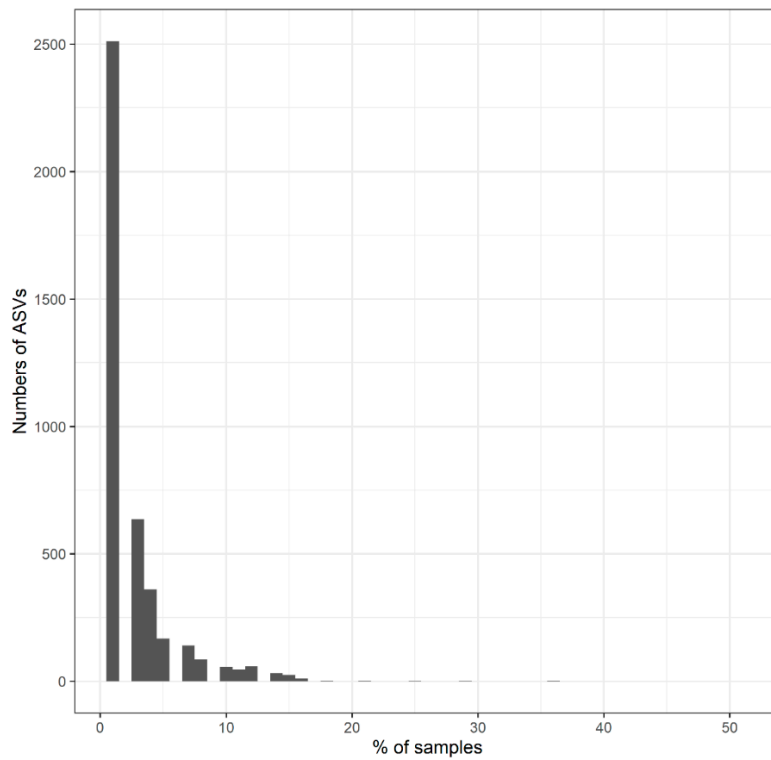


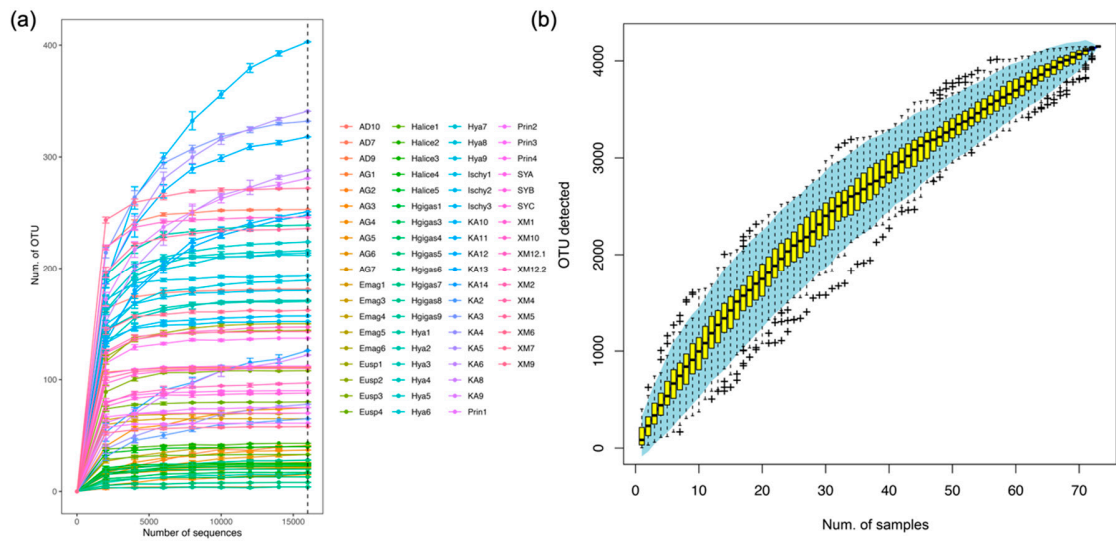
Supplemental Information for:

**Comparably characterizing the gut microbial communities of
amphipods from littoral to hadal zones**

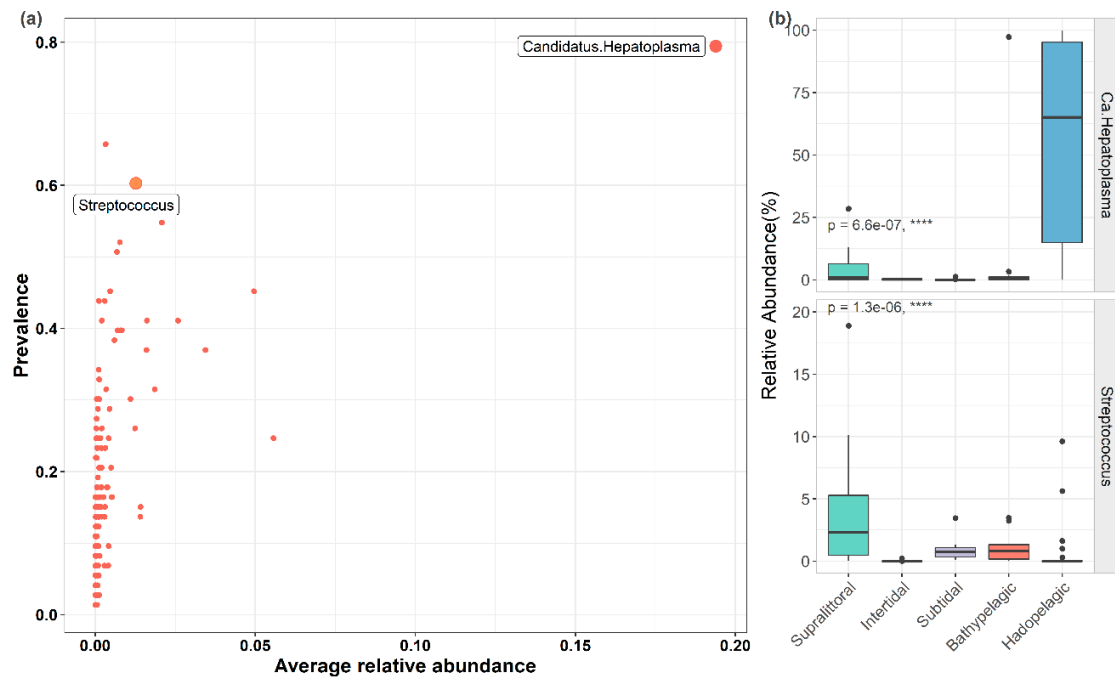
Tao-Shu Wei, Yan-wen Liao, Yong Wang, Jun-yuan Li, Xi-kun Song, Li-Sheng He



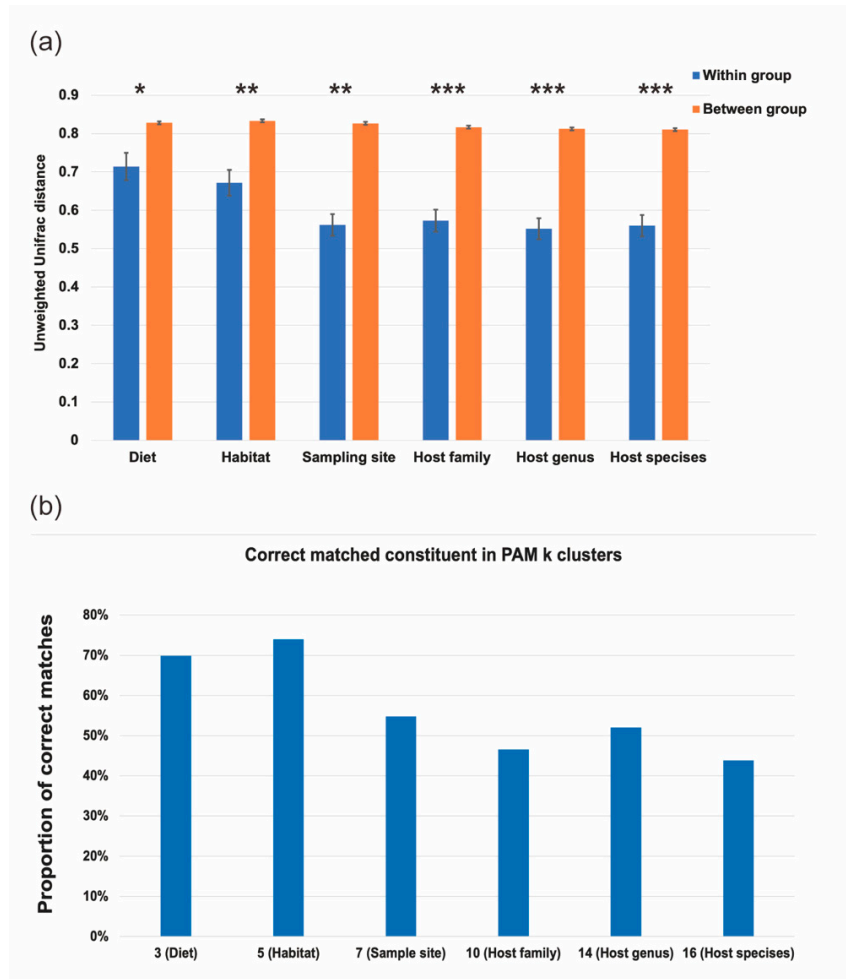
Supplementary Figure S1. Distribution of the prevalence for ASVs across all amphipod samples. X-axis represented the percentage of samples where ASV was detected.



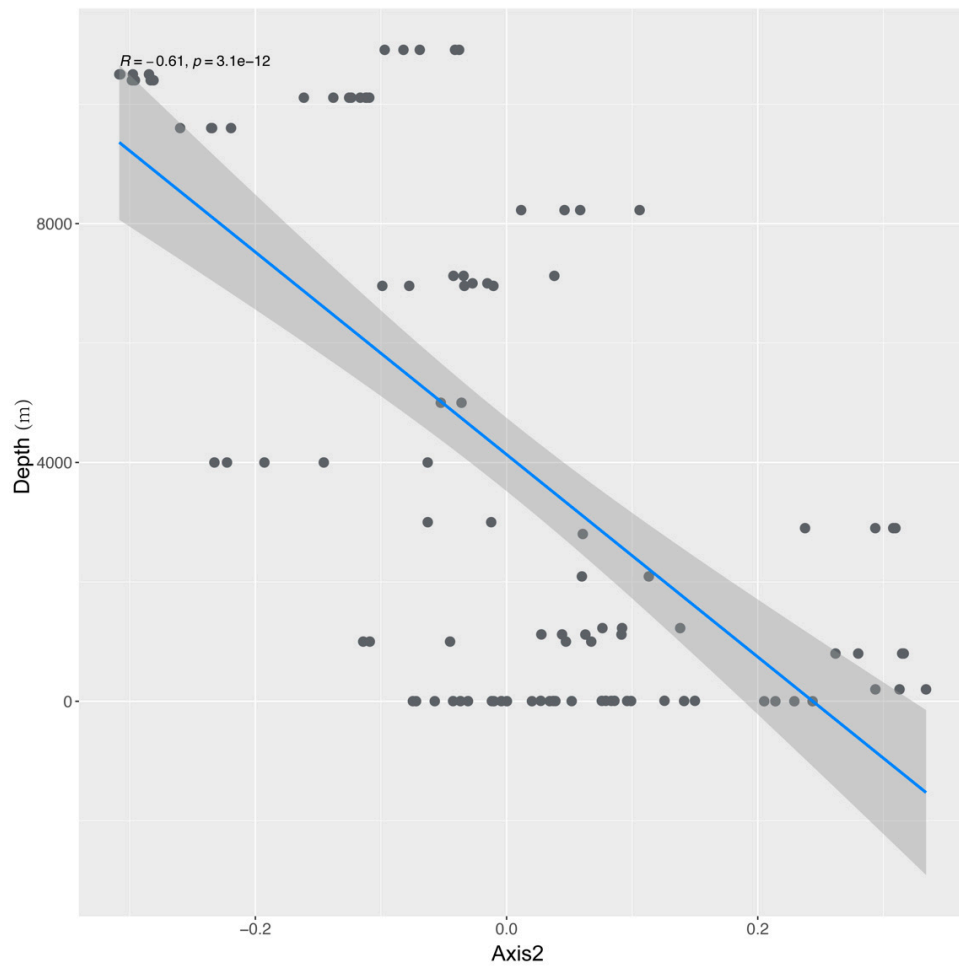
Supplementary Figure S2. Rarefaction curves (a) and species accumulation curves (b) of 73 amphipod gut samples.



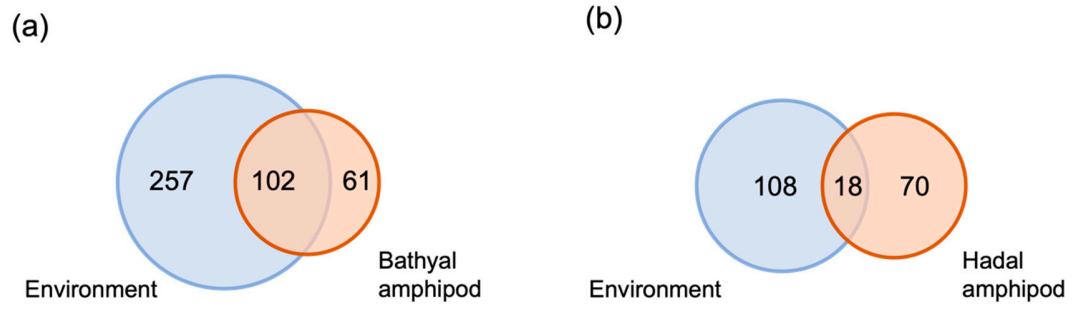
Supplementary Figure S3. Most prevalent genera among the entire amphipod dataset (a) Abundance and prevalence of bacteria at genus level among the amphipods. Genera with average relative abundance > 1% and prevalence > 0.6 were labeled. (b) Variability in the relative abundance of the two most prevalent genera across habitats. (Kruskal-Wallis with Hochberg correction on p-value, $p < 0.05$) Statistical significance was indicated by value and asterisks. The bands show the median value for each group; the bottom and top of boxes show the first and third quartiles, and whiskers show maximum and minimum values with 1.5 of IQR of upper and lower quartiles.



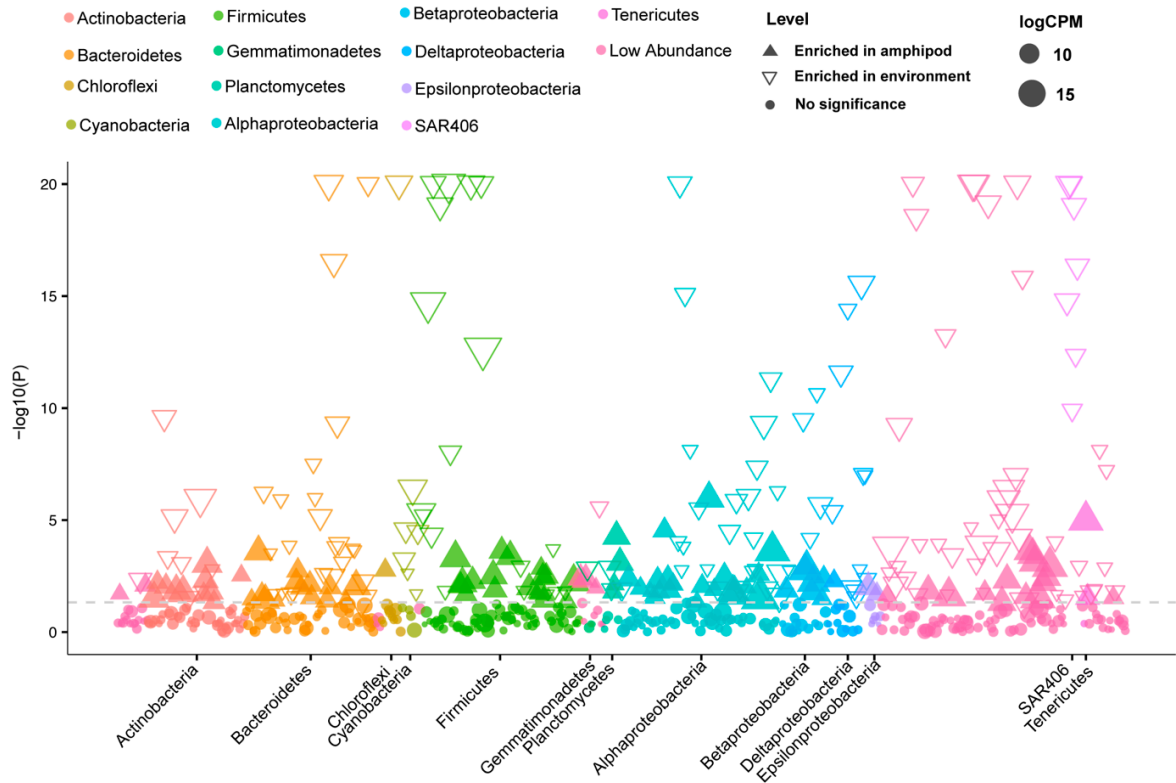
Supplementary Figure S4. The influence of environmental and genetic factors on the amphipod gut microbial community by a clustering analysis. (a) Comparisons of beta diversity in the amphipod gut microbiome within and between groups, based on diverse environmental and genetic factors. (b) The partitioning around medoids (PAM) clustering algorithm was used, which is based on the Calinski-Harabasz (CH) index. The proportion of correctly matched constituents on PAManalysis.



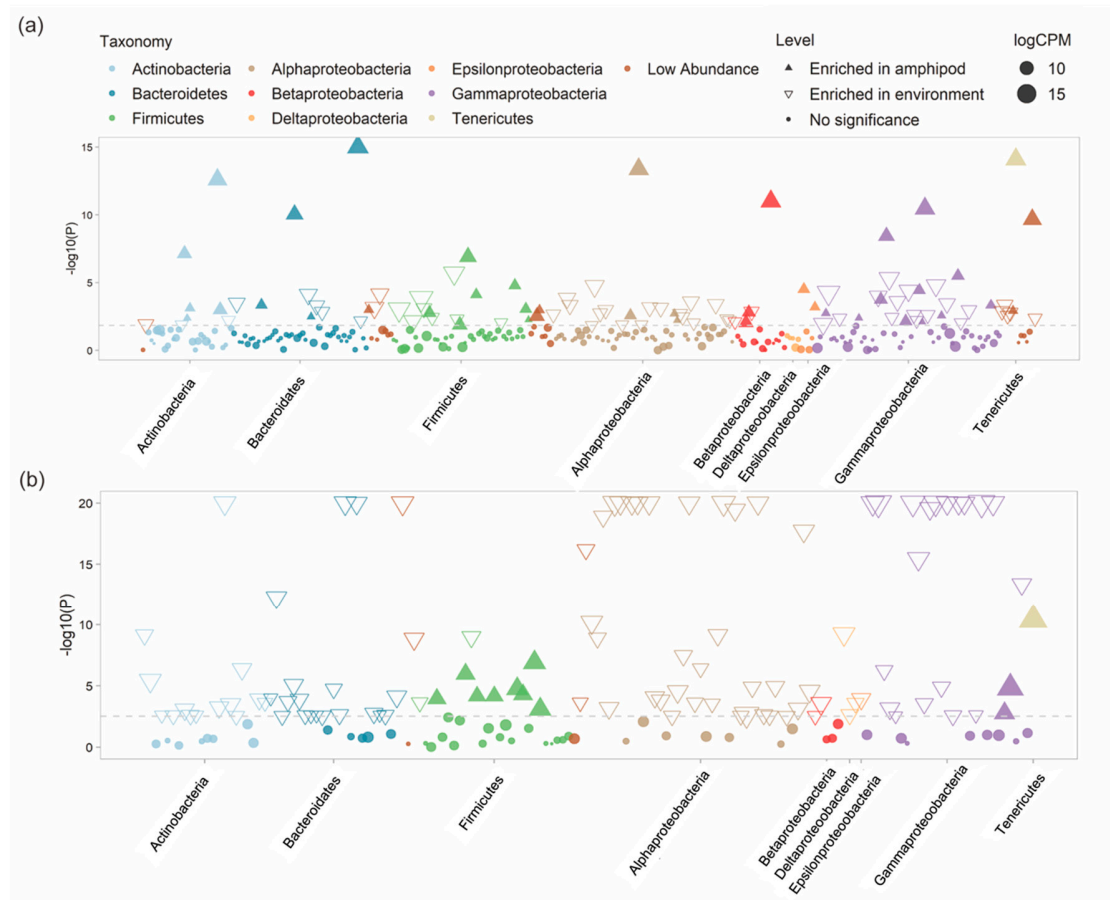
Supplementary Figure S5. Linear regression relationship between depth and PCoA Axis2 of marine amphipod and environmental microbial communities.



Supplementary Figure S6. Overlapping and non-overlapping counts of genera differentially abundant in deep-sea amphipods and environment. (a) Overlapping genera in bathyal amphipods and environment. (b) Overlapping genera in hadal amphipods and environment.



Supplementary Figure S7. Microbial genera enriched in shallow-water amphipod gut or amphipod and overlapping genera between shallow-water amphipod gut and environment. Manhattan plot showing the enriched bacteria in the intestine of supralittoral, intertidal and subtidal amphipod or environment. Each dot or triangle represents a single genus. Genera enriched in the intestine of bathyal amphipod or environment were represented by filled or empty triangles, respectively (FDR adjusted $p < 0.05$, Wilcoxon rank-sum test). Genera were arranged in taxonomic order and colored according to the phylum or, for Proteobacteria, the class.



Supplementary Figure S8. Microbial genera enriched in bathyal amphipod gut or amphipod and overlapping genera between bathyal amphipod gut and environment.

(a) Manhattan plot showing the enriched bacteria in the intestine of bathyal amphipod or environment. (b) Manhattan plot showing the enriched bacteria in the intestine of hadal amphipod or environment. Each dot or triangle represents a single genus. Genera enriched in the intestine of bathyal amphipod or environment were represented by filled or empty triangles, respectively (FDR adjusted $p < 0.05$, Wilcoxon rank-sum test). Genera were arranged in taxonomic order and colored according to the phylum or, for Proteobacteria, the class.