

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Detailed geological information on collected sediments.

File Name: Supplementary Data 2

Description: Characteristics of 238 deep-sea prokaryotic metagenome-assembled genomes (MAGs).

File Name: Supplementary Data 3

Description: Characteristics of 238 MAGs for genes encoding enzymes involved in the breakdown of proteins.

File Name: Supplementary Data 4

Description: Characteristics of 238 MAGs for genes encoding enzymes involved in the breakdown of polysaccharides.

File Name: Supplementary Data 5

Description: Characteristics of 238 MAGs for genes encoding enzymes involved in the breakdown of nucleic acids.

File Name: Supplementary Data 6

Description: Characteristics of 238 MAGs for genes encoding enzymes involved in the breakdown of lipids.

File Name: Supplementary Data 7

Description: Metagenomic analysis of the number of carbohydrate enzymes in MAGs.

File Name: Supplementary Data 8

Description: Metatranscriptomic analysis of the transcript abundances of glycoside hydrolase (GH) in MAGs.

File Name: Supplementary Data 9

Description: Metatranscriptomic analysis of the transcript abundances of

glycosyltransferase (GT) in MAGs.

File Name: Supplementary Data 10

Description: Metatranscriptomic analysis of the transcript abundances of polysaccharide Lyase (PL) in MAGs.

File Name: Supplementary Data 11

Description: Metatranscriptomic analysis of the transcript abundances of carbohydrate esterase (CE) in MAGs.

File Name: Supplementary Data 12

Description: Metatranscriptomic analysis of the transcript abundances of auxiliary activities (AA) in MAGs.

File Name: Supplementary Data 13

Description: Metatranscriptomic analysis of the transcript abundances of carbohydrate-binding module (CBM) in MAGs.

File Name: Supplementary Data 14

Description: The relative abundance of the 10 selected marker genes based on metatranscriptomic data .

File Name: Supplementary Data 15

Description: Abundance of genes encoding GH and GT within these MAGs from metatranscriptomic data. The relative abundance (fold change) of each gene was normalized against the average abundance of the 10 selected marker genes (three replicates per site).

File Name: Supplementary Data 16

Description: Distribution of isolation sources and geographical locations for currently cultured PVC superphylum bacteria.

File Name: Supplementary Data 17

Description: Analysis of laminarin-degrading glycoside hydrolases (GHs) in the PVC superphylum bacteria.