Corrigendum: Dual RNA-seq of trunk kidneys extracted from channel catfish infected with *Yersinia ruckeri* reveals novel insights into host-pathogen interactions

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A Corrigendum on:

Dual RNA-Seq of Trunk Kidneys Extracted From Channel Catfish Infected With *Yersinia ruckeri* Reveals Novel Insights Into Host-Pathogen Interactions.

Yang Y, Zhu X, Zhang H, Chen Y, Song Y and Ai X (2021) Dual RNA-Seq of Trunk Kidneys Extracted From Channel Catfish Infected With *Yersinia ruckeri* Reveals Novel Insights Into Host-Pathogen Interactions. *Front. Immunol.* 12:775708. doi: 10.3389/fimmu.2021.775708

In the published article, there was an error in Figure 6A as published. Figure 5A was used instead of Figure 6A in the revision of the article. The corrected Figure 6A appears below.

In the published article, there was an error in the legend of Figure 1 as published. There was one mistake in the species names. The corrected legend appears below.

"Figure 1. The gene expression profiles for channel catfish and *Y. ruckeri* during infection. A volcanic plot depicting the differences in the expression profiles of channel catfish and *Y. ruckeri*. The X-axis represents a log2 (fold change) and the Y-axis represents

FIGURE 1

The gene expression profiles for channel catfish and *Y. ruckeri* during infection. A volcanic plot depicting the differences in the expression profiles of channel catfish and *Y. ruckeri*. The X-axis represents a lo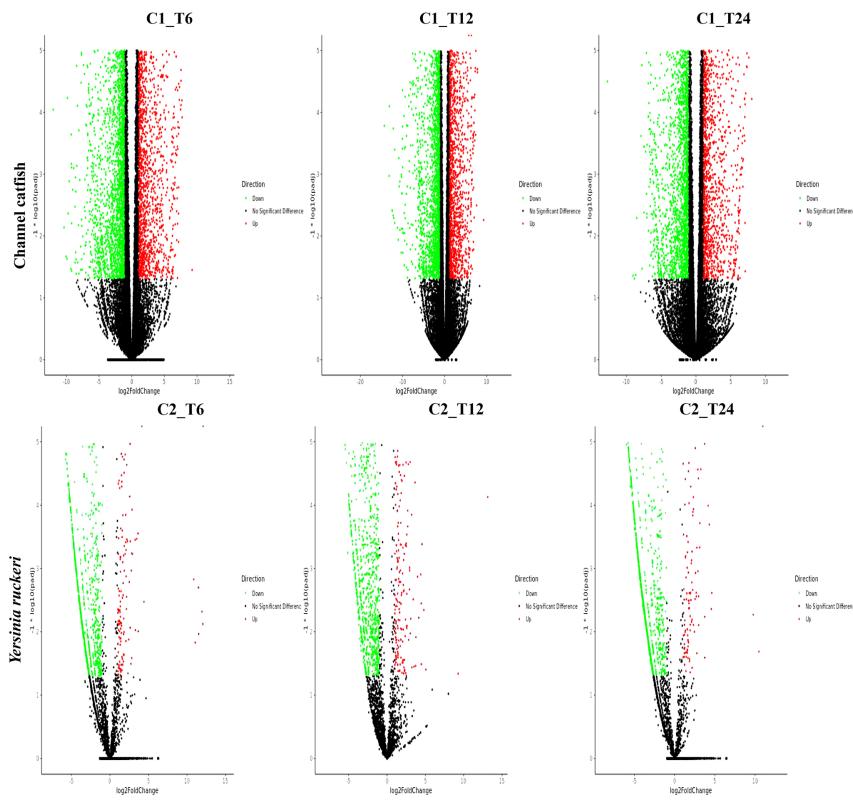g2 (fold change) and the Y-axis represents -log10 (p value). Red represents significantly upregulated genes whereas green represents significantly downregulated genes. Each dot represents a single gene. C1_T6(C2_T6) represents 6 hpi, C1_T12(C2_T12) represents the 12 hpi and C1_T24 (C2_T24) stands for 24 hpi.
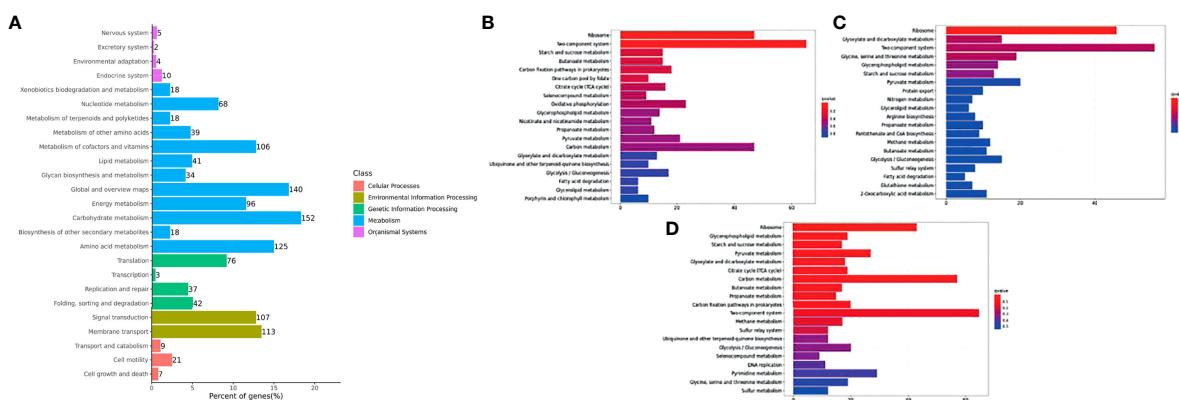
FIGURE 6

Histogram of the top 20 enriched KEGG pathways of DEGs in *Y. ruckeri* at different time points. The Y-axis represents the KEGG pathway categories. The X-axis represents statistical significance of the enrichment. **(A)** represents the classification of total KEGG, **(B)** represents the top 20 KEGG pathways in the C2_T6 group, **(C)** represents the top 20 KEGG pathways in the C2_T12 group and **(D)** represents the top 20 KEGG pathways in the C2_T24 group.

-log10 (p value). Red represents significantly upregulated genes whereas green represents significantly downregulated genes. Each dot represents a single gene. C1_T6(C2_T6) represents 6 hpi, C1_T12(C2_T12) represents the 12 hpi and C1_T24(C2_T24) stands for 24 hpi."

In the published article, there was an error. A correction has been made to **DISCUSSION**, Paragraph 7. This sentence previously stated:

"The pathogen HlyA was severely down-regulated by the host, indicating that the pathogen did not rely on hemolysin to cause harm in the host trunk kidney."

The corrected sentence appears below:

"The pathogen HlyB was up-regulated in the infection, indicating that the pathogen rely on hemolysin to cause harm in the host trunk kidney."

The authors apologize for these errors and state that they do not change the scientific conclusions of the article in any way. The original article has been updated.

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