

**Supplementary material for**

**Microbial drivers of high aquaculture productivity: Decoupling of taxonomic and functional profiles enables efficient nitrogen cycling in greenhouse shrimp farming**

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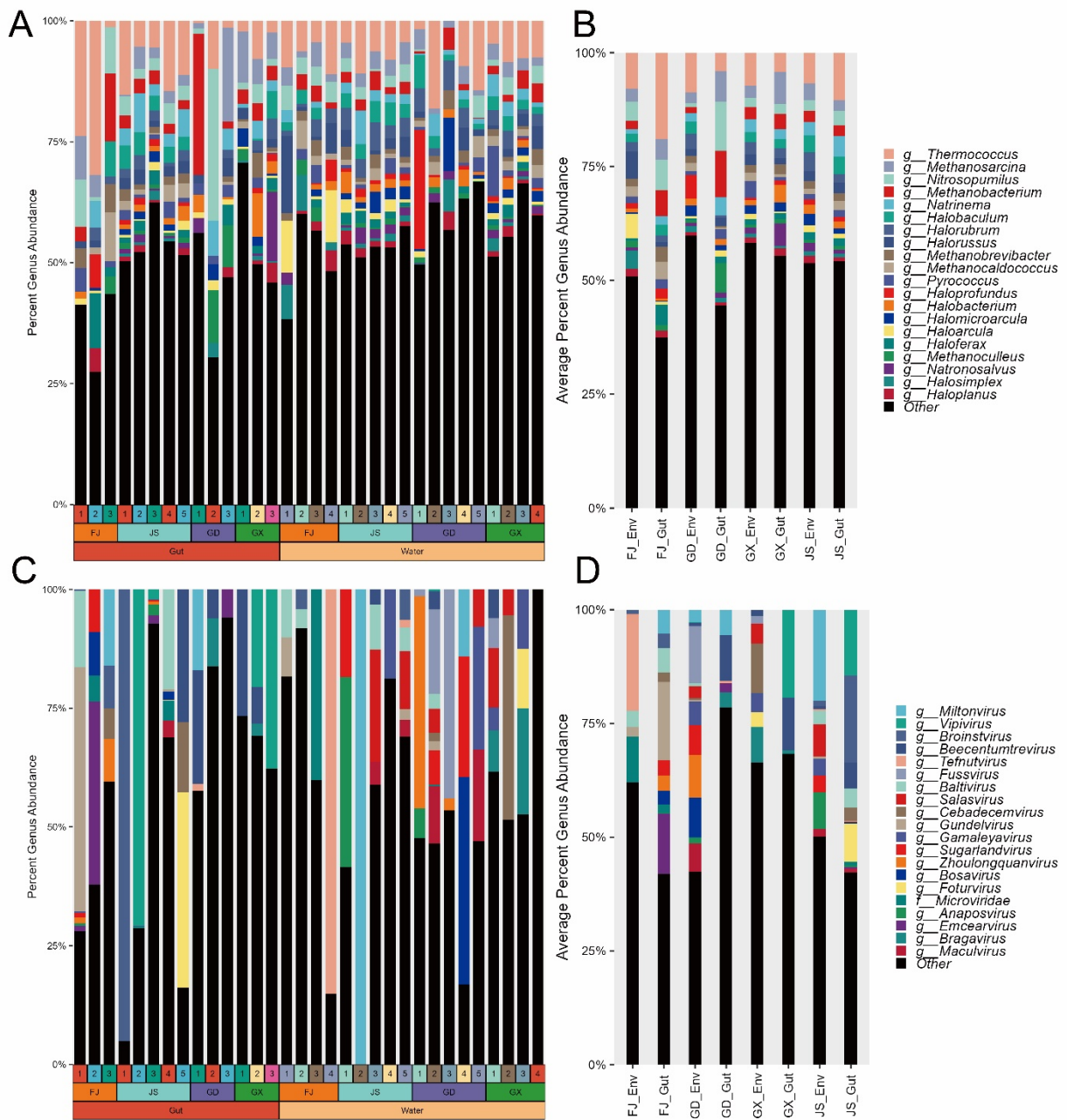
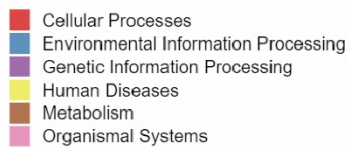
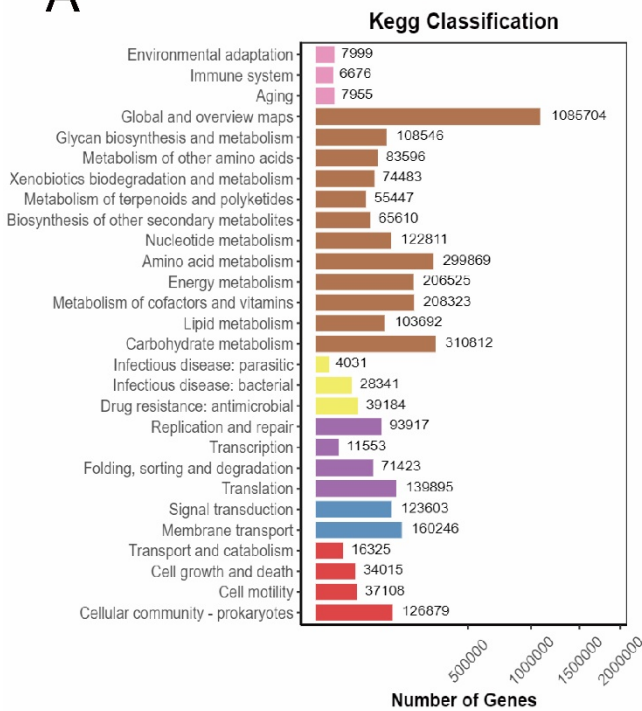


Fig. S1 Species composition abundance. (A) Archaeal microbial communities, (B) Viral microbial communities.

**A**



**B**

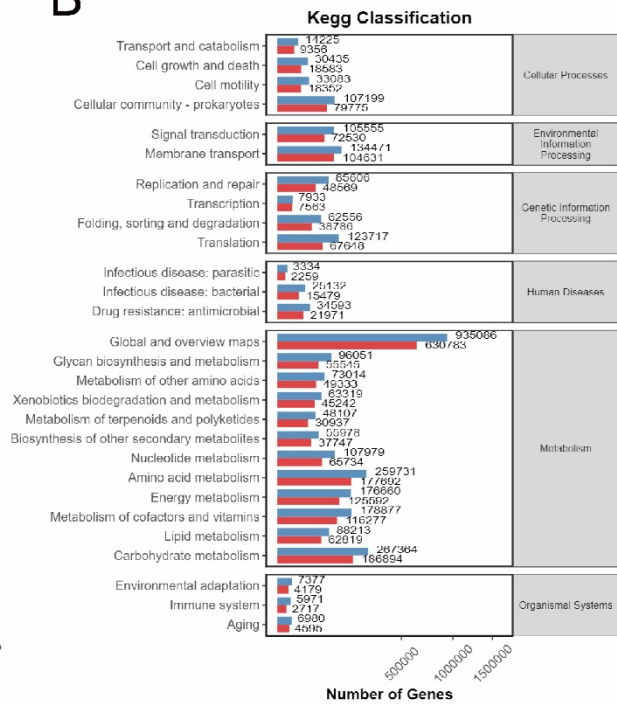
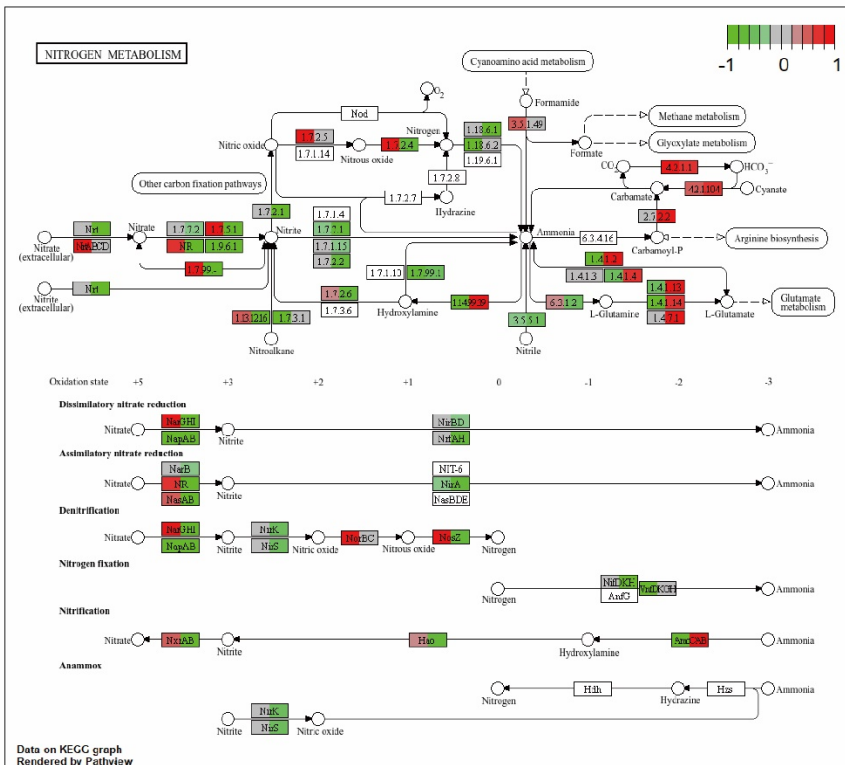


Fig. S2 Functional annotation results based on the KEGG database. (A) Categorized by sample region, (B) Categorized by sample type.

A



B

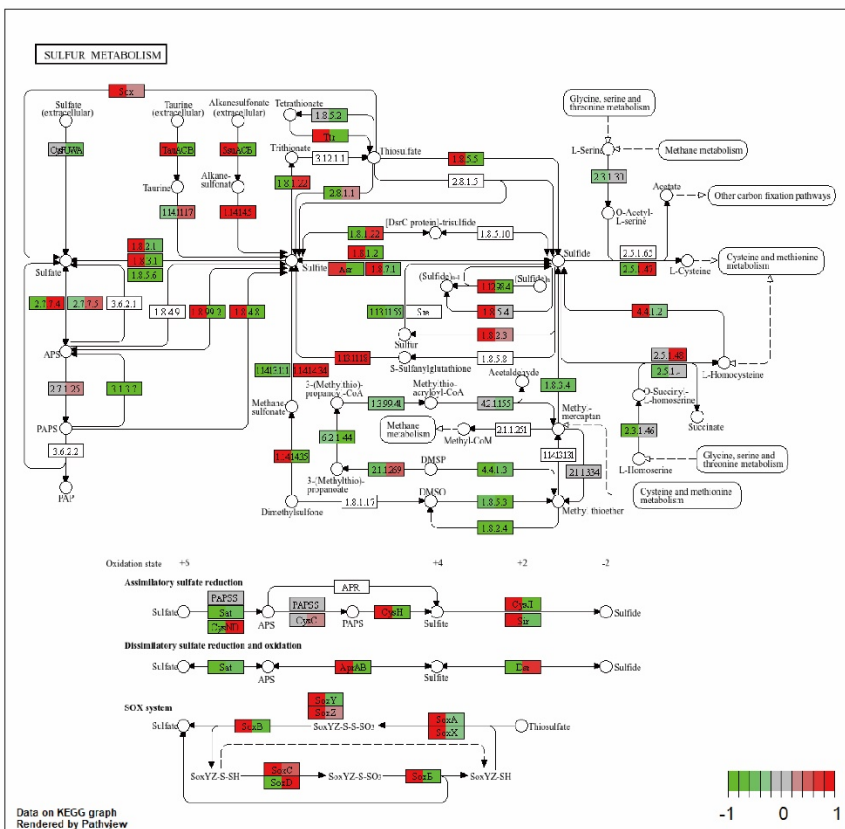
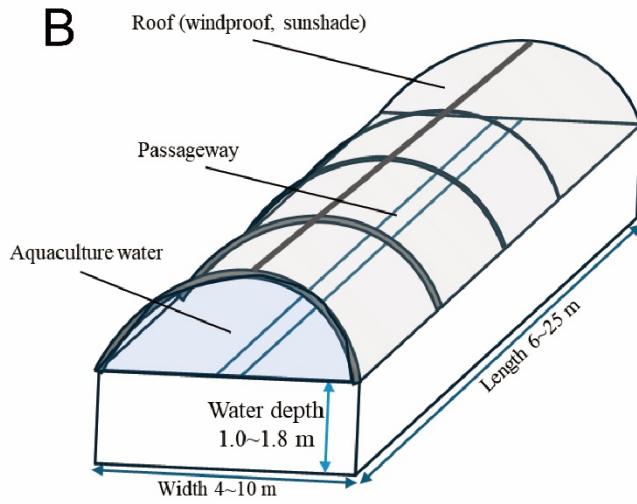


Fig. S3 Gene abundance annotation of biogeochemical cycling pathways by sample origin (former: gut samples; latter: aquatic environmental samples). (A) Nitrogen cycling pathways, (B) Sulfur cycling pathways.

A



B



C



Fig. S4 Sampling information. (A) Sampling map, (B) Schematic diagram of aquaculture model, (C) Aerial view of aquaculture systems in sampling regions.