



Figure S1. Microbial community diversity and phylogenetic composition. **(a)** Rarefaction curves labeled with the Shannon diversity index (H). **(b, c, d, e)** Bacterial community composition at the phylum level by 16S rRNA pyrotag **(b)**, by metagenome genes from 38 IMG/M phylogenetic marker COGs **(c)**, and by all genes with function prediction in the metagenomes **(d)** and in the *de novo* assembled metatranscriptomes **(e)**, respectively. In **(c, d, e)**, sequence homology-based classification was performed by Blastp against NR, and taxonomy was assigned by using the lowest common ancestor algorithm of MEGAN. Taxonomic distribution was then weighted by read depths or expression levels of individual genes for metagenomes or metatranscriptomes respectively.