpha-amino acid metabolic process	2.16	29	5.33e-03
GO:BP	negative regulation of cell cycle phase transition	2.30	25	6.05e-03
GO:BP	regulation of cellular response to stress	2.09	30	6.75e-03
GO:BP	fatty acid oxidation	3.27	14	7.85e-03
GO:BP	lipid oxidation	3.21	14	9.33e-03

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	negative regulation of cell cycle process	2.15	27	9.53e-03
GO:BP	purine nucleoside diphosphate metabolic process	3.61	12	1.02e-02
GO:BP	negative regulation of cell cycle	2.03	30	1.10e-02
GO:BP	cell cycle DNA replication	4.68	9	1.22e-02
GO:BP	nuclear DNA replication	4.68	9	1.22e-02
GO:BP	regulation of chromosome segregation	3.10	14	1.27e-02
GO:BP	ribosomal small subunit assembly	6.31	7	1.33e-02
GO:BP	alpha-amino acid biosynthetic process	3.05	14	1.48e-02
GO:BP	peptidyl-proline modification	4.51	9	1.58e-02
GO:BP	mitochondrion organization	1.81	38	1.58e-02
GO:BP	microtubule-based process	1.44	85	1.63e-02
GO:BP	glycolytic process	3.63	11	1.81e-02
GO:BP	regulation of DNA metabolic process	2.01	28	1.89e-02
GO:BP	import into the mitochondrion	3.14	13	1.89e-02
GO:BP	carbohydrate derivative metabolic process	1.42	89	1.91e-02
GO:BP	regulation of apoptotic signaling pathway	2.11	25	1.93e-02
GO:BP	centromere complex assembly	4.92	8	2.09e-02
GO:BP	ADP catabolic process	3.54	11	2.13e-02
GO:BP	regulation of mitotic metaphase/anaphase transition	3.87	10	2.13e-02
GO:BP	proteinogenic amino acid biosynthetic process	3.09	13	2.14e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	L-amino acid biosynthetic process	3.09	13	2.14e-02
GO:BP	cellular component disassembly	2.06	26	2.14e-02
GO:BP	nucleoside diphosphate metabolic process	2.91	14	2.17e-02
GO:BP	formation of translation preinitiation complex	9.66	5	2.30e-02
GO:BP	positive regulation of signal transduction by p53 class mediator	9.66	5	2.30e-02
GO:BP	ribonucleoside diphosphate metabolic process	3.25	12	2.30e-02
GO:BP	nucleoside monophosphate biosynthetic process	3.25	12	2.30e-02
GO:BP	catabolic process	1.30	138	2.31e-02
GO:BP	pyruvate metabolic process	2.87	14	2.38e-02
GO:BP	mitotic cell cycle phase transition	2.87	14	2.38e-02
GO:BP	purine nucleoside diphosphate catabolic process	3.46	11	2.38e-02
GO:BP	ADP metabolic process	3.46	11	2.38e-02
GO:BP	purine ribonucleoside diphosphate catabolic process	3.46	11	2.38e-02
GO:BP	pyridine nucleotide catabolic process	3.46	11	2.38e-02
GO:BP	regulation of metaphase/anaphase transition of cell cycle	3.76	10	2.42e-02
GO:BP	maturity of LSU-rRNA	3.76	10	2.42e-02
GO:BP	double-strand break repair via homologous recombination	2.29	20	2.53e-02
GO:BP	regulation of apoptotic process	1.53	60	2.68e-02
GO:BP	cell cycle phase transition	2.83	14	2.68e-02
GO:BP	GMP biosynthetic process	6.76	6	2.73e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	ribonucleoside diphosphate catabolic process	3.38	11	2.75e-02
GO:BP	pyridine-containing compound catabolic process	3.38	11	2.75e-02
GO:BP	purine ribonucleoside diphosphate metabolic process	3.38	11	2.75e-02
GO:BP	ribonucleotide biosynthetic process	2.04	25	2.81e-02
GO:BP	nucleobase-containing compound catabolic process	1.84	32	2.83e-02
GO:BP	deoxyribonucleotide metabolic process	4.51	8	3.17e-02
GO:BP	cellular modified amino acid metabolic process	2.19	21	3.21e-02
GO:BP	2'-deoxyribonucleotide metabolic process	5.26	7	3.23e-02
GO:BP	recombinational repair	2.24	20	3.24e-02
GO:BP	purine ribonucleotide biosynthetic process	2.09	23	3.25e-02
GO:BP	mitotic DNA integrity checkpoint signaling	3.06	12	3.38e-02
GO:BP	positive regulation of apoptotic process	2.00	25	3.42e-02
GO:BP	peptidyl-amino acid modification	1.78	34	3.42e-02
GO:BP	XMP metabolic process	13.53	4	3.42e-02
GO:BP	'de novo' XMP biosynthetic process	13.53	4	3.42e-02
GO:BP	XMP biosynthetic process	13.53	4	3.42e-02
GO:BP	mitochondrial electron transport, succinate to ubiquinone	13.53	4	3.42e-02
GO:BP	purine-containing compound biosynthetic process	1.93	27	3.50e-02
GO:BP	'de novo' IMP biosynthetic process	8.46	5	3.63e-02
GO:BP	purine nucleotide biosynthetic process	1.95	26	3.69e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:BP	tetrahydrofolate metabolic process	6.24	6	3.75e-02
GO:BP	regulation of mitotic sister chromatid separation	3.80	9	4.04e-02
GO:BP	regulation of translation	2.00	24	4.09e-02
GO:BP	deoxyribose phosphate metabolic process	4.98	7	4.10e-02
GO:BP	signal transduction in response to DNA damage	2.54	15	4.38e-02
GO:BP	macromolecule catabolic process	1.43	72	4.46e-02
GO:BP	meiosis I cell cycle process	2.43	16	4.50e-02
GO:BP	regulation of chromosome organization	2.35	17	4.54e-02
GO:BP	DNA-templated DNA replication maintenance of fidelity	3.69	9	4.84e-02
GO:BP	nucleoside monophosphate metabolic process	2.90	12	4.90e-02
GO:BP	regulation of double-strand break repair	2.90	12	4.90e-02
Cellular Component				
GO:CC	ribosome	6.68	108	4.42e-59
GO:CC	ribonucleoprotein complex	3.78	177	5.05e-54
GO:CC	ribosomal subunit	7.04	93	1.92e-53
GO:CC	cytosolic ribosome	8.63	76	4.32e-52
GO:CC	intracellular anatomical structure	1.23	1,265	8.08e-52
GO:CC	intracellular organelle	1.29	1,087	1.05e-42
GO:CC	organelle	1.26	1,100	9.05e-39
GO:CC	mitochondrion	2.39	235	6.18e-36

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:CC	non-membrane-bounded organelle	1.72	460	2.54e-35
GO:CC	intracellular non-membrane-bounded organelle	1.72	459	4.71e-35
GO:CC	protein-containing complex	1.54	570	5.76e-32
GO:CC	cytosol	1.95	302	3.27e-30
GO:CC	cytosolic large ribosomal subunit	8.46	44	4.02e-29
GO:CC	cytoplasm	1.28	929	7.97e-28
GO:CC	membrane-enclosed lumen	1.94	275	3.97e-27
GO:CC	organelle lumen	1.94	275	3.97e-27
GO:CC	intracellular organelle lumen	1.94	275	3.97e-27
GO:CC	small ribosomal subunit	8.11	41	3.74e-26
GO:CC	large ribosomal subunit	6.31	51	3.76e-26
GO:CC	intracellular membrane-bounded organelle	1.28	905	4.52e-26
GO:CC	membrane-bounded organelle	1.26	933	9.54e-25
GO:CC	cytosolic small ribosomal subunit	9.54	31	1.85e-22
GO:CC	nuclear lumen	1.85	224	6.28e-19
GO:CC	nucleus	1.36	561	2.14e-17
GO:CC	mitochondrial protein-containing complex	3.58	59	2.73e-16
GO:CC	chromosome	2.09	131	2.56e-14
GO:CC	mitochondrial matrix	3.48	50	4.42e-13
GO:CC	nucleoplasm	1.80	169	1.02e-12

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:CC	mitochondrial inner membrane	2.94	60	2.55e-12
GO:CC	organelle inner membrane	2.73	64	1.16e-11
GO:CC	catalytic complex	1.64	188	1.31e-10
GO:CC	nucleolus	2.34	76	1.62e-10
GO:CC	inner mitochondrial membrane protein complex	3.86	34	4.75e-10
GO:CC	organelle envelope	1.93	104	2.99e-09
GO:CC	mitochondrial envelope	2.13	73	3.18e-08
GO:CC	mitochondrial membrane	2.17	69	4.32e-08
GO:CC	chromosomal region	2.85	41	6.00e-08
GO:CC	chromosome, centromeric region	2.94	34	7.34e-07
GO:CC	nuclear protein-containing complex	1.60	136	7.62e-07
GO:CC	condensed chromosome	2.77	36	1.29e-06
GO:CC	mitochondrial proton-transporting ATP synthase complex	6.43	13	4.00e-06
GO:CC	oxidoreductase complex	4.24	19	4.39e-06
GO:CC	spindle	2.33	45	4.67e-06
GO:CC	proton-transporting ATP synthase complex	6.21	13	5.94e-06
GO:CC	mitochondrial small ribosomal subunit	6.65	12	8.40e-06
GO:CC	organellar small ribosomal subunit	6.65	12	8.40e-06
GO:CC	organellar ribosome	3.68	21	9.69e-06
GO:CC	mitochondrial ribosome	3.68	21	9.69e-06

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:CC	translation preinitiation complex	9.59	9	1.15e-05
GO:CC	spliceosomal complex	2.45	37	1.52e-05
GO:CC	eukaryotic 48S preinitiation complex	11.08	8	1.63e-05
GO:CC	eukaryotic translation initiation factor 3 complex	8.90	9	2.36e-05
GO:CC	eukaryotic 43S preinitiation complex	9.23	8	9.12e-05
GO:CC	kinetochore	2.89	24	1.01e-04
GO:CC	respiratory chain complex	5.86	11	1.01e-04
GO:CC	cytochrome complex	5.86	11	1.01e-04
GO:CC	respirasome	5.25	11	3.03e-04
GO:CC	condensed chromosome, centromeric region	2.70	24	3.03e-04
GO:CC	protein-DNA complex	1.72	65	3.03e-04
GO:CC	microtubule cytoskeleton	1.48	111	4.41e-04
GO:CC	U2-type spliceosomal complex	3.64	15	5.33e-04
GO:CC	small nuclear ribonucleoprotein complex	3.64	15	5.33e-04
GO:CC	centrosome	1.78	55	5.33e-04
GO:CC	proteasome core complex	6.23	9	5.43e-04
GO:CC	proton-transporting two-sector ATPase complex	3.58	15	6.27e-04
GO:CC	aminoacyl-tRNA synthetase multienzyme complex	8.08	7	1.12e-03
GO:CC	U4 snRNP	10.39	6	1.12e-03
GO:CC	mitochondrial respirasome	5.66	9	1.12e-03

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:CC	spliceosomal snRNP complex	3.59	14	1.12e-03
GO:CC	Sm-like protein family complex	3.21	16	1.16e-03
GO:CC	preribosome	2.74	20	1.16e-03
GO:CC	chromatin	1.69	58	1.18e-03
GO:CC	catalytic step 2 spliceosome	3.02	17	1.37e-03
GO:CC	replication fork	3.53	13	2.44e-03
GO:CC	spliceosomal tri-snRNP complex	4.47	10	2.72e-03
GO:CC	U2 snRNP	5.54	8	3.72e-03
GO:CC	intracellular protein-containing complex	1.44	89	4.68e-03
GO:CC	U5 snRNP	7.55	6	6.68e-03
GO:CC	pICln-Sm protein complex	9.89	5	8.41e-03
GO:CC	respiratory chain complex IV	5.70	7	9.06e-03
GO:CC	cleavage furrow	4.82	8	9.12e-03
GO:CC	Arp2/3 protein complex	6.92	6	1.02e-02
GO:CC	microtubule organizing center	1.54	60	1.02e-02
GO:CC	U1 snRNP	5.10	7	1.67e-02
GO:CC	mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)	5.93	6	2.21e-02
GO:CC	U12-type spliceosomal complex	4.62	7	2.88e-02
GO:CC	eukaryotic translation initiation factor 3 complex, eIF3m	11.08	4	3.24e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:CC	small-subunit processome	2.77	12	3.26e-02
GO:CC	tricarboxylic acid cycle heteromeric enzyme complex	6.92	5	3.76e-02
GO:CC	nuclear chromosome	1.95	22	3.89e-02
GO:CC	proton-transporting ATP synthase complex, coupling factor F(o)	5.19	6	3.99e-02
GO:CC	mitotic spindle	2.16	17	4.58e-02
Molecular Function				
GO:MF	structural constituent of ribosome	7.30	95	1.45e-55
GO:MF	RNA binding	2.37	182	6.82e-26
GO:MF	structural molecule activity	2.26	125	1.73e-15
GO:MF	nucleic acid binding	1.49	340	2.94e-13
GO:MF	organic cyclic compound binding	1.30	544	9.27e-12
GO:MF	rRNA binding	6.56	24	3.02e-11
GO:MF	translation regulator activity	3.92	32	1.15e-08
GO:MF	translation factor activity, RNA binding	4.28	25	2.61e-07
GO:MF	aminoacyl-tRNA ligase activity	5.08	20	5.57e-07
GO:MF	ligase activity, forming carbon-oxygen bonds	5.08	20	5.57e-07
GO:MF	translation regulator activity, nucleic acid binding	3.93	26	5.88e-07
GO:MF	ligase activity	2.63	45	6.96e-07
GO:MF	catalytic activity, acting on a nucleic acid	1.91	87	7.53e-07
GO:MF	catalytic activity, acting on a tRNA	3.17	29	8.40e-06

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:MF	translation initiation factor activity	4.37	16	1.74e-04
GO:MF	oxidoreductase activity	1.61	96	3.56e-04
GO:MF	NAD binding	3.78	17	5.51e-04
GO:MF	identical protein binding	1.77	67	5.59e-04
GO:MF	catalytic activity, acting on RNA	1.89	51	1.40e-03
GO:MF	electron transfer activity	5.21	11	1.73e-03
GO:MF	mRNA binding	1.99	42	2.32e-03
GO:MF	catalytic activity, acting on DNA	2.07	38	2.37e-03
GO:MF	heterocyclic compound binding	1.24	247	8.80e-03
GO:MF	nucleoside phosphate binding	1.25	236	9.04e-03
GO:MF	nucleotide binding	1.25	236	9.04e-03
GO:MF	catalytic activity	1.13	553	9.04e-03
GO:MF	isomerase activity	2.20	28	9.04e-03
GO:MF	single-stranded DNA binding	2.84	17	1.33e-02
GO:MF	oxidoreductase activity, acting on NAD(P)H	3.71	12	1.38e-02
GO:MF	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor	5.69	8	1.42e-02
GO:MF	ATP-dependent activity, acting on DNA	2.32	23	1.60e-02
GO:MF	oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	6.63	7	1.60e-02

GO Category	GO:Term	Fold	Number of	P-value
		Enrichment	DEGs	(Adjusted)
GO:MF	NAD+ binding	6.22	7	2.33e-02
GO:MF	proton transmembrane transporter activity	2.41	20	2.45e-02
GO:MF	binding	1.05	999	2.45e-02
GO:MF	translation elongation factor activity	5.53	7	4.38e-02

Table 4A: Significantly Enriched KEGG Pathways from DEGs identified at 12 and 24-hpi (Results from the DAVID online resource)

Time Point	Regulation	KEGG Term	DEG Count	Fold	P-value
				Enrichment	(Adjusted)
12-hpi	down	Ribosome	80	6.68	3.16e-49
12-hpi	down	Oxidative phosphorylation	37	3.22	1.08e-08
12-hpi	down	DNA replication	18	6.01	1.09e-08
12-hpi	down	Ribosome biogenesis in eukaryotes	27	4.03	1.09e-08
12-hpi	down	Spliceosome	30	2.50	1.25e-04
12-hpi	down	Nucleocytoplasmic transport	22	2.29	1.00e-02
12-hpi	down	Base excision repair	13	3.10	1.13e-02
12-hpi	down	Mismatch repair	9	4.29	1.13e-02
12-hpi	down	Nucleotide excision repair	14	2.86	1.29e-02
12-hpi	up	Steroid biosynthesis	10	6.14	1.65e-03
12-hpi	up	Autophagy - animal	29	2.34	2.12e-03
12-hpi	up	Cell cycle	27	2.30	3.90e-03

Table 4A: Significantly Enriched KEGG Pathways from DEGs identified at 12 and 24-hpi (Results from the DAVID online resource)

Time Point	Regulation	KEGG Term	DEG Count	Fold Enrichment	P-value (Adjusted)
12-hpi	up	Influenza A	22	2.13	4.74e-02
24-hpi	down	Ribosome	88	5.54	2.81e-49
24-hpi	down	Oxidative phosphorylation	50	3.28	2.71e-13
24-hpi	down	Carbon metabolism	39	2.98	1.08e-08
24-hpi	down	Aminoacyl-tRNA biosynthesis	22	3.78	1.10e-06
24-hpi	down	Biosynthesis of amino acids	24	3.02	2.50e-05
24-hpi	down	Citrate cycle (TCA cycle)	15	4.36	2.50e-05
24-hpi	down	DNA replication	15	3.78	1.93e-04
24-hpi	down	Spliceosome	33	2.08	1.09e-03
24-hpi	down	Metabolic pathways	225	1.22	3.04e-03
24-hpi	down	Cell cycle	36	1.89	3.04e-03
24-hpi	down	Propanoate metabolism	12	3.24	7.53e-03
24-hpi	down	Fatty acid degradation	14	2.86	7.77e-03
24-hpi	down	Glycolysis / Gluconeogenesis	17	2.42	1.19e-02
24-hpi	down	One carbon pool by folate	9	3.78	1.35e-02
24-hpi	down	Nucleotide excision repair	15	2.31	3.73e-02
24-hpi	down	Pyruvate metabolism	12	2.59	4.20e-02
24-hpi	up	Steroid biosynthesis	11	5.15	1.92e-03

Table 4A: Significantly Enriched KEGG Pathways from DEGs identified at 12 and 24-hpi (Results from the DAVID online resource)

Time Point	Regulation	KEGG Term	DEG Count	Fold Enrichment	P-value (Adjusted)
24-hpi	up	Lysosome	29	2.24	3.94e-03
24-hpi	up	Terpenoid backbone biosynthesis	9	4.43	1.73e-02
24-hpi	up	Glycosaminoglycan biosynthesis - heparan sulfate / heparin	10	3.90	1.73e-02
24-hpi	up	Protein processing in endoplasmic reticulum	30	1.94	1.73e-02
24-hpi	up	Autophagy - animal	30	1.85	3.19e-02

Table 4B: Significantly Enriched KEGG Pathways from DEGs identified at 12 and 24-hpi (Results from the gprofiler2 R package)

Time Point	Regulation	KEGG Term	DEG Count	P-value (Adjusted)
12-hpi	down	Ribosome	35	7.70e-24
12-hpi	down	DNA replication	11	5.07e-07
12-hpi	down	Oxidative phosphorylation	19	3.10e-04
12-hpi	down	Base excision repair	9	1.15e-03
12-hpi	down	One carbon pool by folate	6	1.27e-03
12-hpi	down	Mismatch repair	6	3.49e-03
12-hpi	down	Ribosome biogenesis in eukaryotes	9	1.77e-02
12-hpi	down	Nucleotide excision repair	8	3.36e-02

Table 4B: Significantly Enriched KEGG Pathways from DEGs identified at 12 and 24-hpi (Results from the gprofiler2 R package)

Time Point	Regulation	KEGG Term	DEG Count	P-value (Adjusted)
12-hpi	up	Autophagy - animal	13	2.09e-02
24-hpi	down	Ribosome	41	4.71e-28
24-hpi	down	Aminoacyl-tRNA biosynthesis	12	3.04e-04
24-hpi	down	Oxidative phosphorylation	22	4.35e-04
24-hpi	down	Base excision repair	9	1.15e-02
24-hpi	down	Carbon metabolism	14	3.14e-02
24-hpi	down	Propanoate metabolism	6	3.99e-02
24-hpi	up	Ubiquitin mediated proteolysis	17	7.26e-03
24-hpi	up	Steroid biosynthesis	5	2.63e-02

²⁵⁸ **SUPPLEMENTARY INFORMATION/MATERIALS**