Methanogens and iron-reducing bacteria: the overlooked members of mercury methylating microbial communities in boreal lakes

Running tittle: **Overlooked mercury methylators in boreal lakes**

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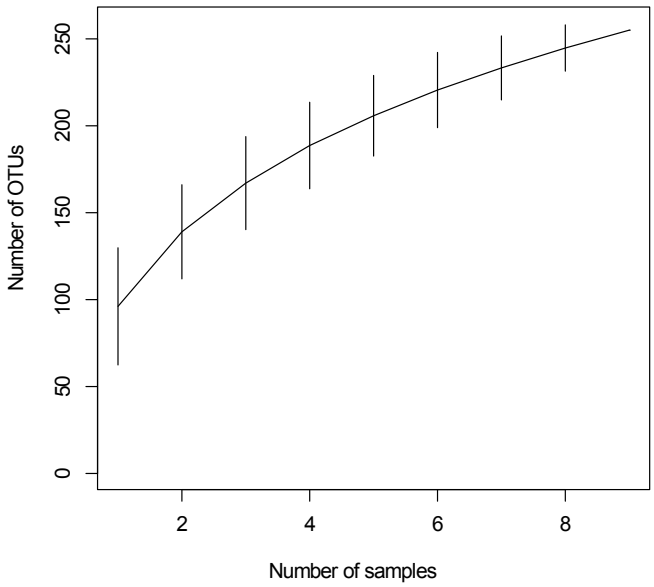
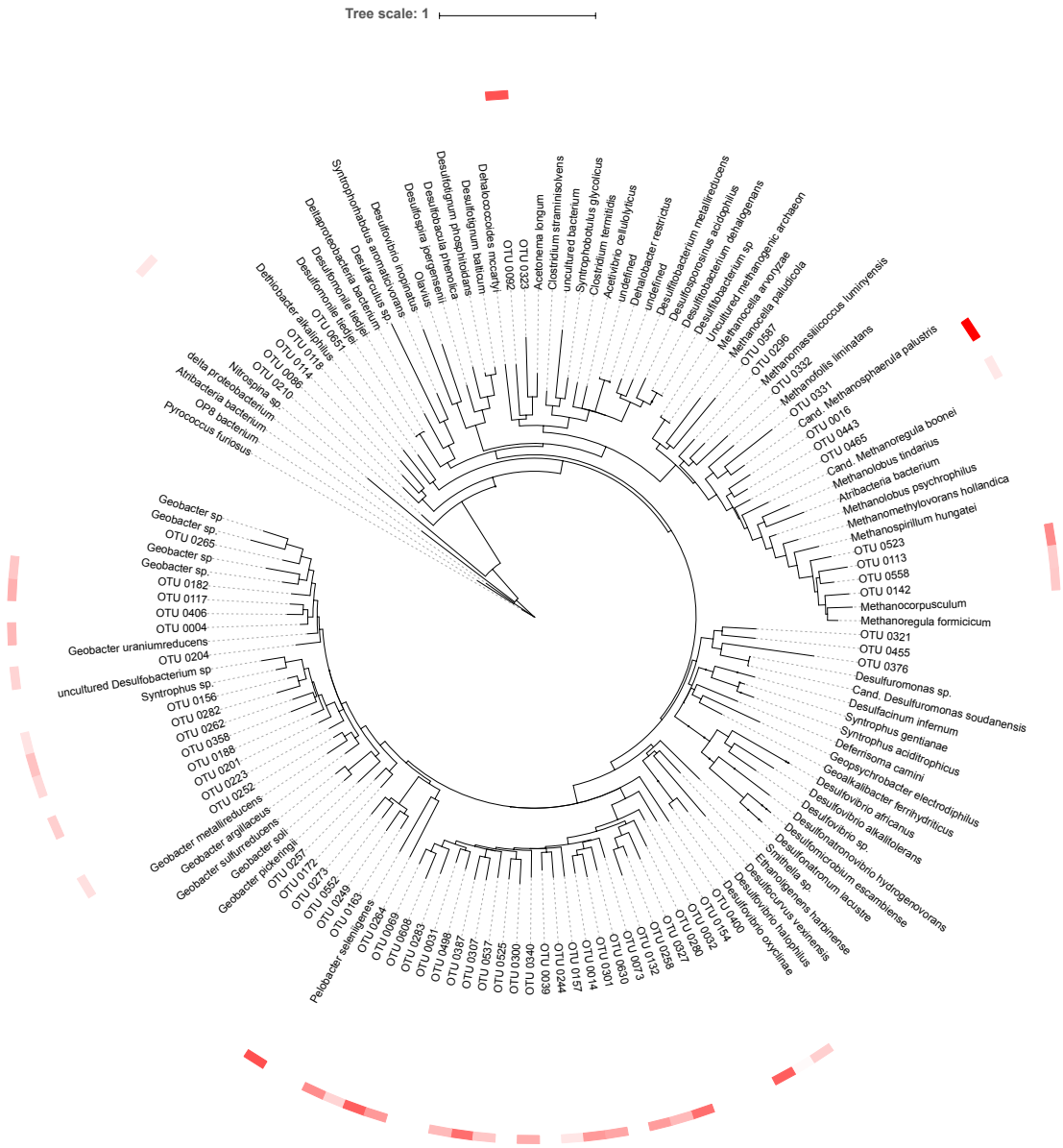
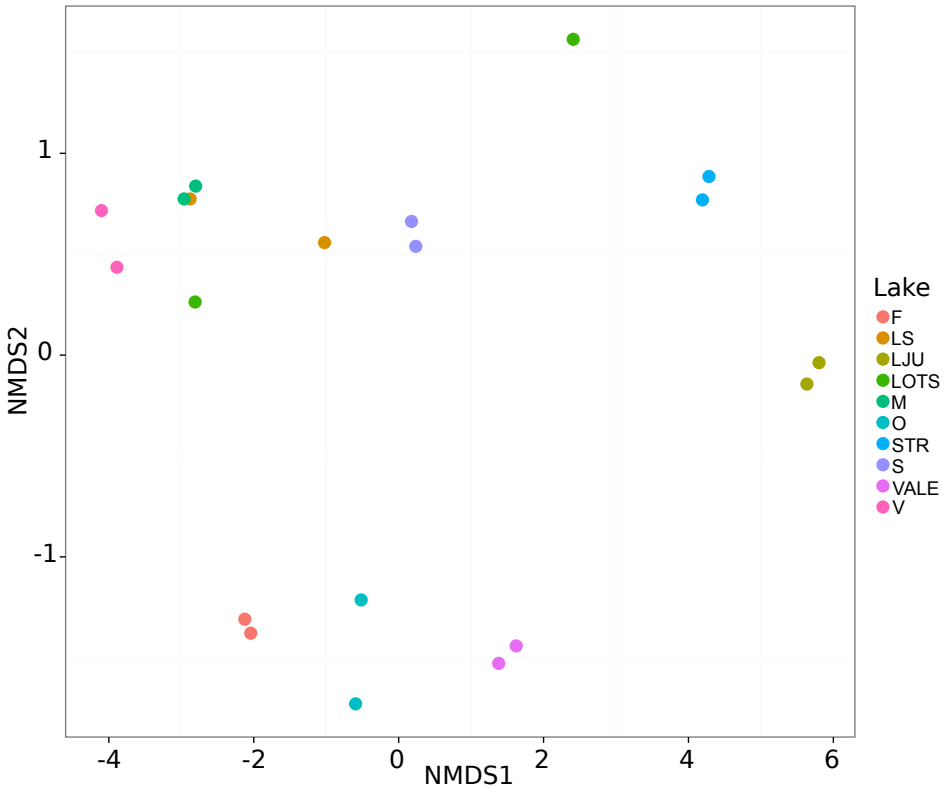
Supplementary Figure S1. Rarefaction curve of the *hgcA* genes. The x-axis represents the number of collected samples while the y-axis represents the total OTUs detected in this study.



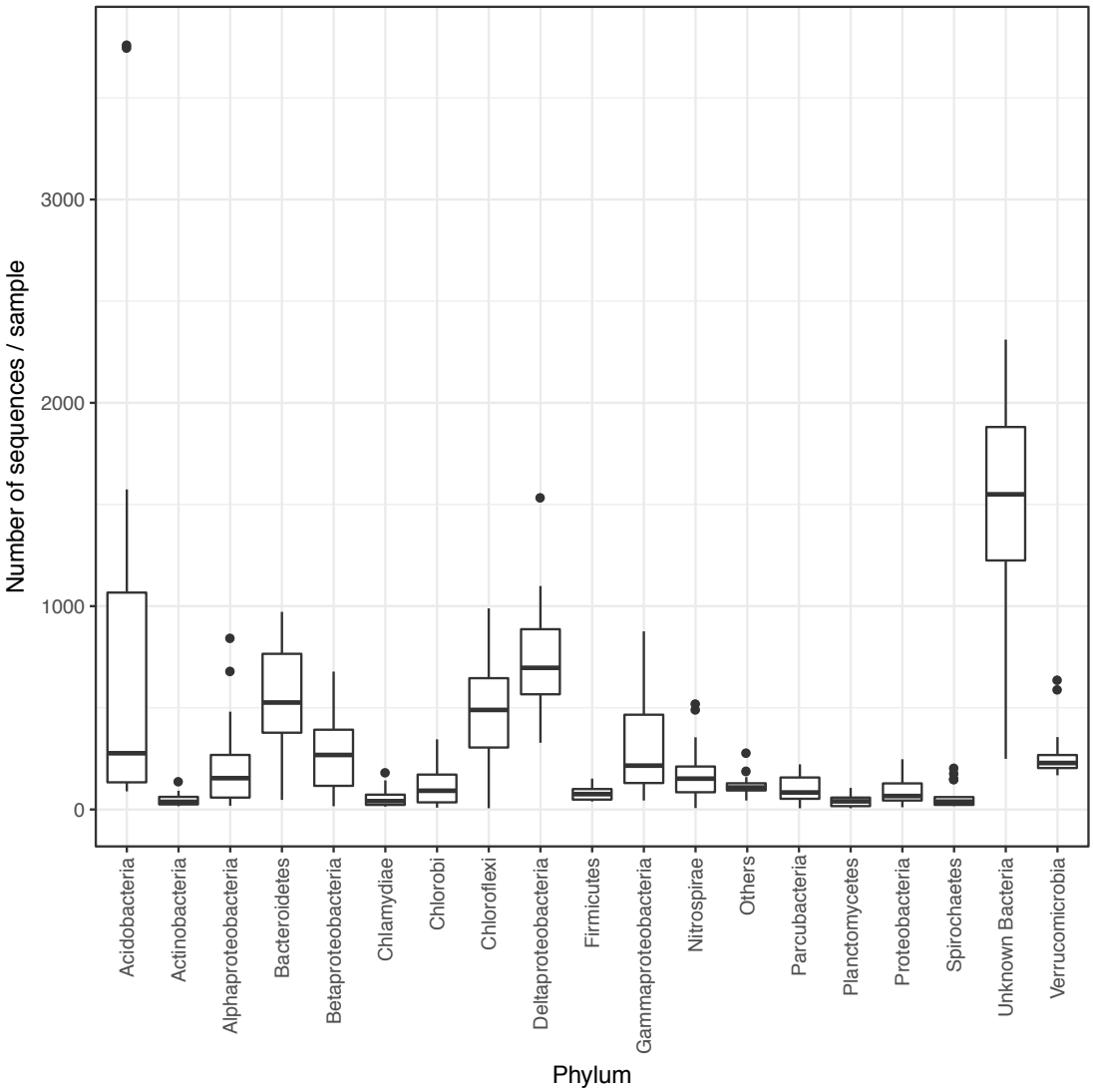
Supplementary Figure S2. Phylogenetic tree and abundance of *hgcA* functional gene OTUs. The outside colors illustrate the abundance of the sequences (total number of 78 642 sequences).



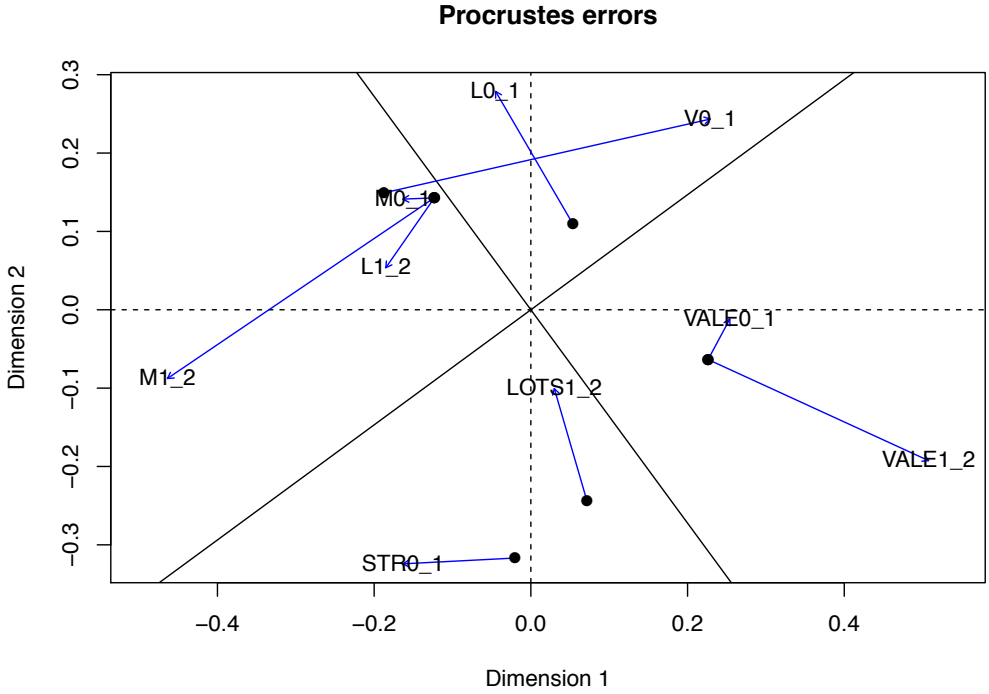
Supplementary Figure S3. NMDS (2D stress = 0.04) plot visualizing the composition of the bacterial community based on Bray-Curtis distances of the 16S rRNA gene data.



Supplementary Figure S4. Distribution of abundance at phylum-level (except *Proteobacteria* which is shown at class level) across the studied boreal lake sediments.



Supplementary Figure S5. NMDS plot of procrustes rotation of the Bray-Curtis distance matrices of 16S rRNA gene and *hgcA* gene data. Points represent sample ordination based on 16S rRNA gene data with arrows illustrating the position of corresponding *hgcA* gene sample.



Supplementary Figure S6. Significant ($p < 0.05$) correlations between different OM compounds (colored by classes). The ellipses have their eccentricity parametrically scaled to the Pearson correlation value (narrower ellipses represents higher correlation values). The orientation of the ellipse indicates negative (red) or positive (blue) correlations (scale on the right).