Accepted Manuscript

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PII: S1050-4648(18)30131-1

DOI: 10.1016/j.fsi.2018.03.014

Reference: YFSIM 5169

To appear in: *Fish and Shellfish Immunology*

Received Date: 1 September 2017

Revised Date: 7 March 2018

Accepted Date: 8 March 2018

Please cite this article as: Hwang JY, Markkandan K, Kwon MG, Seo JS, Yoo S-i, Hwang SD, Son M-H, Park J, Transcriptome analysis of olive flounder (*Paralichthys olivaceus*) head kidney infected with moderate and high virulent strains of infectious *viral hemorrhagic septicaemia virus* (VHSV), *Fish and Shellfish Immunology* (2018), doi: 10.1016/j.fsi.2018.03.014.

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Abstract

Olive flounder (*Paralichthys olivaceus*) is one of the most valuable marine aquatic species in South Korea and faces tremendous exposure to the viral hemorrhagic septicemia virus (VHSV). Given the growing importance of flounder, it is therefore essential to understand the host defense of *P. olivaceus* against VHSV infection, but studies on its immune mechanism are hindered by the lack of genomic resources. In this study, the *P. olivaceus* was infected with disease-causing VHSV isolates, ADC-VHS2012-11 and ADC-VHS2014-5 which showed moderate virulent (20% mortality) and high virulent (65% mortality), in order to