

Supplementary figures

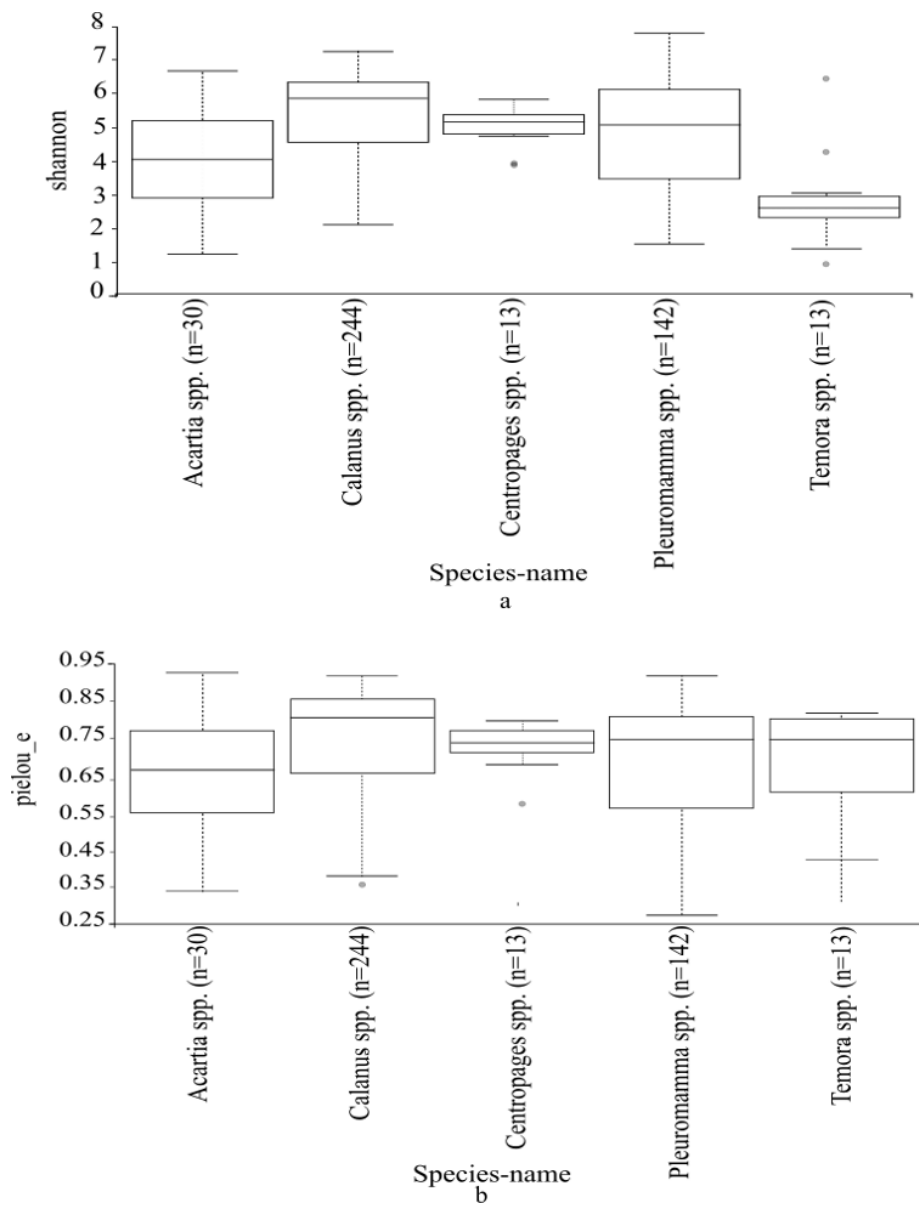


Figure. S1 The Kruskal-Wallis analysis between the CAB with a) Shannon and b) evenness. Different copepods genera had significantly different alpha diversity and similar evenness values.

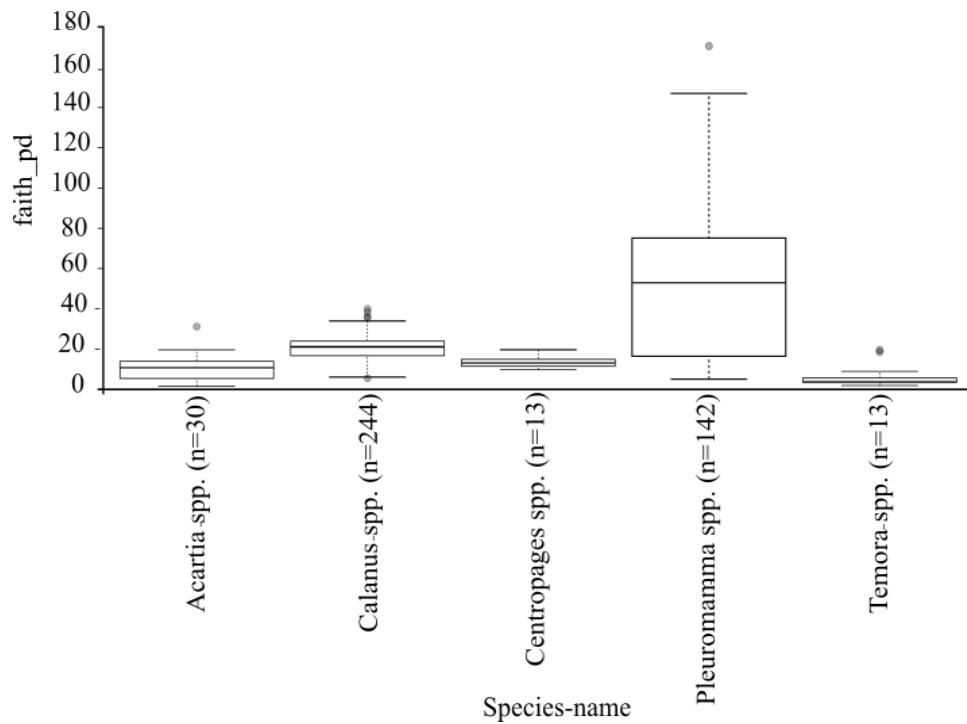


Figure S2: Kruskal-Wallis test reveals *Pleuromamma* spp. to have maximum Faith phylogenetic diversity (Faith_PD) of microbiome (52.0 ± 35.6).

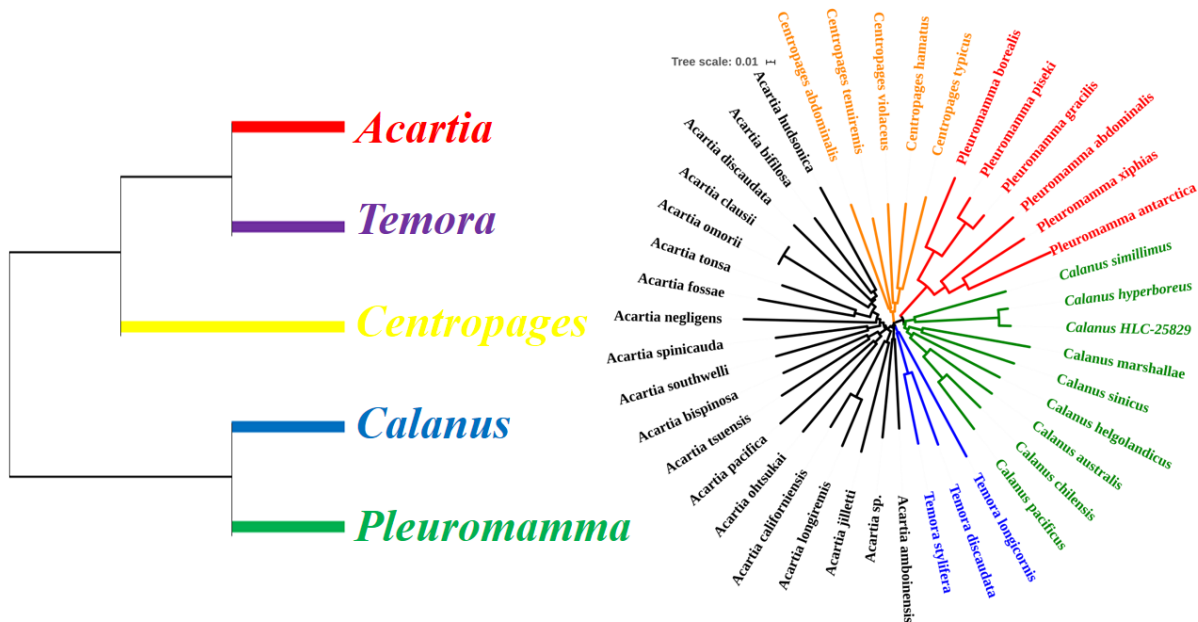


Figure S3: Phylogenetic tree of five copepod genera (Left) drawn from the actual tree (right) consisting of 19, 3, 9 and 6 species of *Acartia* spp., *Temora* spp., *Calanus* spp., *Pleuromamma* spp., and *Centropages* spp., respectively.

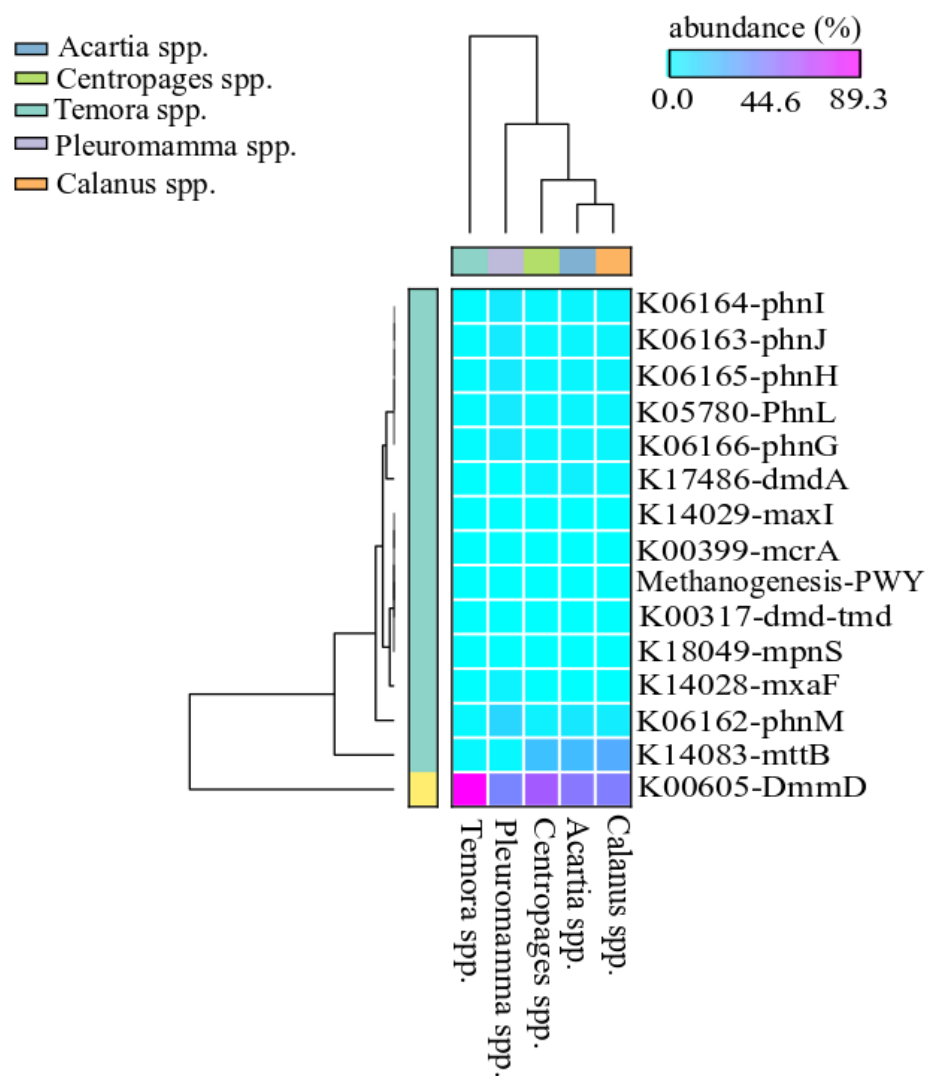


Figure S4. The heatmap represents the relative proportion of methanogenesis and methanotrophic genes observed in CAB of five copepods genera with KEGG id and gene name.

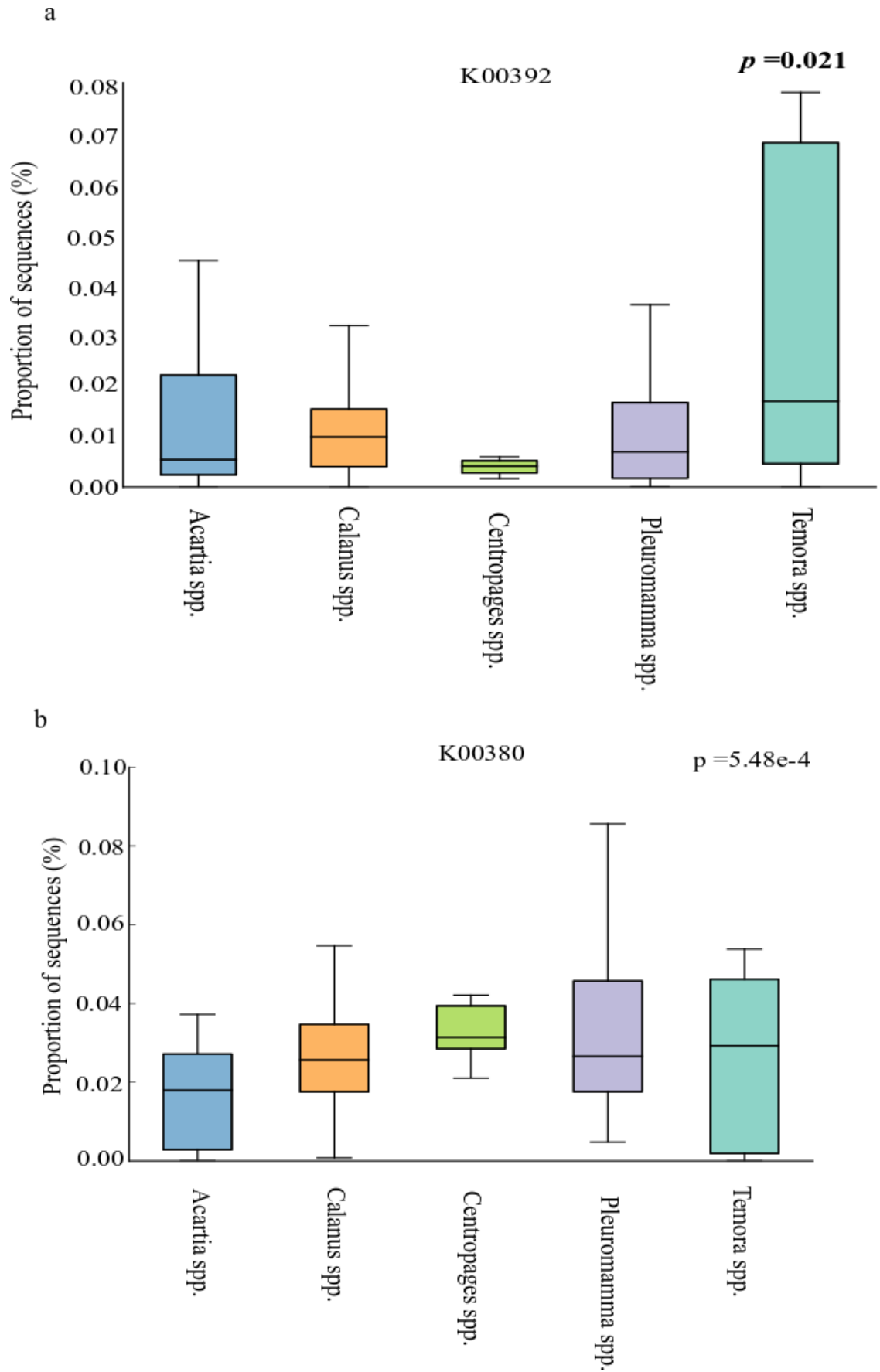


Figure S5 Relative abundance of a) Sulfite reductase (ferredoxin) b) Sulfite reductase (NADPH) flavoprotein alpha-component in CAB of copepods genera.

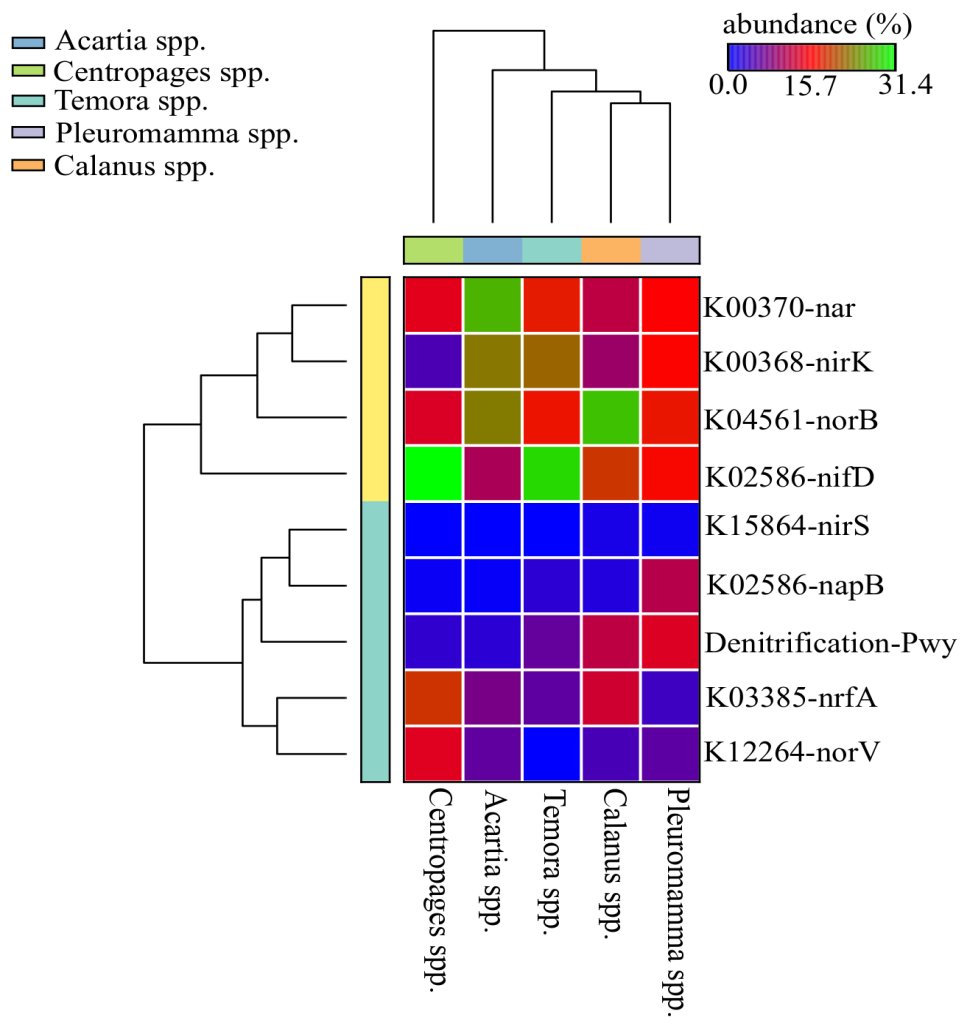


Figure S6. The heat map represents the relative proportion of nitrogen cycle gene observed in CAB of five copepods genera with KEGG id and gene name.

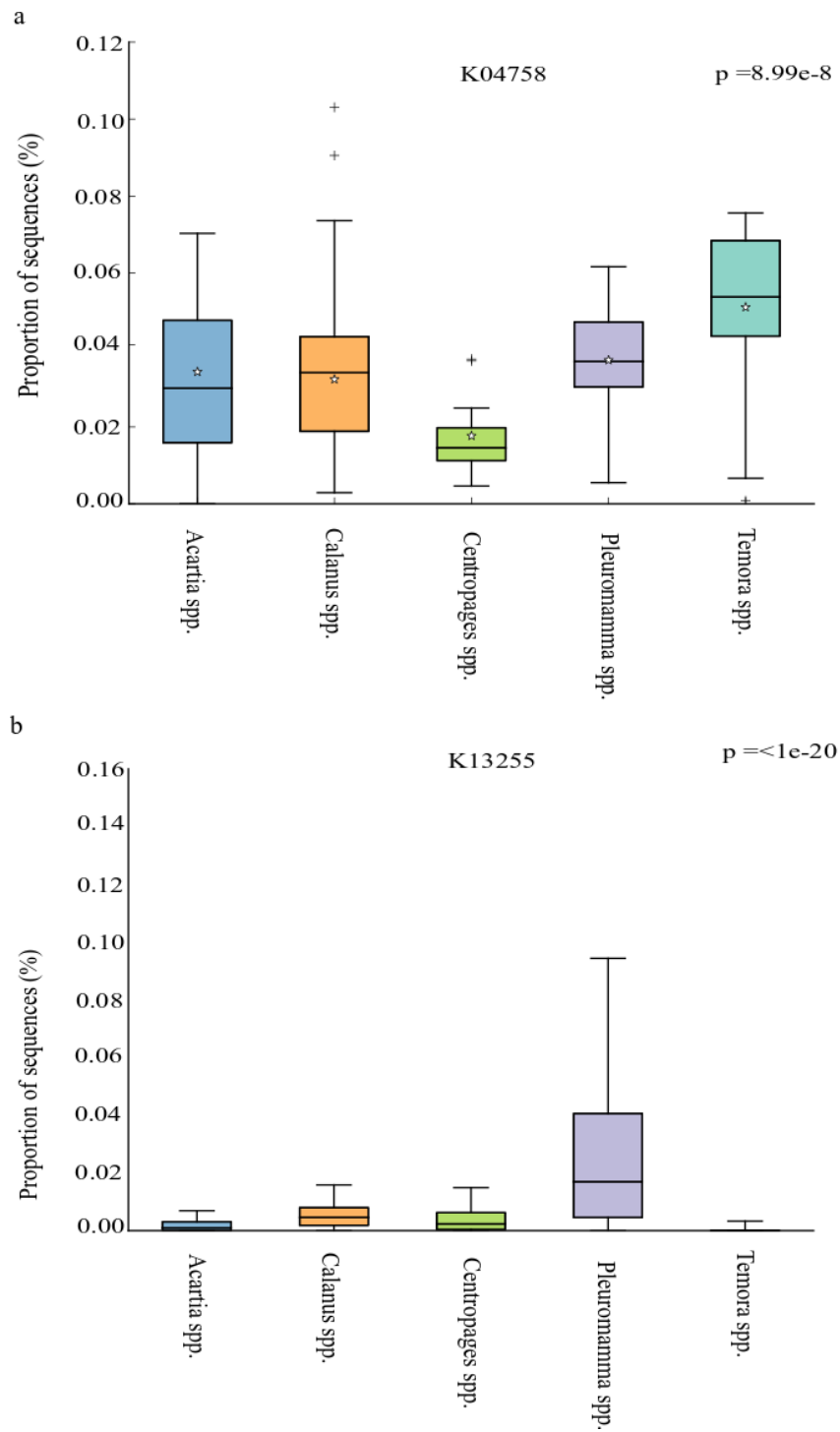


Figure S7. Relative abundances of a) PEPC genes, b). Bacterial chitinase genes observed in CAB of copepods genera.

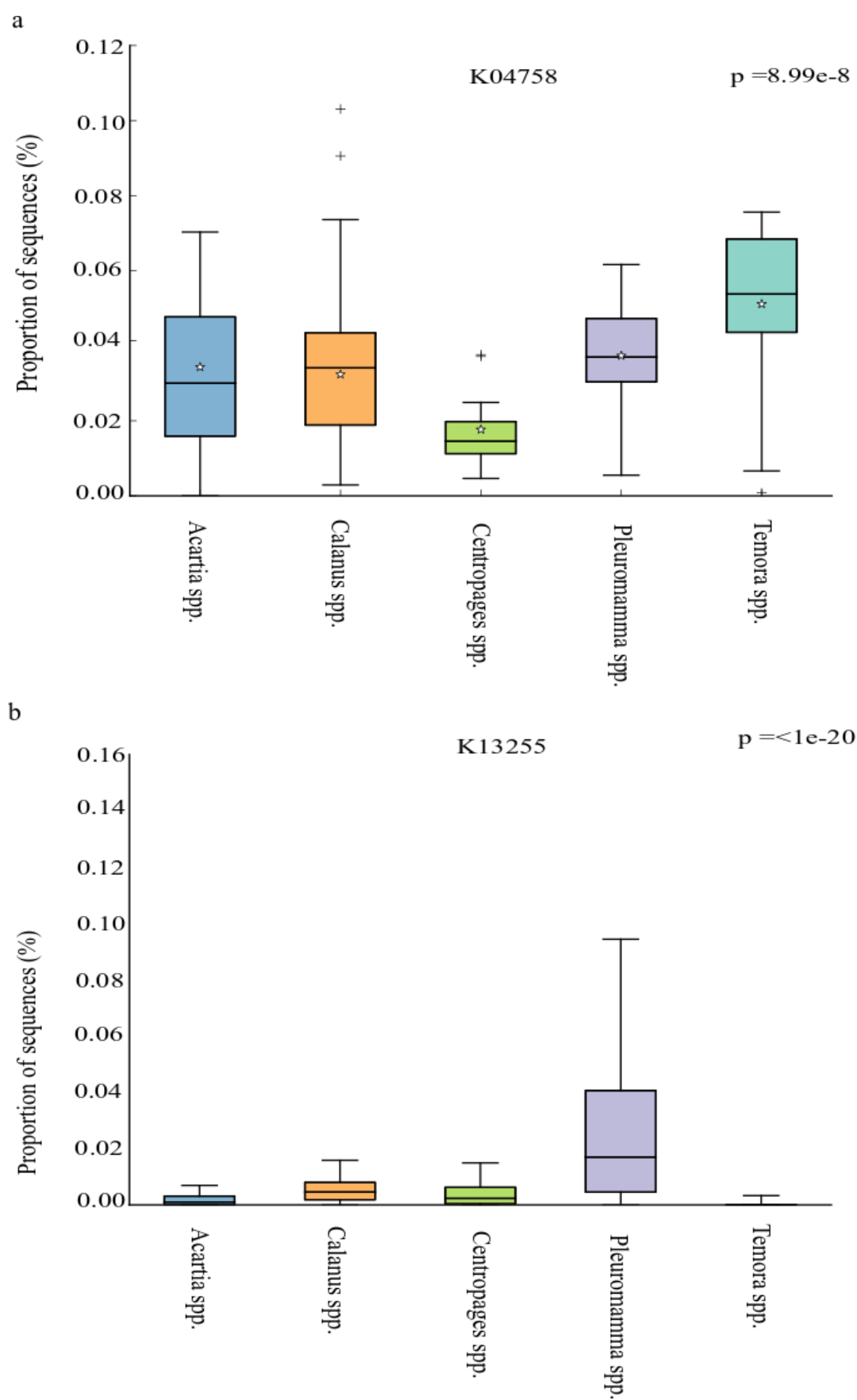


Figure S8 Relative proportions of a) *feoA* protein b) *fluF* genes observed in CAB of copepods genera.

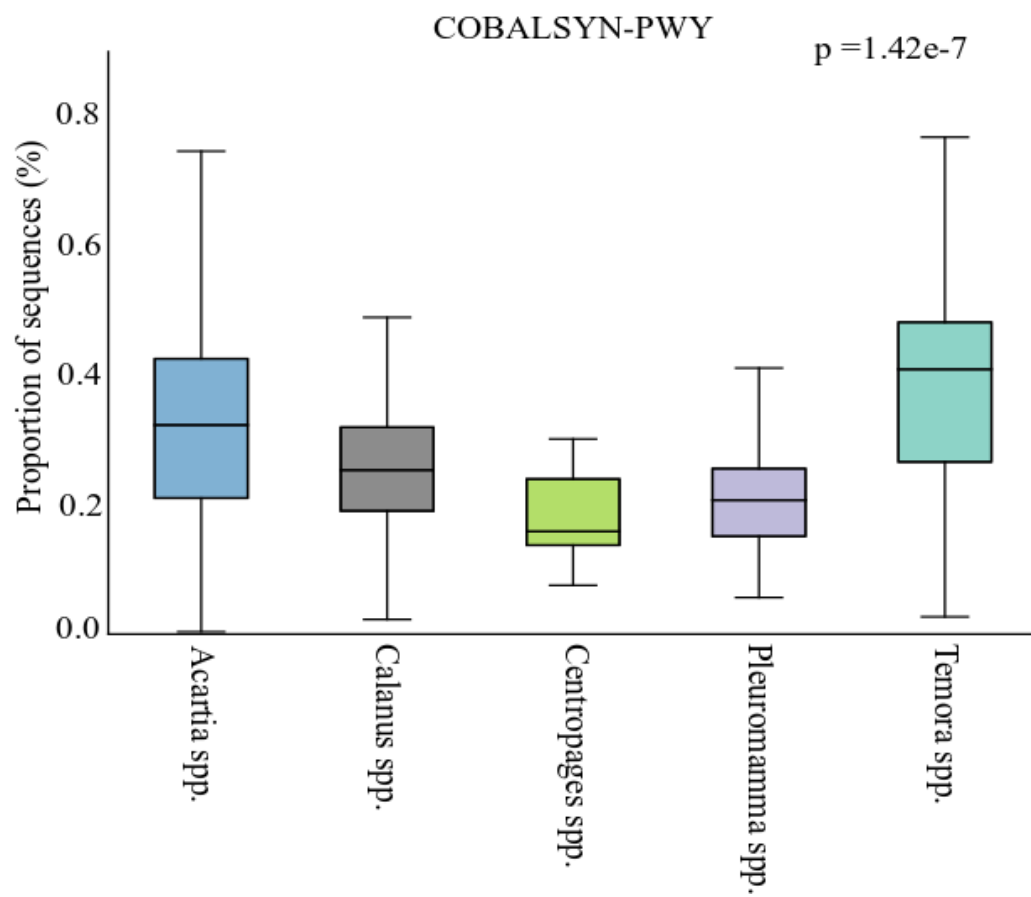


Figure S9. Relative proportions of Vitamin B12 synthesising prokaryotes associated with copepods genera.