Supplementary Information for

Multi-omics and cultivation reveal laminarin-degrading PVC bacteria in the deep sea

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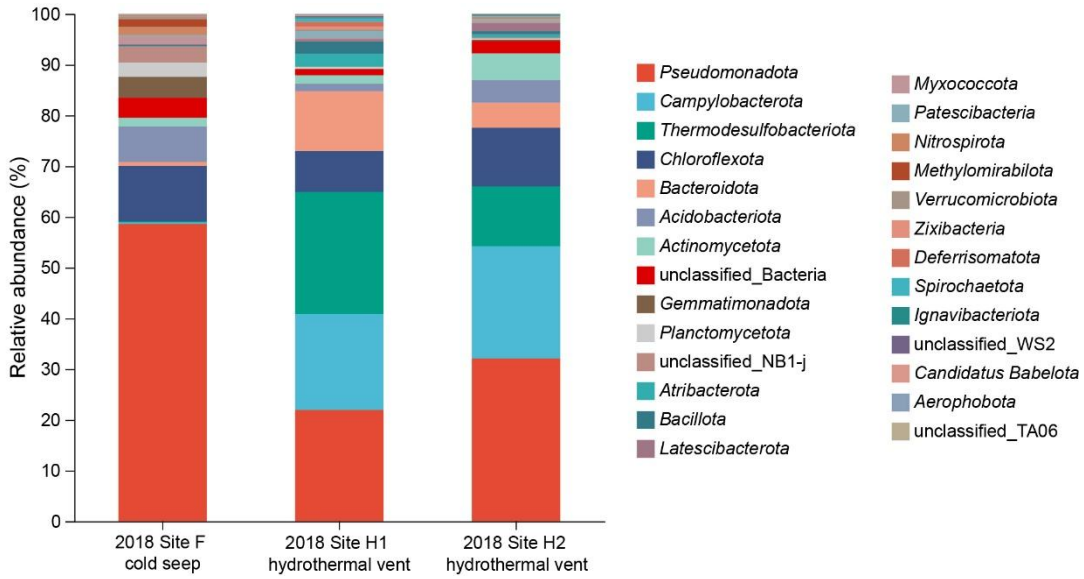
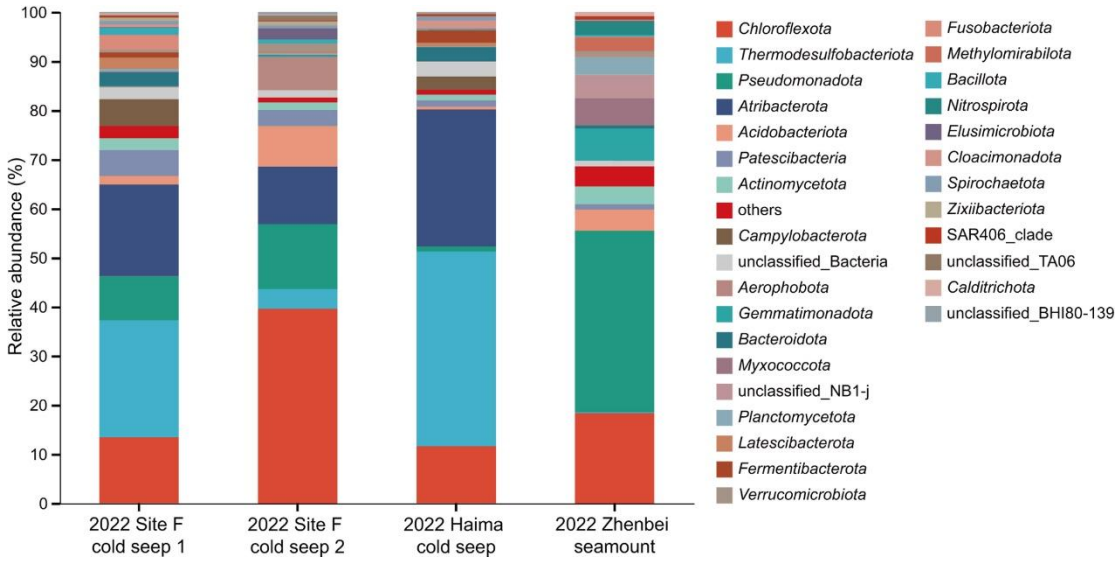
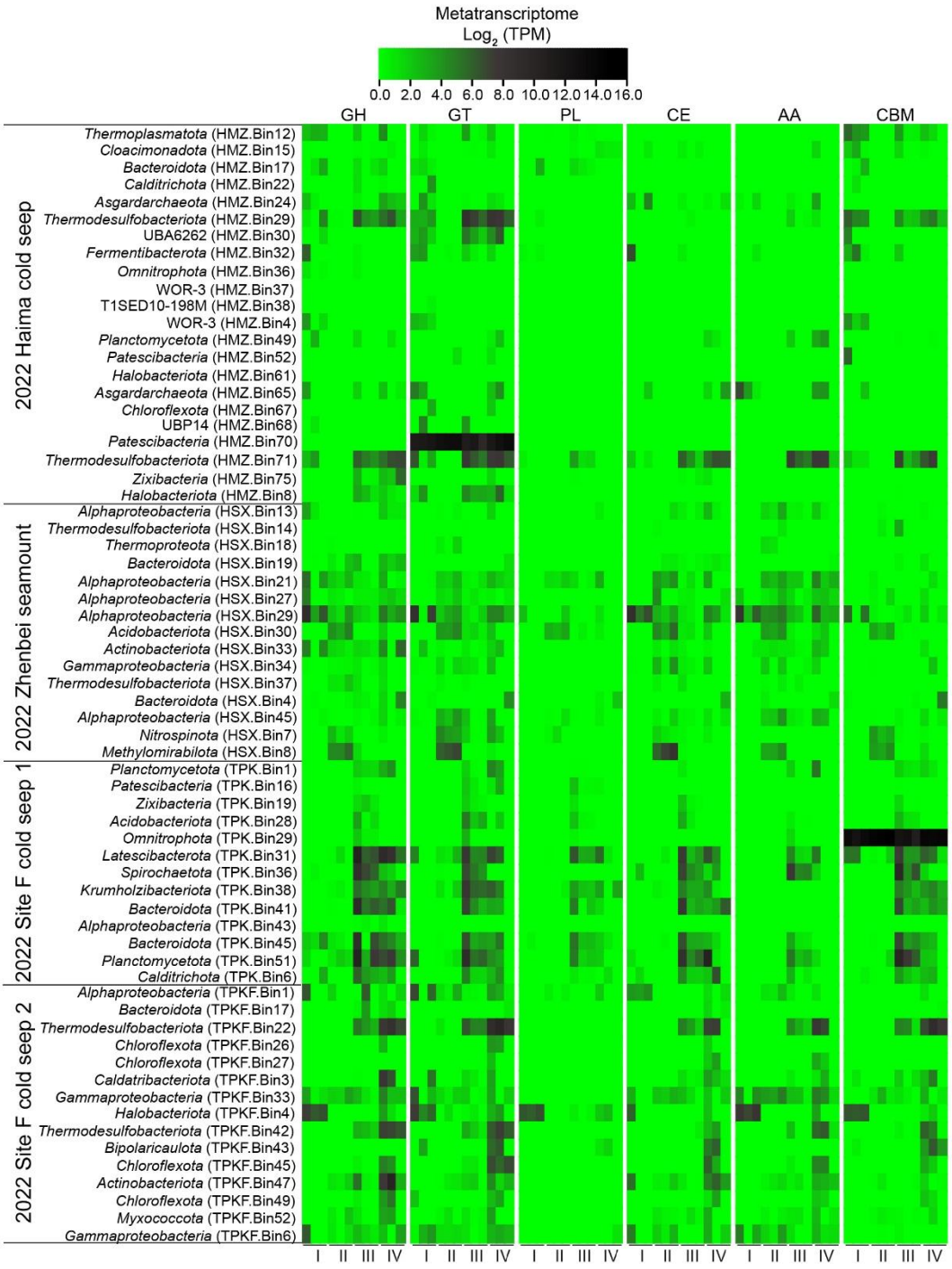
Supplementary Figures



Supplementary Fig. 1 | Relative abundances of dominant prokaryotic communities in deep-sea cold seep and hydrothermal vent sediments (collected in 2018) at the phylum level. Source data are provided as a Source Data file.

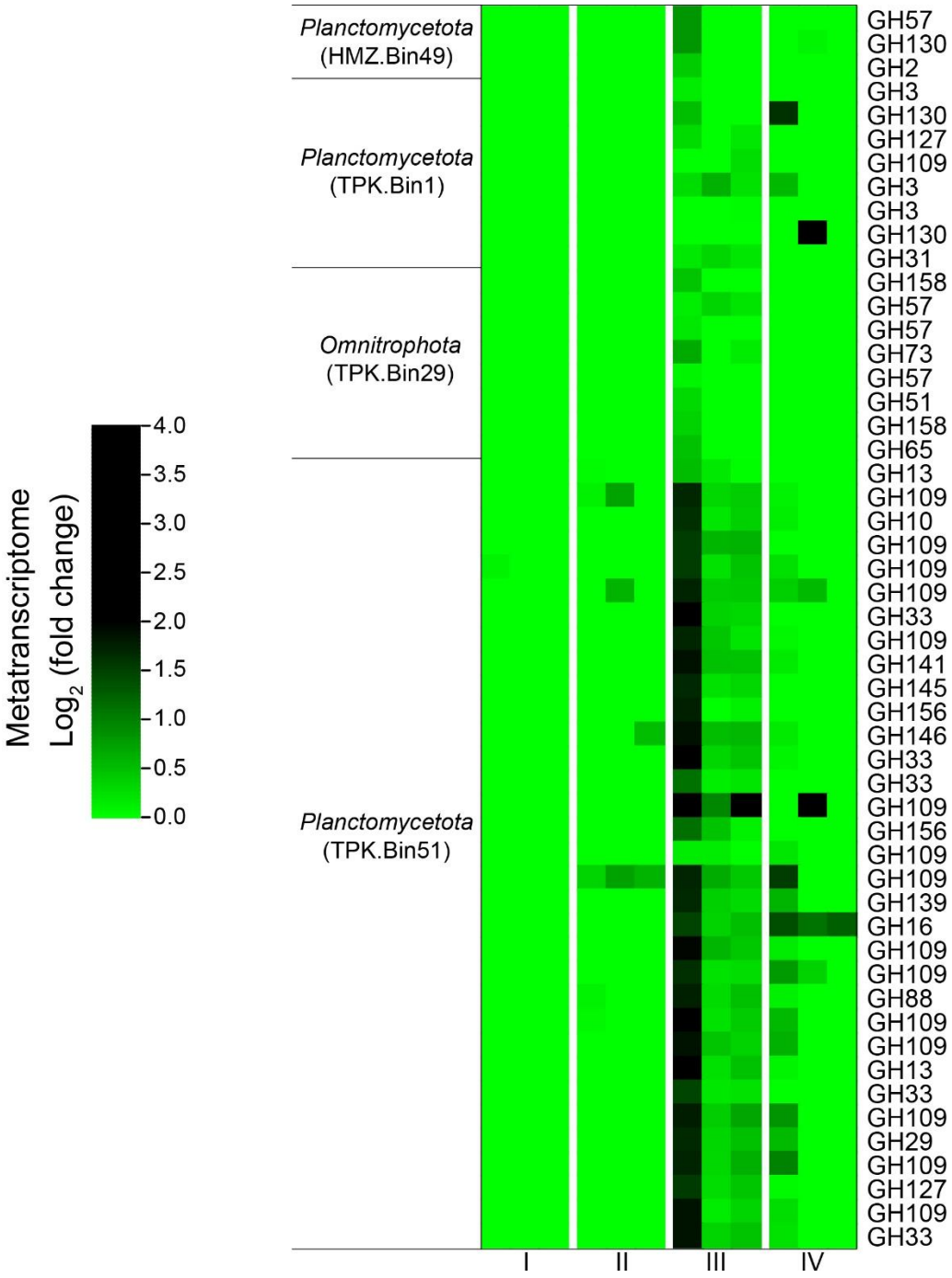


Supplementary Fig. 2 | Relative abundances of dominant prokaryotic communities in deep-sea cold seep and seamount sediments (collected in 2022) at the phylum level. Source data are provided as a Source Data file.



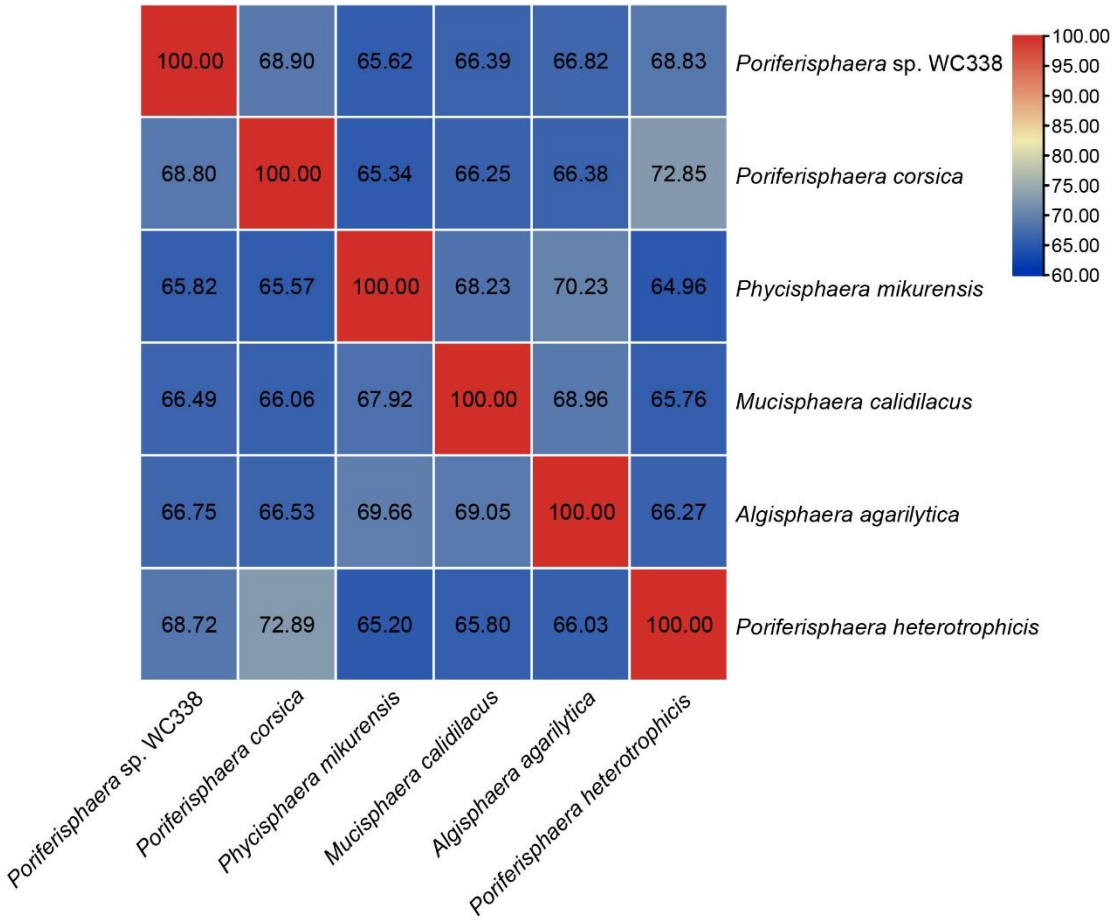
Supplementary Fig. 3 | Metatranscriptomic profiling of relative carbohydrate-active enzyme gene abundances across deep-sea microbial communities. Transcript abundances are shown in transcripts per million (TPM). To ensure comparability between samples, TPM values were normalized and quantified as $\log_2$-transformed TPM ($\log_2$ TPM) based on metatranscriptomic data (three replicates per site). Sites are denoted as follows: I, 2022 Haima cold seep (HMZ); II, 2022 Zhenbei seamount (HSX);

III, 2022 Site F cold seep 1 (TPK); IV, 2022 Site F cold seep 2 (TPKF). Source data are provided as a Source Data file.

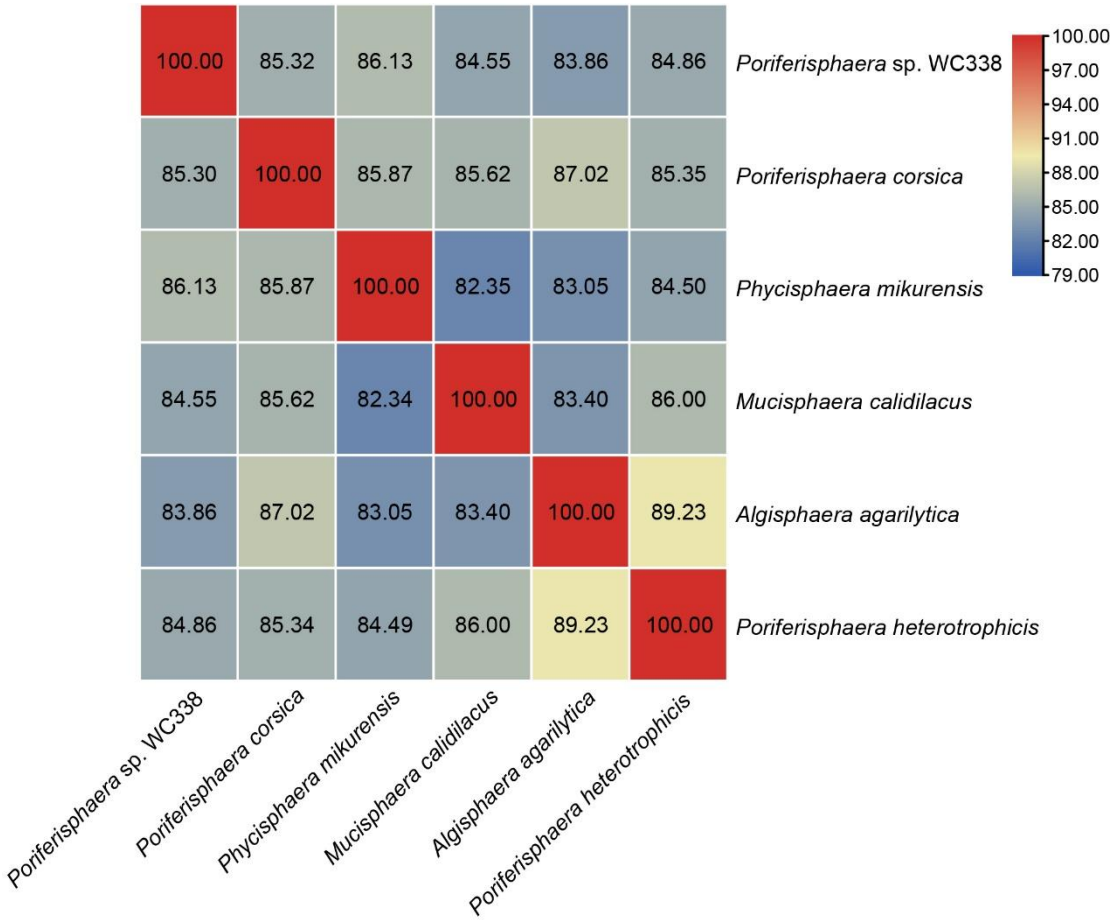


Supplementary Fig. 4 | Metatranscriptomic profiling of relative glycoside hydrolase gene abundances across deep-sea microbial communities. The relative abundance of each gene was normalized against the average abundance of the 10 selected marker genes and quantified as $\log_2$-transformed fold change ($\log_2$ fold change) based on metatranscriptomic data (three replicates per site). Sites are denoted as follows: I, 2022 Haima cold seep (HMZ); II, 2022 Zhenbei seamount (HSX); III, 2022 Site F

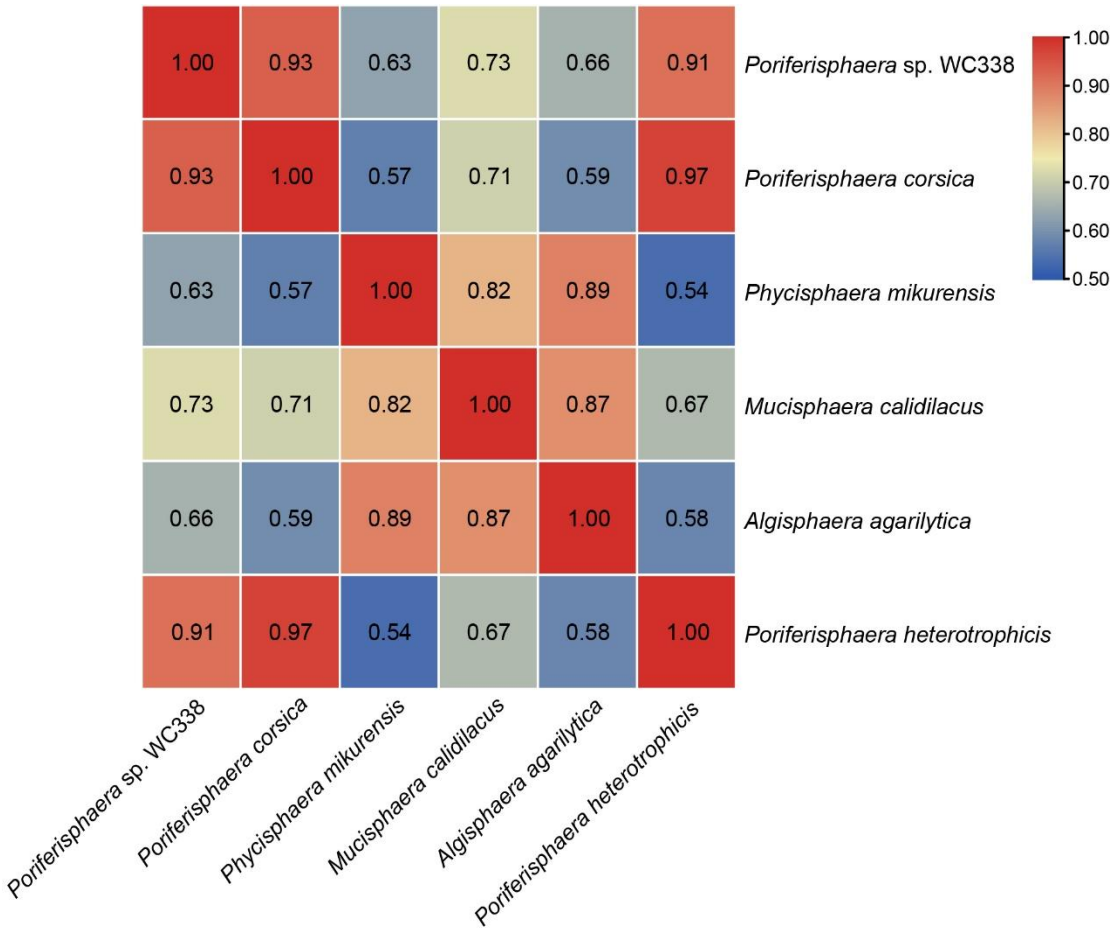
cold seep 1 (TPK); IV, 2022 Site F cold seep 2 (TPKF). Source data are provided as a Source Data file.



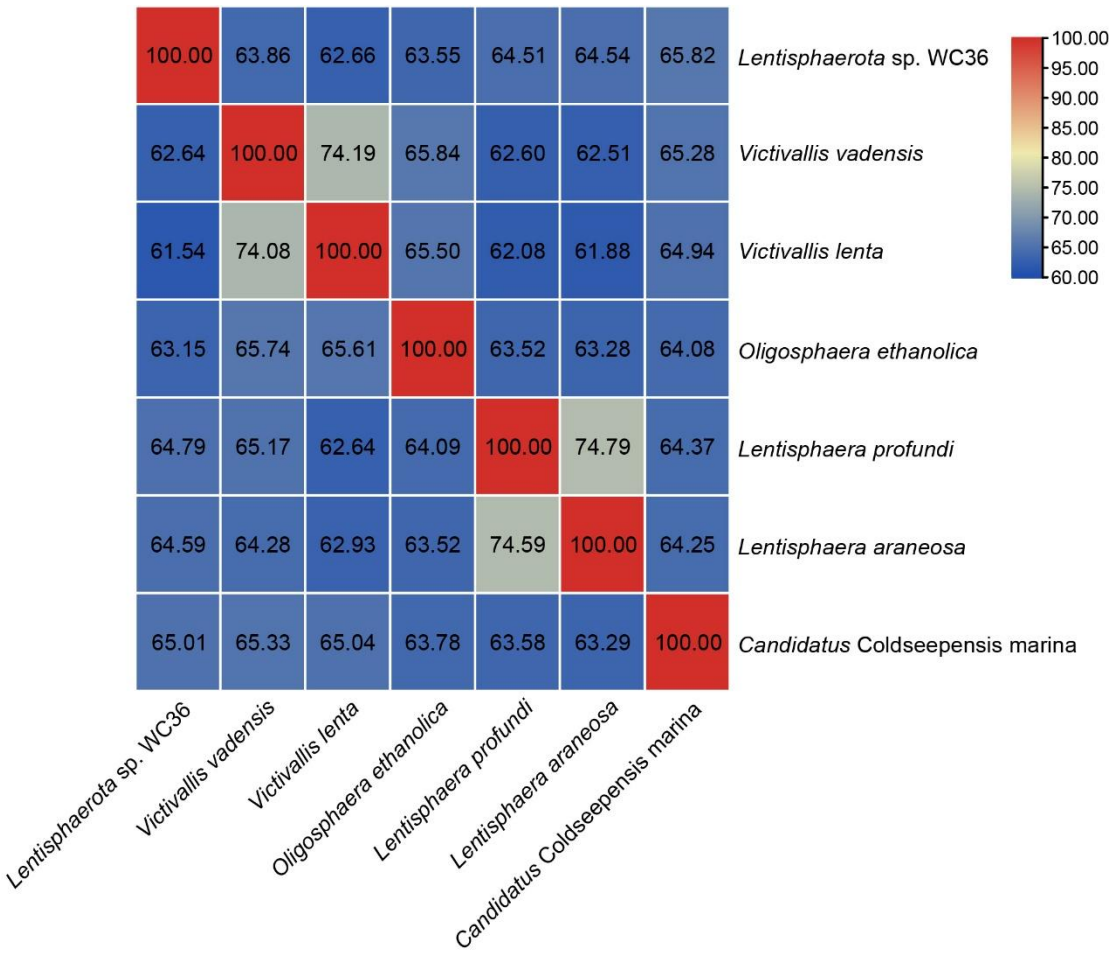
Supplementary Fig. 5 | Average nucleotide identity based on BLAST+ (ANIb) of *Poriferisphaera* sp. WC338 compared with those of other closely related species. Source data are provided as a Source Data file.



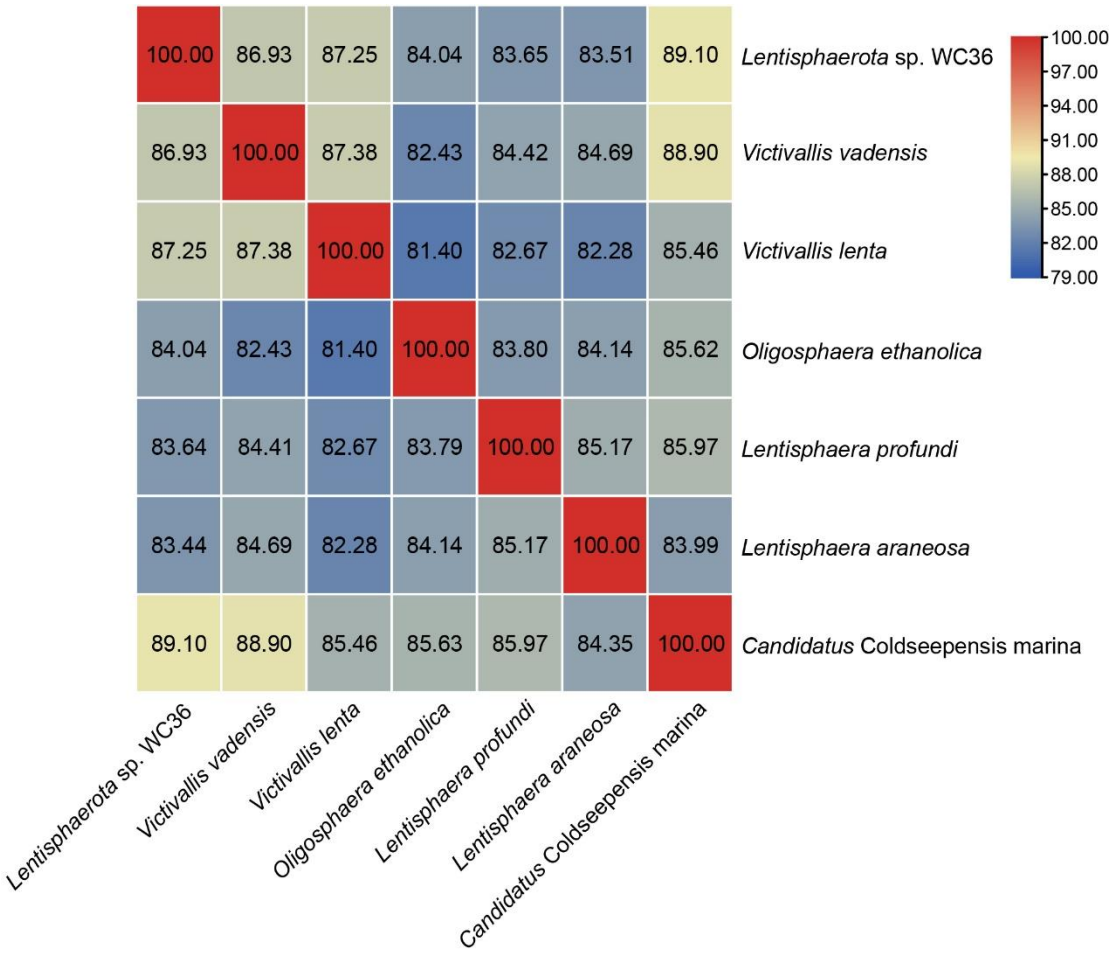
Supplementary Fig. 6 | Average nucleotide identity based on MUMmer (ANIm) of *Poriferisphaera* sp. WC338 compared with those of other closely related species. Source data are provided as a Source Data file.



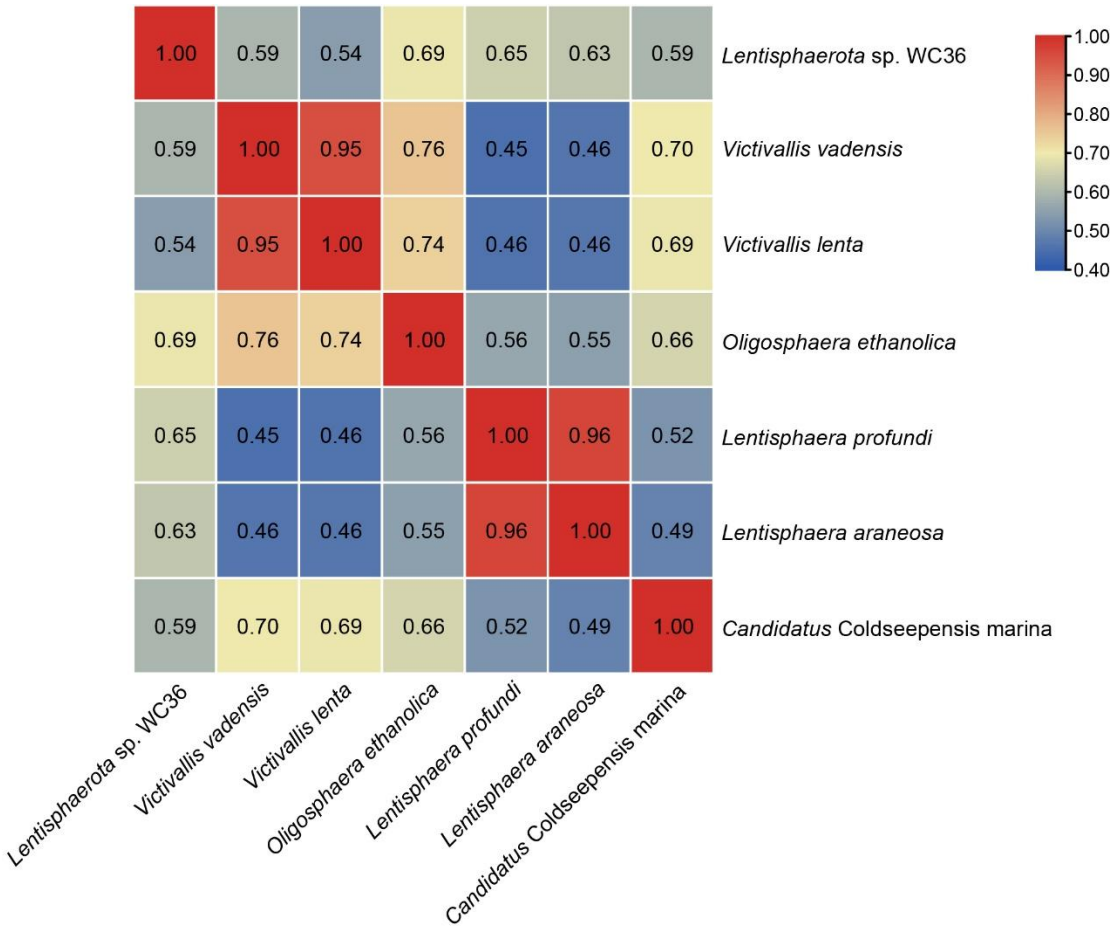
Supplementary Fig. 7 | Tetranucleotide signatures (Tetra) of *Poriferisphaera* sp. WC338 compared with those of other closely related species. Source data are provided as a Source Data file.



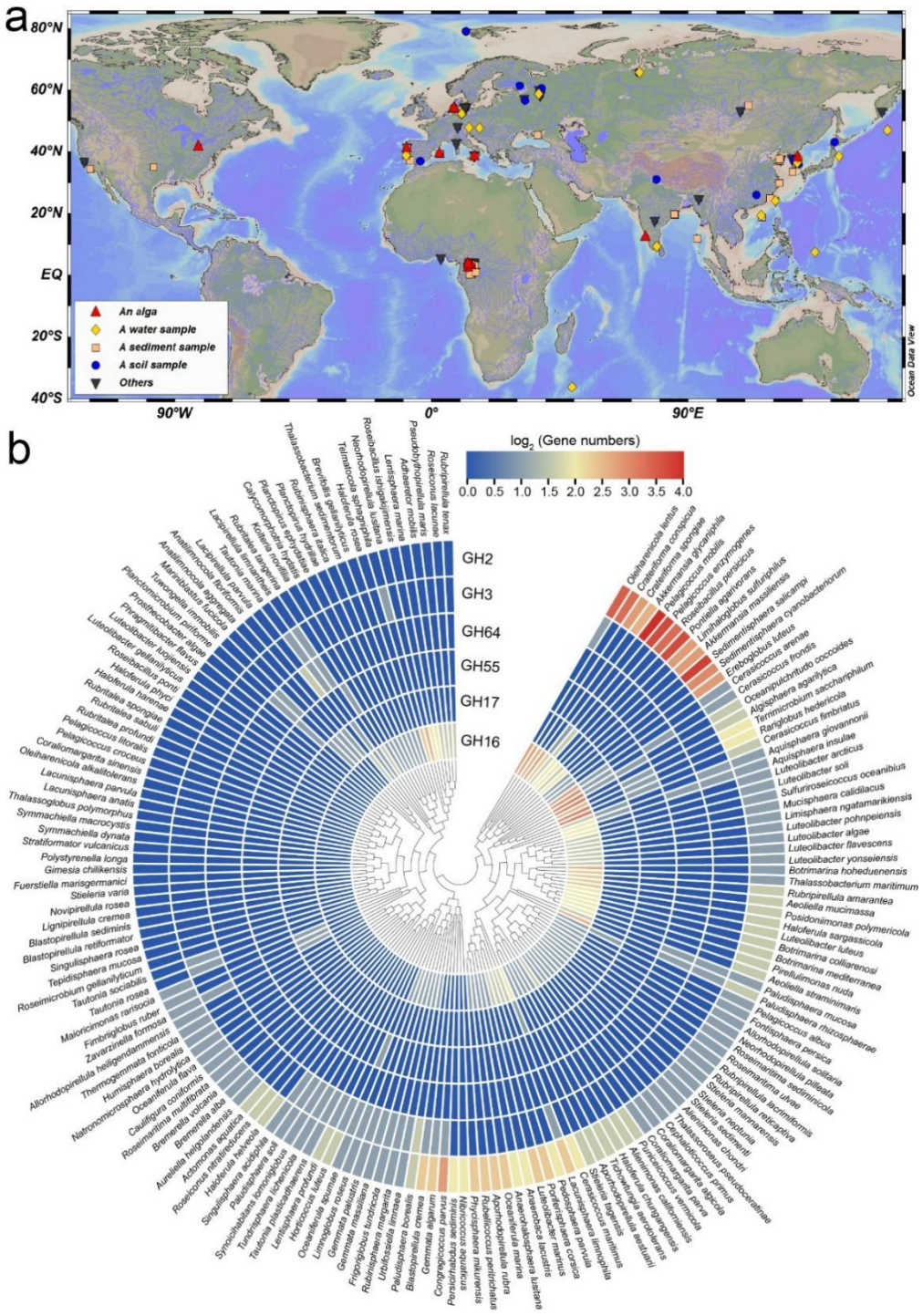
Supplementary Fig. 8 | Average nucleotide identity based on BLAST+ (ANIb) of *Lentisphaerota* sp. WC36 compared with those of other closely related species. Source data are provided as a Source Data file.



Supplementary Fig. 9 | Average nucleotide identity based on MUMmer (ANIm) of *Lentisphaerota* sp. WC36 compared with those of other closely related species. Source data are provided as a Source Data file.



Supplementary Fig. 10 | Tetranucleotide signatures (Tetra) of *Lentisphaerota* sp. WC36 compared with those of other closely related species. Source data are provided as a Source Data file.



Supplementary Fig. 11 | Geographic distribution and glycoside hydrolase gene profiles of PVC superphylum bacteria from diverse environmental sources. a Geographic distribution of PVC superphylum bacteria isolates from various environmental sources. Isolates are classified by environmental source: alga (red triangle), water (yellow diamond), sediment (orange square), soil (blue circle), and others (gray inverted triangle). **b** Clustered heatmap of laminarin-degrading GHs in the

PVC superphylum bacteria. A circular heatmap displays the log_2-transformed GH gene copy numbers associated with laminarin degradation (GH16, GH3, GH17, GH55, GH64, and GH2) for 171 PVC bacterial genomes, arranged according to hierarchical clustering based on GH gene content. Source data are provided as a Source Data file.