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CORRECTION

Corrections to: Interpreting lacustrine bulk sediment $\delta^{15}N$ values using metagenomics in a tropical hypersaline lake system

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In the original publication of this article, the captions of Figures 2–5 were in incorrect order. The correct captions are provided in this correction.

Figure 2: Lake 1 carbon, nitrogen, and stable isotope values, 1400 cal years BP to present. **A** bulk OM $\delta^{15}N$ (‰, air). **B** Percent total nitrogen. **C** bulk OM $\delta^{13}C_{org}$ (‰, VPDB). **D** Percent total organic carbon. **E** C/N ratio. **F** Carbonate matrix $\delta^{13}C$ (‰, VPDB). **G** Carbonate matrix $\delta^{18}O$ (‰, VPDB). Gray bars indicate the surface and buried mat regions.

Figure 3: Relative abundance of the most abundant **A** bacterial and **B** archaeal phyla in Kiritimati sediment samples from Lake 1. Numbers in parentheses of each pool indicate the depth of the corresponding DNA pool. The results represent SSU rRNA results extracted from the phyloFlash pipeline.

Figure 4: Constrained Correspondence Analysis (CCA) plot based on Bray–Curtis matrix for taxa results obtained in Lake 1. Each dot represents an operational taxonomic unit (OTU) discovered in metagenomes, and different color of dots represent the top 10 most abundant phyla observed in Lake 1. The different shapes represent the five metagenomes. Environmental factors are plotted as gray vectors in the plot.

Figure 5: Heatmap of N-related functional genes annotated from KEGG from 5 metagenomes. The color bar is in log2fold scale, and the raw counts of genes are normalized by the normalization function in DESeq2 package in R. Each functional gene is followed by the related biochemical reaction (shown in the parentheses) and is marked with colors representing key N-metabolisms discussed in this paper.

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