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Correction: Isolation, phylogenetics, and characterization of a new PDCoV strain that affects cellular gene expression in human cells

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PDCoV, Huh7 cells, phylogenetic tree, transcriptome analysis, immune response

A Correction on

Isolation, phylogenetics, and characterization of a new PDCoV strain that affects cellular gene expression in human cells

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There was a mistake in Figure 9 as published. The bands representing the PDCoV N protein in interferon-related pathway and autophagy-related pathway were the same. This error occurred while we rearranged Figure 9D in the final version by selecting the same band of PDCoV N twice.

The corrected figure and its caption appear below.

The original version of this article has been updated.

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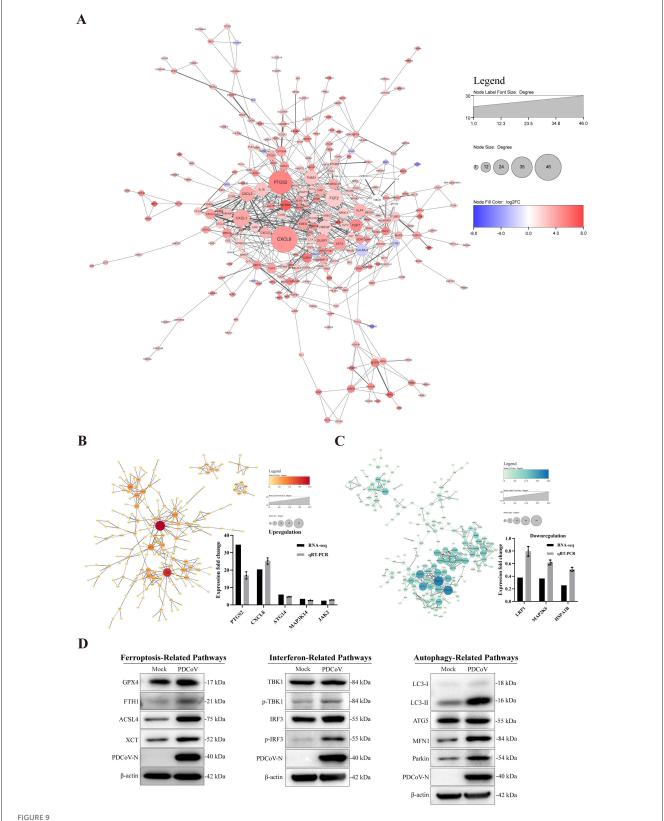
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Yang et al. 10.3389/fmicb.2025.1646820



Interacting network of differentially expressed proteins. (A) PPI network of the DEGs. (B, C) PPI network of up-regulated and down-regulated DEGs and RT-qPCR verified results. (D) The related protein expression level of ferroptosis, autophagy and immune response in the context of PDCoV infection using western blotting. β -actin was used as an internal reference. All PPI networks were based on STRING analysis. Each node represented a protein, and each edge represented the interaction between proteins. The upregulated proteins are shown in red shadow, and the downregulated proteins are shown in blue.