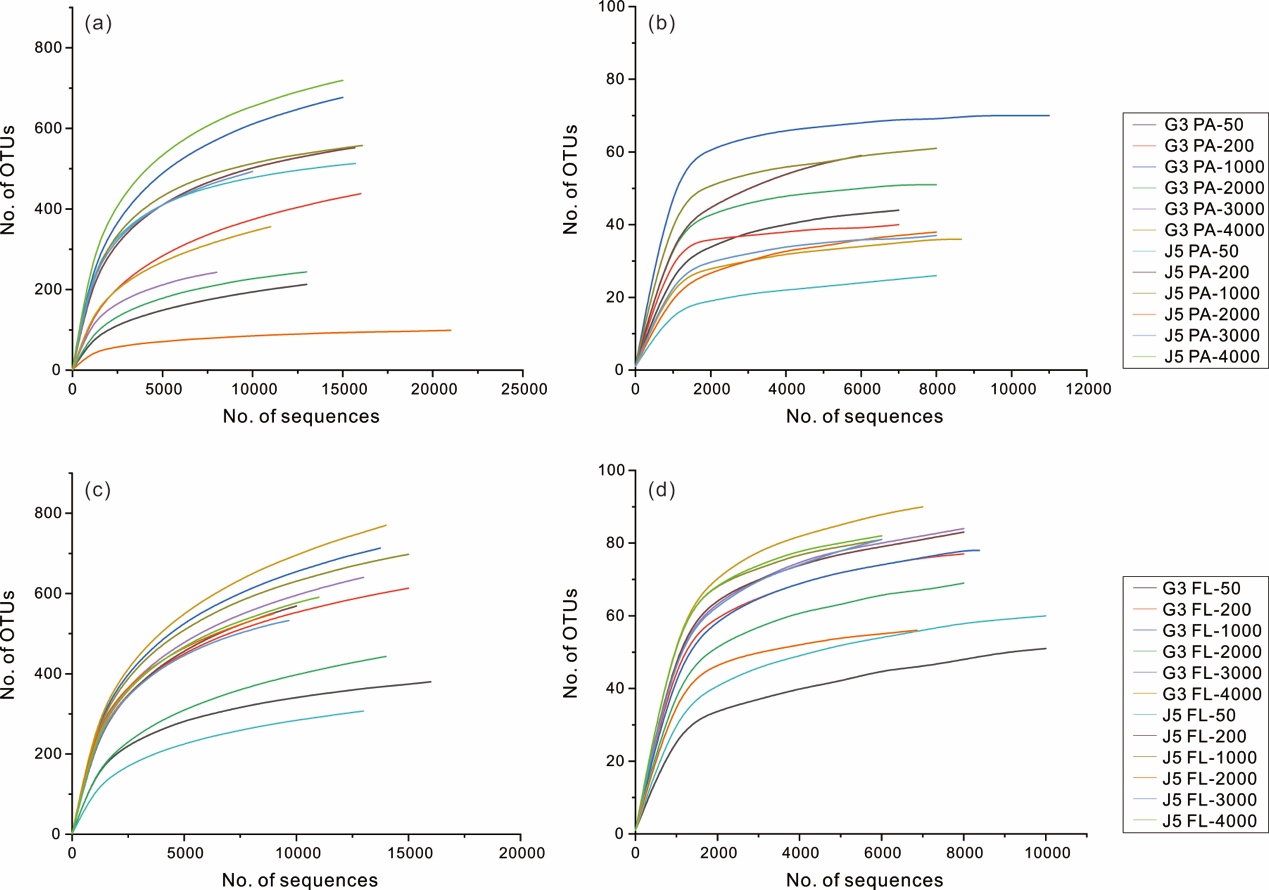
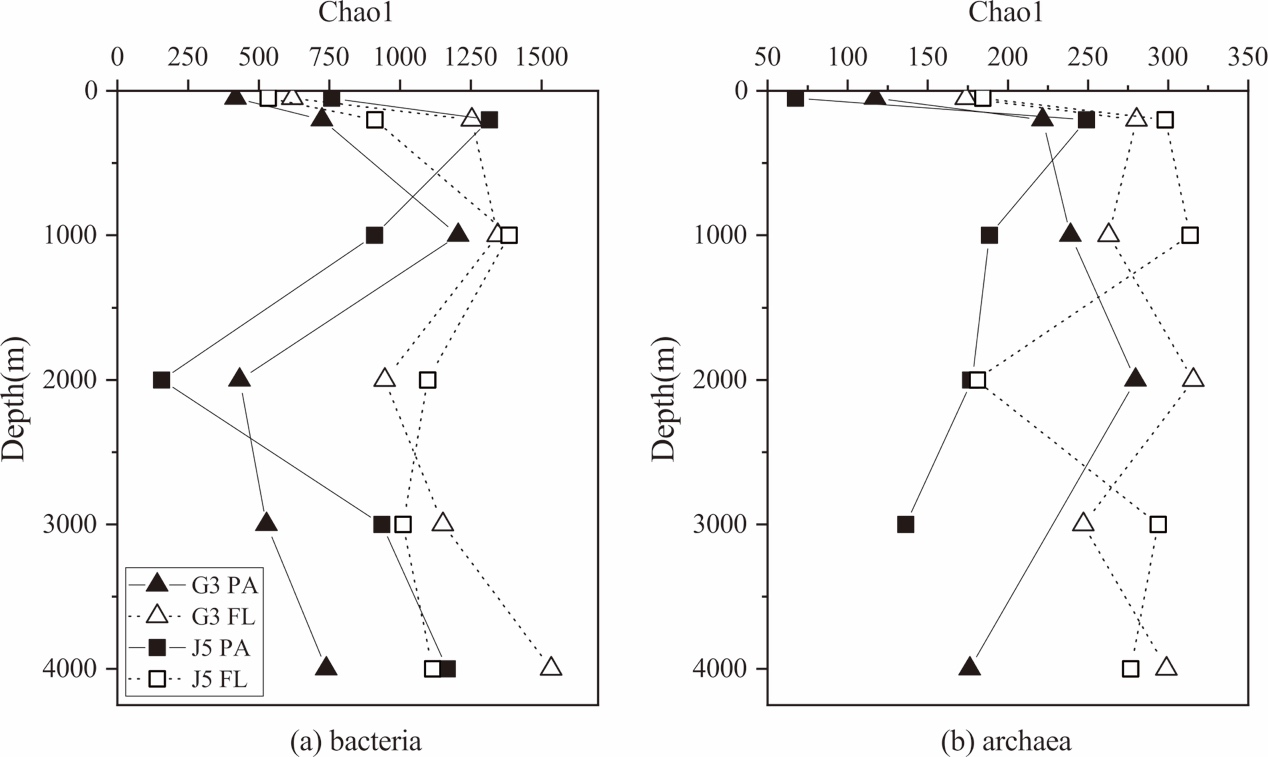


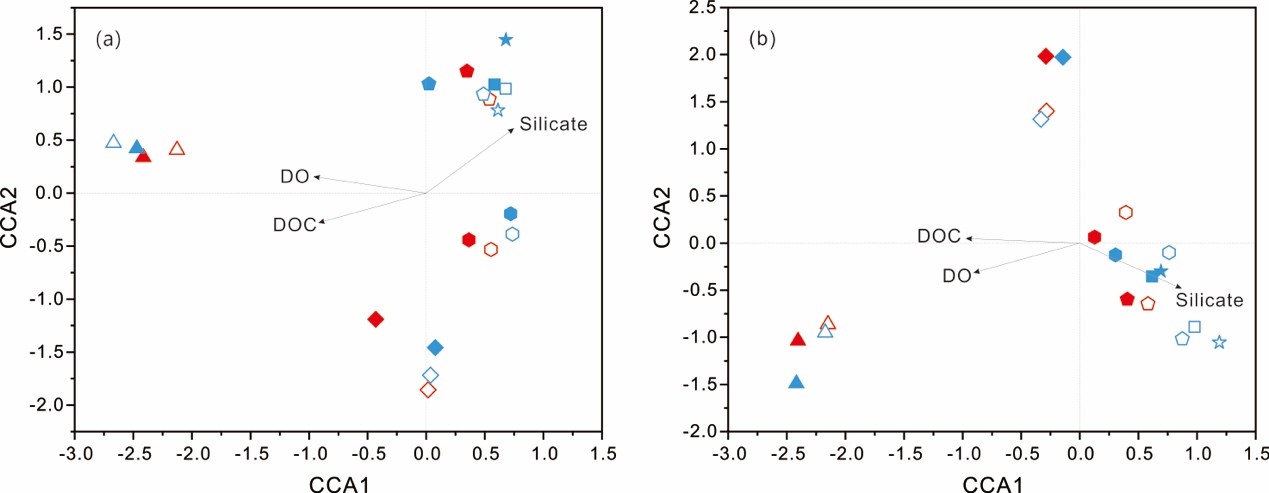
**Figure S1**. Bathymetric map of the South China Sea showing sampling locations (+) of the two water columns (G3 and J5 stations) in this study.



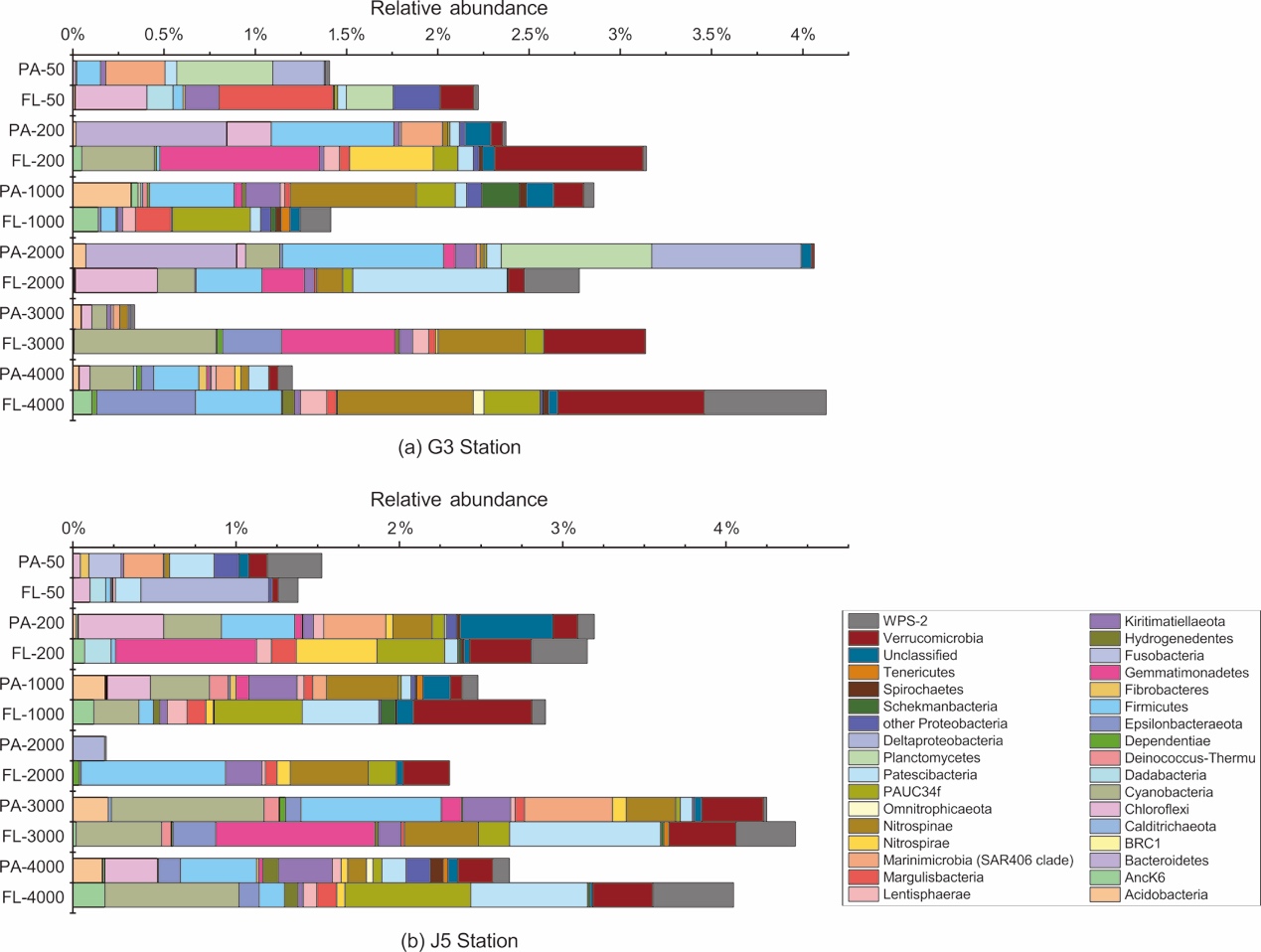
**Figure S2.** Rarefaction curves for PA and FL microbial fractions at G3 and J5 stations. (a) and (b): Rarefaction curves of PA bacterial and archaeal fractions at both G3 and J5 stations, respectively. (c) and (d): Rarefaction curves of FL bacterial and archaeal fractions at both G3 and J5 stations, respectively.

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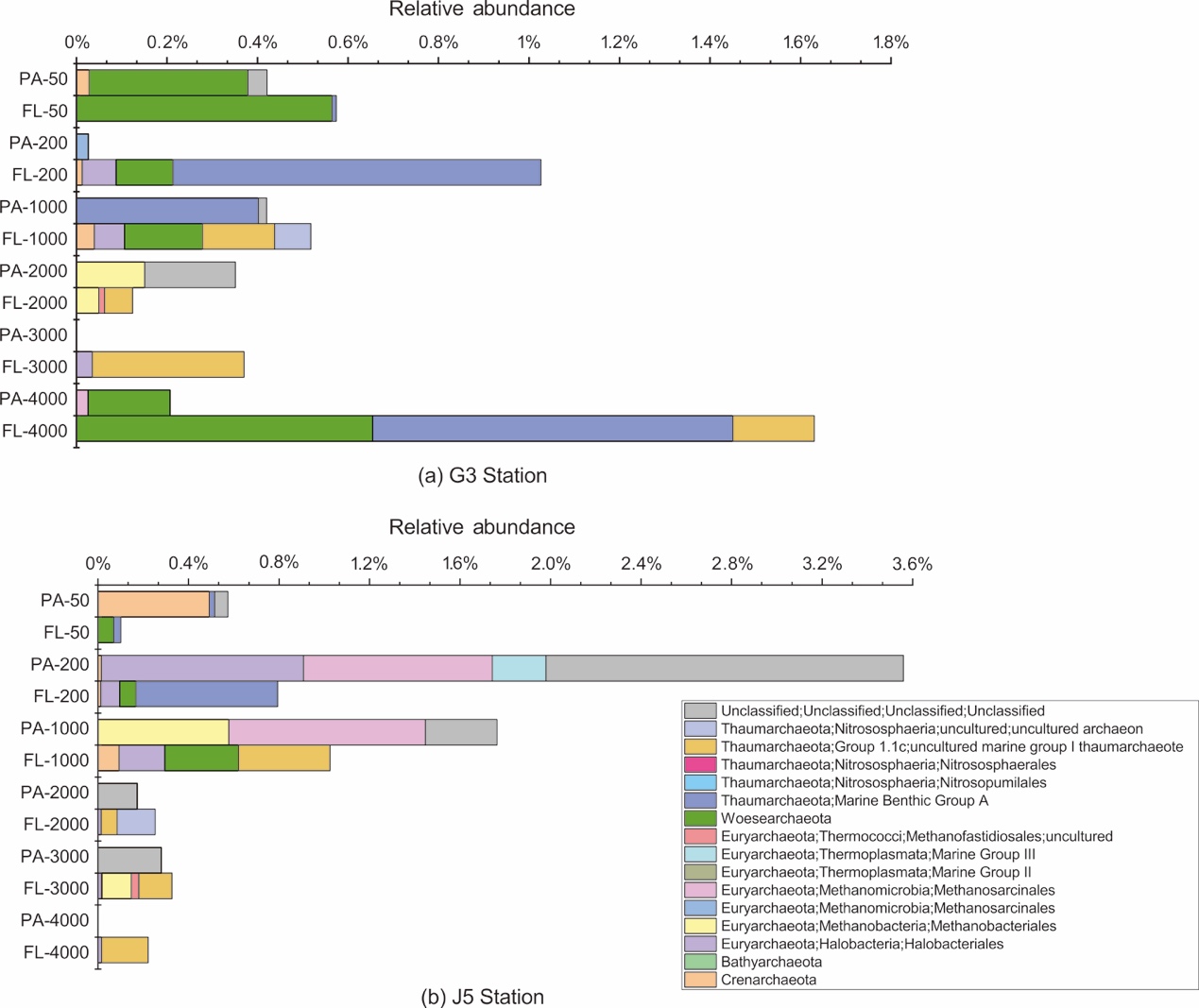
**Figure S3.** Chao1 index calculated for all bacterial and archaeal communities of seawaters collected at different depths from G3 station and J5 station in the South China Sea.

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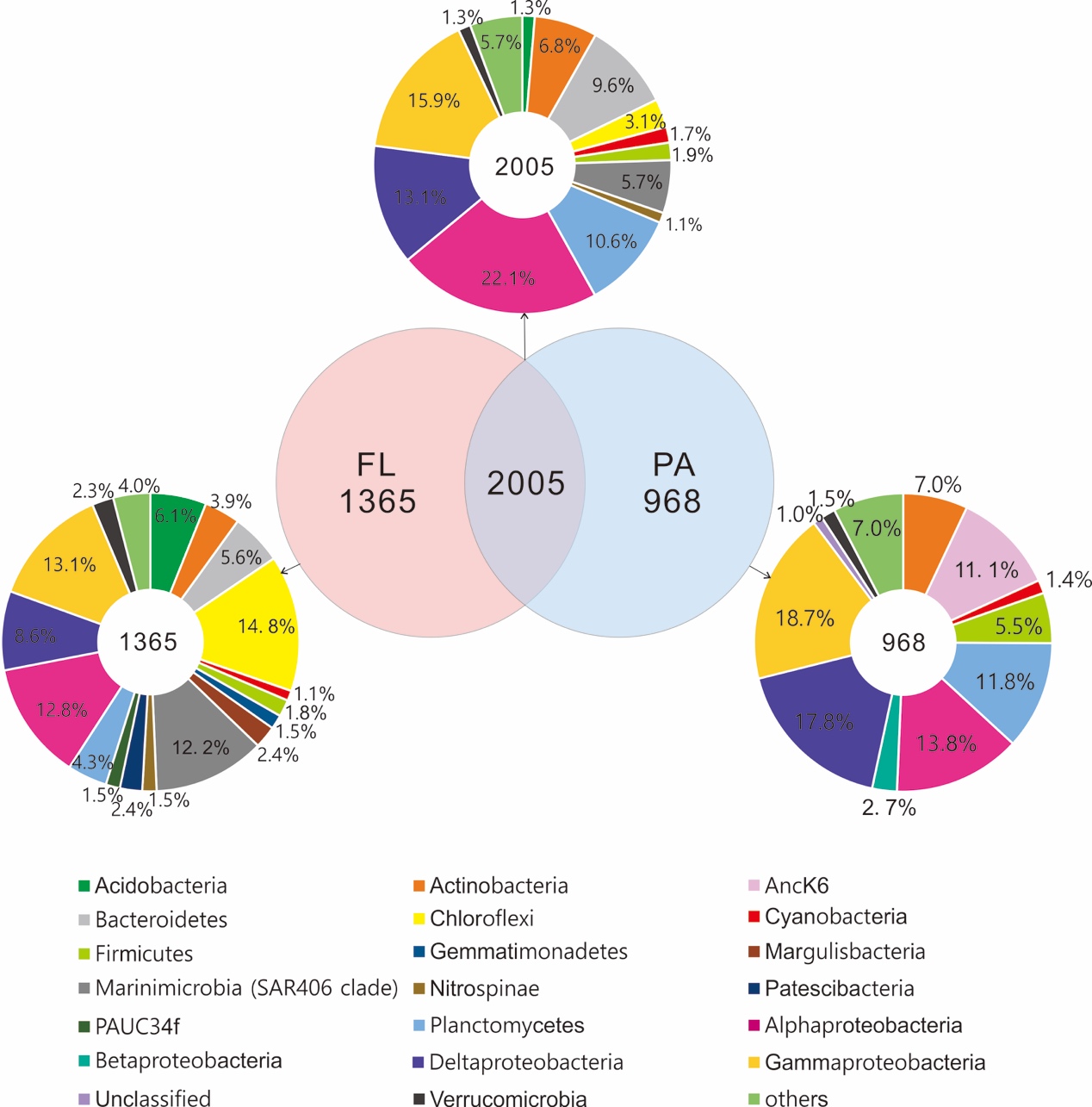
**Figure S4.** Results of CCAanalysis to correlated environmental factors to PA and FL microbial communities collected from seawater columns of the South China Sea. (a) PA and FL bacteria; (b) PA and FL archaea. Triangle: 50 m; rhombus: 200 m; hexagon: 1000 m; star: 2000 m; square: 3000 m; pentagon: 4000 m. Blue color: J5 station; red color: G3 station. Filled: particle-attached fraction; open: free-living fraction.

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**Figure S5.** Taxonomic compositions of bacterial “others” groups comprised of the phylum or class with less than 1% proportions in seawater bacterial communities of two fractions. (a) G3 station; (b) J5 station.



**Figure S6.** Taxonomic compositions of archaeal “others” groups comprised of the phylum or class with less than 1% proportions in seawater archaeal communities of two fractions. (a) G3 station; (b) J5 station. PA-3000 at G3 station and PA-4000 at J5 station indicate the samples failing in the sequencing of archaeal 16S rRNA gene.



**Figure S7**. Numbers of each OTU sets including those exclusively found in PA fraction, FL fraction, and those shared by PA and FL fractions. Pie charts represent relative proportions of each bacterial lineages at phylum/class level.