

Cover pages for the supporting information

Title:

Quantitative proteomic analysis of porcine intestinal epithelial cells infected with porcine deltacoronavirus using iTRAQ-coupled LC-MS/MS

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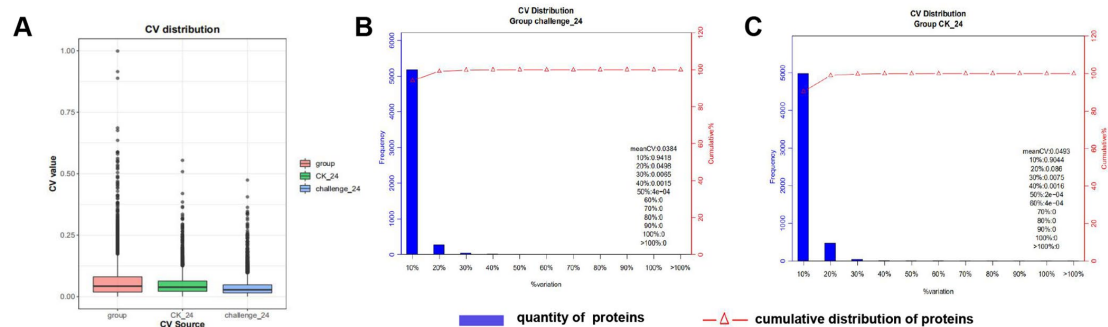
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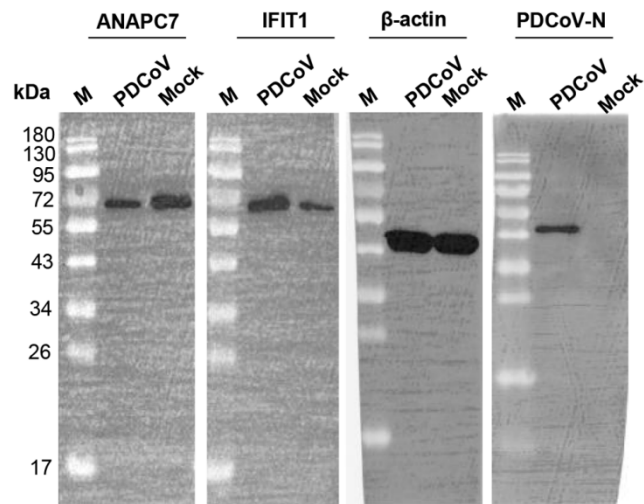
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Table. All supplementary components

File Names	Description of supporting files
Supplementary Figure S1	Repeatability analysis of different biological replicates used for iTRAQ-coupled LC–MS/MS proteomic analysis. (A) The coefficient of variation (CV) distribution between groups. (B) Repeatability analysis of three technical replicates of PDCoV-infected IPEC-J2 cells. (C) Repeatability analysis of three technical replicates of mock-infected IPEC-J2 cells. The x-axis represents the variation levels of proteins in PDCoV- or mock-infected IPEC-J2 cells between three technical replicates. The left y-axis represents the frequency of quantitative proteins (histograms) and the right y-axis represents the cumulative percentage of proteins at different variation levels (line graph).
Supplementary Figure S2	The original images of the entire PVDF membranes containing the target western blots of Figure 2C. The expected size of ANAPC7, IFIT1, β -actin and PDCoV-N proteins are 63, 57, 42 and 41 kDa, respectively.
Supplementary File S1	A total of 5502 proteins identified in PDCoV- and mock-infected IPEC-J2 cells using iTRAQ-coupled LC-MS analysis.
Supplementary File S2	Viral proteins identified in PDCoV-infected IPEC-J2 cells.
Supplementary File S3	GO function annotation of the 78 differentially expressed proteins.
Supplementary File S4	COG function classification of the 78 differentially expressed proteins.
Supplementary File S5	KEGG pathway analysis of the 78 differentially expressed proteins.
Supplementary File S6	The top 20 KEGG pathway of the 23 significantly upregulated proteins.
Supplementary File S7	The top 20 KEGG pathway of the 55 significantly downregulated proteins.



Supplementary Figure S1. Repeatability analysis of different biological replicates used for iTRAQ-coupled LC–MS/MS proteomic analysis. (A) The coefficient of variation (CV) distribution between groups. (B) Repeatability analysis of three technical replicates of PDCoV-infected IPEC-J2 cells. (C) Repeatability analysis of three technical replicates of mock-infected IPEC-J2 cells. The x-axis represents the variation levels of proteins in PDCoV- or mock-infected IPEC-J2 cells between three technical replicates. The left y-axis represents the frequency of quantitative proteins (histograms) and the right y-axis represents the cumulative percentage of proteins at different variation levels (line graph).



Supplementary Figure S2. The original images of the entire PVDF membranes containing the target western blots of Figure 2C. The expected size of ANAPC7, IFIT1, β -actin and PDCoV-N proteins are 63, 57, 42 and 41 kDa, respectively.