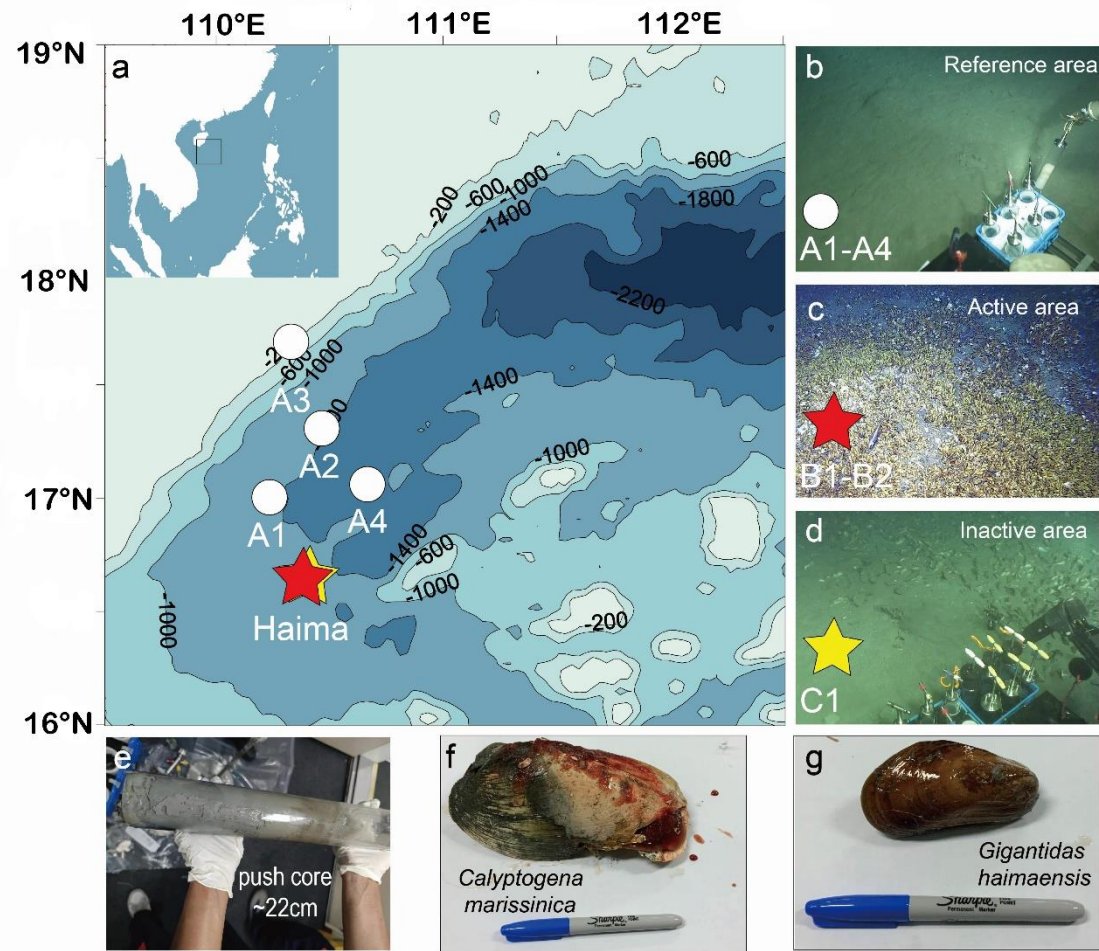
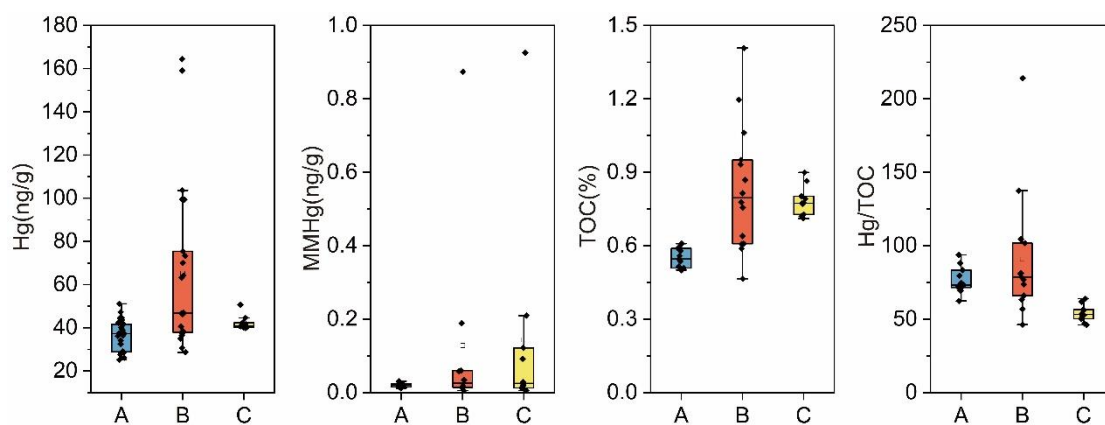
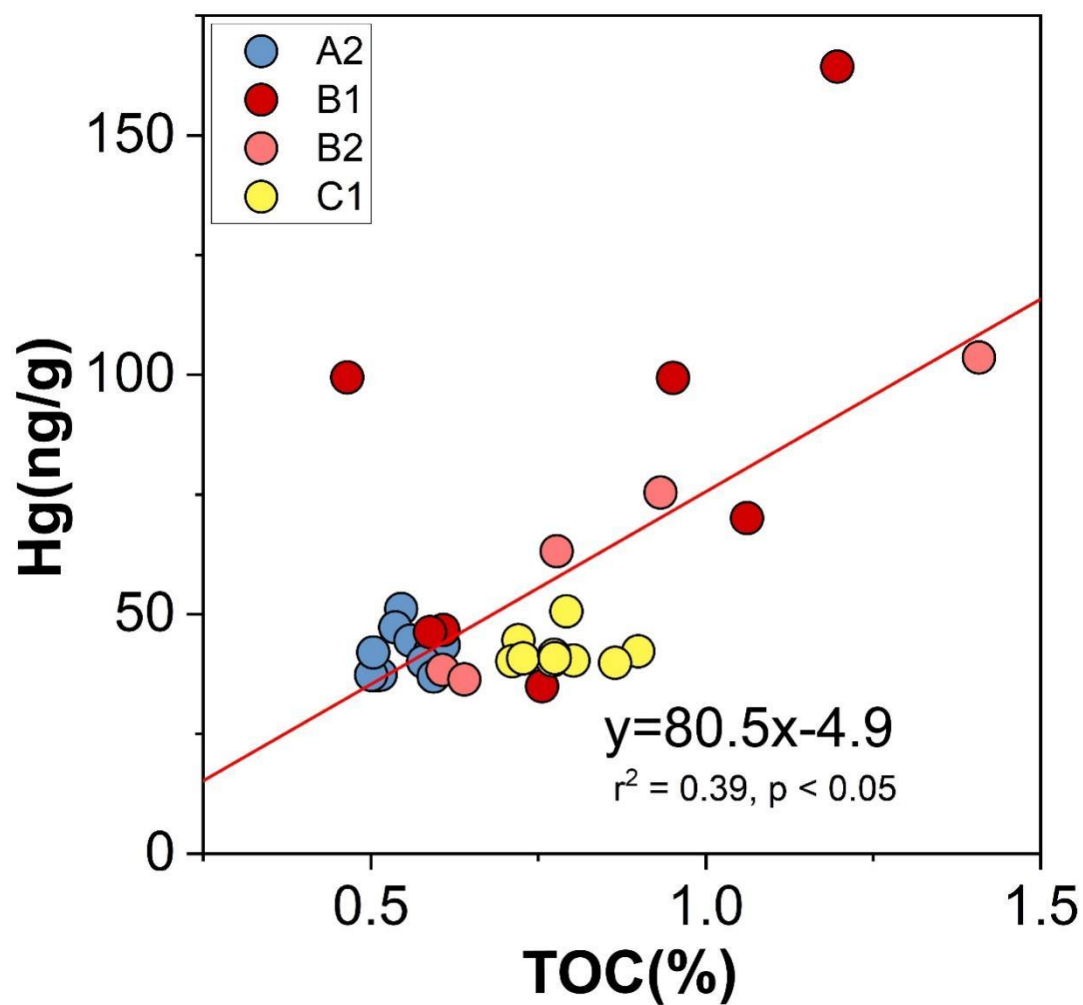




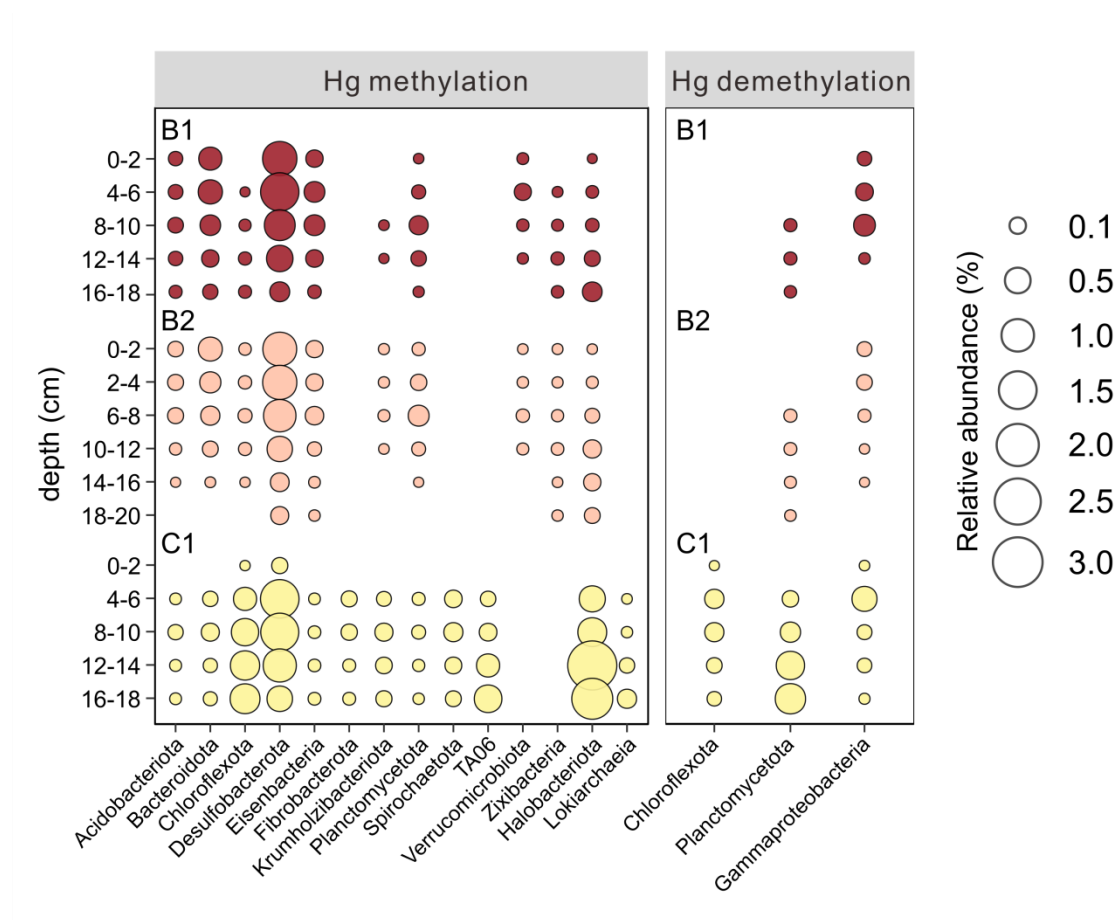
Supplementary Figure 1 Sampling sites in and around the Haima cold seep, South China Sea. a. Location of sampling sites in the South China Sea. b. Seafloor at the reference area. Core A1-A4 were collected from this area. c. Active seep area located at a water depth of 1367m in the Haima cold seep with living *G. haimaensis*. Core B1 and B2 were collected from this area. d. Inactive seep area located at water depth of 1360 m in the Haima cold seep with dead *C. marissinica*. Core C1 was collected from this area. e. The representing push core collected from the cold seep area. f. The image of *C. marissinica* collected from the inactive seep area. g. The picture of *G. haimaensis* collected from active seep area.



Supplementary Figure 2 Box-type diagram of TOC, Hg, MMHg and Hg/TOC in the sediment cores of the Haima cold seep, South China Sea. Data were from core A1-A4 (A) in the reference area, B1-B2 (B) in the active seep area, and C1 (C) in the active seep area. In the boxplots, the center line marks the median value of the distribution. The two box ends represent the first and third quartile of data. The “□” represents the mean value, and dots correspond to outliers. The whiskers extend from the box to the 5th and 95th percentile of data.



Supplementary Figure 3 Plots of TOC versus total-Hg in the Haima cold seep sediments, South China Sea. Data were from core A2 in the reference area, B1 and B2 in the active seep area, and C1 in the inactive seep area.



Supplementary Figure 4 The distribution pattern of Hg-methylating and demethylating MAGs, in these sediment metagenomes from the Haima cold seep, South China Sea. Data were from core B1 and B2 in the active seep area, and C1 in the inactive seep area. Detail information of abundance can be found in **Supplementary Table 4**.