## **Figure captions**

- Fig. 1 CH<sub>4</sub> (A), H<sub>2</sub>S (B) and CS<sub>2</sub> fluxes from Meiliang Bay in Lake Taihu and a relationship between CH<sub>4</sub> and H<sub>2</sub>S fluxes.
- **Fig. 2** CH<sub>4</sub> oxidation potential (A), organic matter content (B), the regression analysis of the organic <sup>13</sup>C content with the <sup>13</sup>CH<sub>4</sub> consumption (C), the conversion efficiency of CH<sub>4</sub>-derived carbon into total carbon (CE<sub>TC</sub>) (D) and into CO<sub>2</sub>(CE<sub>CO2</sub>) (E) in the groups with CH<sub>4</sub> (M) or CH<sub>4</sub> and CS<sub>2</sub> (MS). Dashed lines denote the gas exchange and CH<sub>4</sub> reinjection to the initial concentration during the incubation. The blue triangle represents the sediment sampling point. \*\* represents P<0.01.
- Fig. 3 The contents of ECPS (A) and ECP (B) of sediments in the MS and M groups at different  $CH_4$  consumptions. \* represents P < 0.05).
- Fig. 4 The contents of TS (A), AVS (B), SO4<sup>2-</sup>-S (C) and percent of SO4<sup>2-</sup>-S increment to CS<sub>2</sub>-S (D) of sediment in the MS and M groups at different CH<sub>4</sub> consumptions. Different lowercase letters mean significant difference at *P*<0.05.</p>
- Fig. 5 Gene abundances of 16S rRNA gene (A), pmoA (B), mmoX (C), and mxaF (D) in the sediments of the MS and M groups at different CH<sub>4</sub> consumptions. \* represents P<0.05, \*\* represents P<0.01.</p>
- Fig. 6 The Chao index based on operational taxonomic unit (OTU) level and the relative abundance of bacteria at the phylum level in total DNA (A and C) and <sup>13</sup>C-DNA (B and D) from the sediments in the MS and M groups at different CH<sub>4</sub> consumptions. \* represents *P*<0.05, \*\* represents *P*<0.01.</li>
- Fig. 7 The redundancy analysis (RDA) of environmental factors and microbial community based on operational taxonomic unit (OTU) in total DNA and <sup>13</sup>C-DNA at 97% similarity level in the MS and M groups.
- Fig. 8 Relative abundance of methanotrophs (A), methylotrophs (B), sulfur oxidizers

(C) and sulfate-reducing bacteria (D) in total DNA and <sup>13</sup>C DNA from the sediments in the MS and M groups at different CH<sub>4</sub> consumptions. \* represents P<0.05, \*\* represents P<0.01).









Fig. 3











Fig. 7



## Fig. 8

