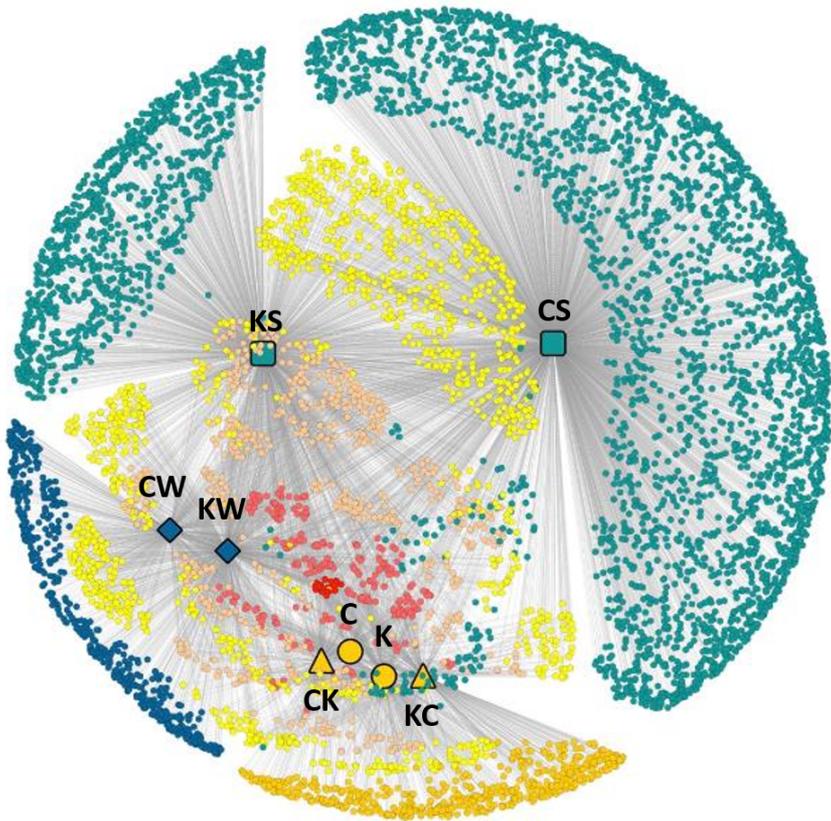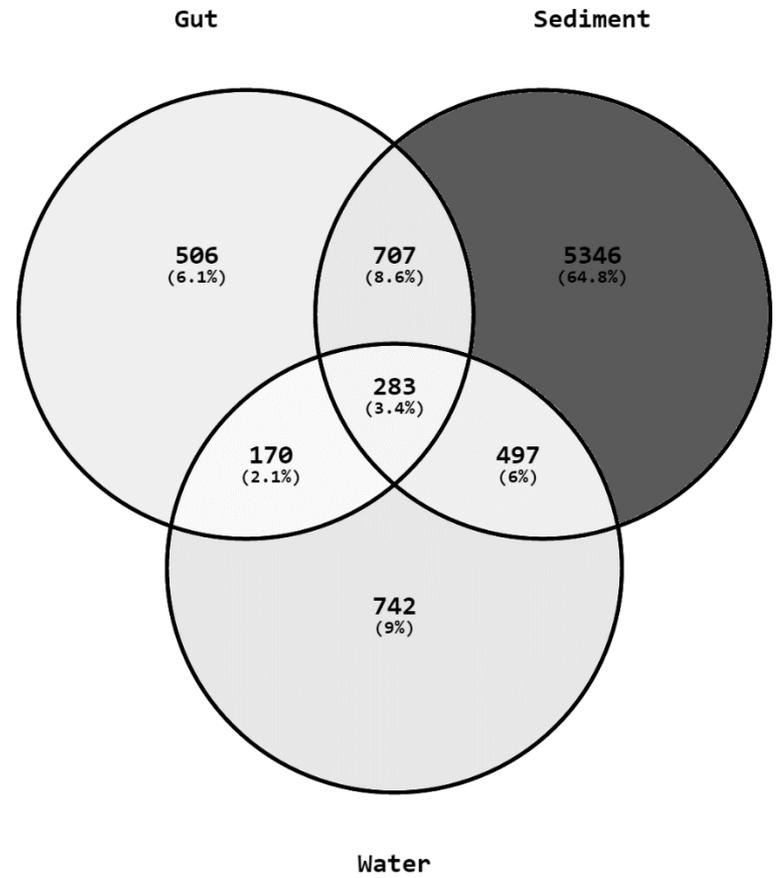**S2 Fig. Relationships between shrimp gut microbes and those from their habitats.**
In the network-based analysis of all gut microbes derived from shrimps and environments (**a**), the average relative abundance of OTUs in replicate samples was represented, and the Edge-weighted Spring Embedded algorithm as implemented in Cytoscape 3.4.0 was used to cluster the OTUs and hosts in this network. Sample nodes correspond to 97% OTUs (yellow circle: native shrimp; yellow triangle: habitat-exchanged shrimp; blue diamond: water; green square: sediment), while color of OTU nodes represent assignments of OTUs to samples nodes that are shared (yellow nodes: OTUs shared between two samples; orange OTU nodes: shared between 3 or 4 samples; pink OTU nodes: shared between 5 or 6 samples; red OTU nodes: shared between 7 or 8 samples). In the numbers of shared OTUs (**b**), the Venn diagrams were produced in Venny 2.1.0 online freeware.