

Supplementary dataset 1: Station information of metaproteomic samples

Supplementary dataset 2: Accession of metagenomics and metatranscriptomic reads for prokaryotic and eukaryotic community

Supplementary dataset 3: KO profile in metaproteome

Supplementary dataset 4: Relative abundance profile of differentially expressed KO between size fractions or depth strata

Supplementary dataset 5: Relative abundance profile of superkingdoms

Supplementary dataset 6: Statistics of major eukaryotic groups in the metaproteome

Supplementary dataset 7: Statistics of major prokaryotic groups in the metaproteome

Supplementary dataset 8 Statistics of major viruses infecting different bacterial hosts in the metaproteome

Supplementary dataset 7: Statistics of cell specific leucine incorporation rate.