

Interactive comment on “Finding immune gene expression differences induced by marine bacterial pathogens in the deep-sea hydrothermal vent mussel *Bathymodiolus azoricus*” by E. Martins et al.

Anonymous Referee #2

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General comments: This study investigates gene expression of several immune genes in the deep-sea hydrothermal vent mussel *Bathymodiolus azoricus* infected with single suspensions of different marine bacterial pathogens. In general the study is a welcome addition to the literature as it provides new insights into the biology and, in particular, innate immunity of hydrothermal vents organisms. However, the paper as it stands is mainly descriptive and needs to be improved and re-organized to properly meet the required standards for publication.

Specific comments: My main concern about this manuscript is that it is not properly

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organized and do not provide, in my opinion, a clear interpretation of the obtained results. The results and discussion section is very long and is mainly a description of results. More discussion should be given by the authors on relevant issues such as the interpretation they provided about the differential immune response to the different pathogens, and how this compare with studies in other bivalves (e.g it would be interesting to compare the immune response to pathogen infections by *B. azoricus* in pristine vents environments to that of closest relatives in impacted environments including species that has been subjected to mass mortality events during the recent years). Another major issue relates to the definition and use of bacterial pathogens for infection experiments. I do expect authors having used reference pathogenic bacterial strains or alternatively isolated strains which should have been characterized for the presence of specific virulence factors. However, no information were given in the manuscript on the types of strains being used in the experiments. In addition, which is the final concentration of bacteria employed for *B. azoricus* infections? *Flavobacterium* was used as non-pathogenic strain in contrasting experiments however this strain induced the highest expression levels of immune recognition, transcription and effector genes at 12h time point. Do you have an explanation for this? To benefit data interpretation, it would have been nice to correlate immune gene expression response to challenge by pathogens to physiological responses linked to the animal health status.

Technical comments: Page 1 “irrelevant” should be “non-pathogenic” Page 1 and elsewhere “*Vibrio. splendidus*” should be “*Vibrio splendidus*” Page 4, line 3: *Vibrio aestuari-
anus* should be possibly added to the list Page 16: “..genes clusters were connected according to its function..” should be “..gene clusters were connected according to their function..”

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