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Transcriptome analysis of the hepatopancreas in *Exopalaemon carinicauda* infected with an AHPND-causing strain of *Vibrio parahaemolyticus*

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ABSTRACT Acute hepatopancreatic necrosis disease (AHPND) caused by *Vibrio parahaemolyticus* carrying toxin-producing plasmid, has led to severe mortalities in multiple shrimp species throughout Asia. In order to understand the immunological response of shrimp to infection by AHPND-causing strain of *V. parahaemolyticus* (VP_{AHPND}), the transcriptomic profiles of the hepatopancreas from severe AHPND-infected (BS_G), AHPND-survived (KB_G) and non-infected (PBS_G) *Exopalaemon carinicauda* groups were obtained using HiSeq™ 2500 (Illumina). In total, 525 million high quality clean reads were obtained in nine libraries and de novo assembled into 130,082 unigenes with an average length of 724 bp. Based on sequence similarity, 22.75% unigenes were annotated in the public databases. Comparative analysis revealed that 3,733 genes differentially expressed in VP_{AHPND} infection compared with the controls, including 1,114 and 3,461 unigenes in BS_G vs

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