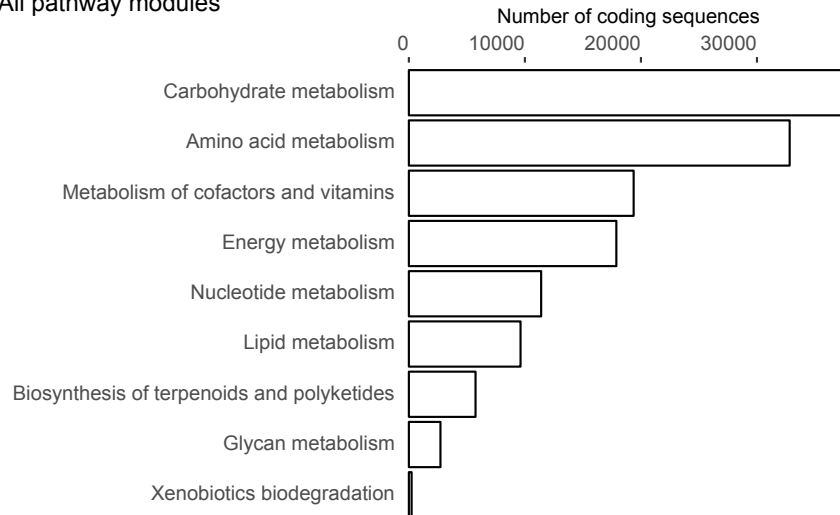
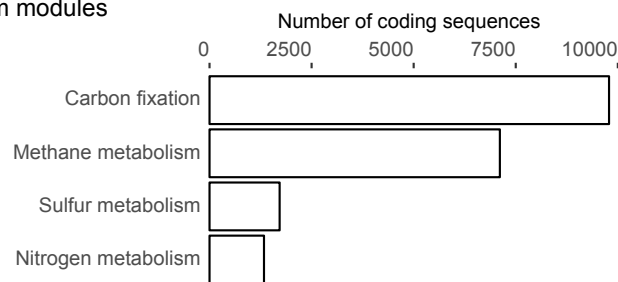


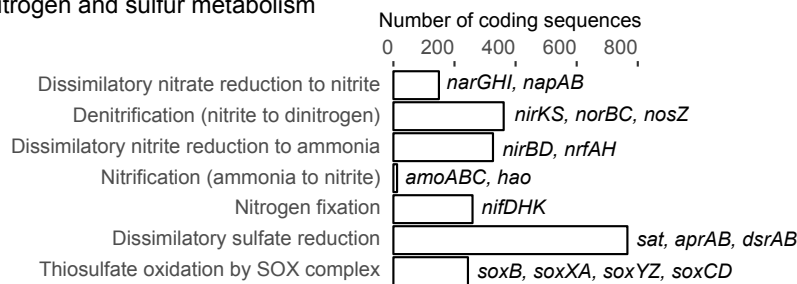
a) All pathway modules



b) Energy metabolism modules



c) Nitrogen and sulfur metabolism



Supplementary Figure 5. Functional classification of the KEGG-annotated transcripts.

In total 582,671 K numbers were assigned to 1,419,467 coding sequences (cds) on the metatranscriptomic contigs. a) Classification of annotated cds to the pathway modules within KEGG mapper. b) Sub-classification of annotated cds within “Energy metabolism”. c) Coding sequences annotated as transcripts of selected marker genes in pathways within the “Nitrogen metabolism” and “Sulfur metabolism”.